

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds  
(without alignments)  
44.518 Million cell updates/sec

Title: US-10-009-122-17  
Perfect score: 29  
Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : PIR 80.\*

- 1: pir1.\*
- 2: pir2.\*
- 3: pir3.\*
- 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	186	1 WRR219	19K globulin precu
2	29	100.0	186	2 JC4784	alpha-globulin pre
3	29	100.0	442	2 H81402	probable integral
4	29	100.0	1144	1 A43271	nitric-oxide synth
5	28	96.6	380	2 F70399	hydrogenase expres
6	27	93.1	447	2 F71039	hypothetical prote
7	26	89.7	33	2 S23094	beta-amyloid prote
8	26	89.7	42	2 PN0512	hypothetical prote
9	26	89.7	57	2 A60045	Alzheimer's diseas
10	26	89.7	57	2 F60045	Alzheimer's diseas
11	26	89.7	57	2 D60045	Alzheimer's diseas
12	26	89.7	57	2 G60045	Alzheimer's diseas
13	26	89.7	57	2 B60045	Alzheimer's diseas
14	26	89.7	81	2 F90736	Alzheimer's diseas
15	26	89.7	81	2 A82251	Alzheimer's diseas
16	26	89.7	81	2 G85586	Alzheimer's diseas
17	26	89.7	81	2 H64814	Alzheimer's diseas
18	26	89.7	82	2 PQ0438	Alzheimer's diseas
19	26	89.7	83	2 AC0598	Alzheimer's diseas
20	26	89.7	152	2 T06645	Alzheimer's diseas
21	26	89.7	193	2 B90157	Alzheimer's diseas
22	26	89.7	207	2 B81256	Alzheimer's diseas
23	26	89.7	231	2 H85138	Alzheimer's diseas
24	26	89.7	293	2 D69355	Alzheimer's diseas
25	26	89.7	294	2 H90318	Alzheimer's diseas
26	26	89.7	300	2 T26245	Alzheimer's diseas
27	26	89.7	330	2 B82822	Alzheimer's diseas
28	26	89.7	339	2 B72402	Alzheimer's diseas
29	26	89.7	339	2 B72402	Alzheimer's diseas

hypothetical prote  
wax synthase limpo  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
conserved hypothet  
hypothetical prote  
Alzheimer's diseas  
Alzheimer's diseas  
Alzheimer's diseas  
Alzheimer's diseas  
glycogen phosphory  
genome polypeptid  
hypothetical prote  
conserved hypothet  
hypothetical prote  
hypothetical prote  
hypothetical prote  
PFS system, IIB co  
hypothetical prote  
hypothetical prote  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
conserved hypothet  
probable permease  
uncharacterized co  
hypothetical prote  
probable polysacch  
hypothetical prote  
hypothetical prote  
transcription regu  
2-deoxy-D-gluconat  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
NAD-dinitrogen-red  
NAD-dinitrogen-red  
hypothetical prote  
hypothetical prote  
hypothetical 21K p  
methionyl-tRNA for  
caspid protein - b  
methionyl-tRNA for  
hypothetical prote  
NADH2 dehydrogenas  
tryptophanyl-tRNA  
cell fusion protei  
hypd' protein - Br  
sorbidol dehydroge  
histidinol-phospha  
hydrogenase isoenz  
pleiotrophic effec  
hydrogenase isoenz  
hydrogenase expres  
hydrogenase homolo  
hypothetical prote  
hypothetical prote  
hypd' protein - Rhi  
proton/sodium-glut  
proton/sodium-glut  
conserved hypothet  
probable LPS biosy  
lipid A-core surfa  
tyrosine-tRNA liga  
hypothetical prote  
probable selenium-  
probable beta-alan

30 26 89.7 349 2 T26247  
31 26 89.7 352 2 T48903  
32 26 89.7 428 2 T48908  
33 26 89.7 477 2 B28988  
34 26 89.7 520 2 A81548  
35 26 89.7 594 2 F86499  
36 26 89.7 603 2 F72237  
37 26 89.7 617 2 A72123  
38 26 89.7 695 1 A49795  
39 26 89.7 695 2 A27485  
40 26 89.7 695 2 S00550  
41 26 89.7 747 2 JQH773  
42 26 89.7 770 1 ORHUA4  
43 26 89.7 817 2 A82511  
44 26 89.7 1016 2 S30236  
45 26 86.2 74 2 B64214  
46 25 86.2 109 2 B72213  
47 25 86.2 136 2 T19479  
48 25 86.2 146 2 B75134  
49 25 86.2 148 2 T32362  
50 25 86.2 156 2 H95252  
51 25 86.2 156 2 F98117  
52 25 86.2 159 2 C71080  
53 25 86.2 162 2 T13659  
54 25 86.2 162 2 T13656  
55 25 86.2 162 2 T13563  
56 25 86.2 162 2 T13487  
57 25 86.2 164 2 T13562  
58 25 86.2 188 2 G70475  
59 25 86.2 190 2 A95895  
60 25 86.2 194 2 B97211  
61 25 86.2 200 2 A81632  
62 25 86.2 232 2 A71495  
63 25 86.2 234 2 T23466  
64 25 86.2 247 2 T32514  
65 25 86.2 253 2 D82405  
66 25 86.2 255 2 C87434  
67 25 86.2 257 2 C83982  
68 25 86.2 261 2 D64166  
69 25 86.2 277 2 T31855  
70 25 86.2 286 2 C84857  
71 25 86.2 295 2 JC4744  
72 25 86.2 295 2 I39751  
73 25 86.2 295 2 C70736  
74 25 86.2 302 2 A99074  
75 25 86.2 302 2 B35961  
76 25 86.2 311 2 S73625  
77 25 86.2 316 2 S61237  
78 25 86.2 318 2 A75275  
79 25 86.2 321 2 H71729  
80 25 86.2 328 2 T11938  
81 25 86.2 330 2 H75505  
82 25 86.2 340 1 NMBE5  
83 25 86.2 347 2 S35229  
84 25 86.2 352 2 A82057  
85 25 86.2 352 2 H97272  
86 25 86.2 373 2 A85922  
87 25 86.2 373 2 A91077  
88 25 86.2 373 2 S15200  
89 25 86.2 373 2 T19743  
90 25 86.2 379 2 G83808  
91 25 86.2 382 2 H64161  
92 25 86.2 384 2 S32877  
93 25 86.2 385 2 G97727  
94 25 86.2 399 2 D71728  
95 25 86.2 399 2 A82842  
96 25 86.2 402 2 E86038  
97 25 86.2 402 2 D91191  
98 25 86.2 405 2 A70146  
99 25 86.2 455 2 T34366  
100 25 86.2 469 2 T02325  
101 25 86.2 477 2 T02505  
102 25 86.2 477 2 T02505



103	25	86.2	512	2	T19806	hypothetical prote	176	24	82.8	241	2	G71045	hypothetical prote
104	25	86.2	572	2	H96685	probable AMP-bindi	177	24	82.8	245	2	T49889	zinc finger transc
105	25	86.2	604	1	QXJL5M	NADH2 dehydrogenas	178	24	82.8	246	2	E90309	hypothetical prote
106	25	86.2	620	2	H69382	ABC transporter, A	179	24	82.8	248	2	F71849	amino acid ABC tra
107	25	86.2	646	2	AD3409	ABC transporter, AT	180	24	82.8	248	2	C64666	glutamine transpor
108	25	86.2	657	2	G86590	exinuclease ABC su	181	24	82.8	254	2	T28170	hypothetical prote
109	25	86.2	657	2	B72034	exinuclease ABC,	182	24	82.8	256	2	AC1561	conserved hypotet
110	25	86.2	657	2	H90523	exinuclease ABC 8	183	24	82.8	256	2	AE1203	conserved hypotet
111	25	86.2	660	1	A28153	gelatinase A (EC 3	184	24	82.8	262	2	D88930	protein R11G11.10
112	25	86.2	662	2	S70365	gelatinase A (EC 3	185	24	82.8	262	2	A81056	conserved hypotet
113	25	86.2	662	2	A42496	gelatinase A (EC 3	186	24	82.8	263	2	C69887	hypothetical prote
114	25	86.2	662	2	S34780	gelatinase A (EC 3	187	24	82.8	269	2	A81820	conserved hypotet
115	25	86.2	663	1	S46492	gelatinase A (EC 3	188	24	82.8	276	2	S05343	NAD ADP-ribosyltra
116	25	86.2	676	2	D81654	exinuclease ABC c	189	24	82.8	278	1	S01065	probable dehydroge
117	25	86.2	681	2	T39814	hypothetical prote	190	24	82.8	281	2	F69400	2-deoxy-D-gluconat
118	25	86.2	774	2	F96639	protein T1P9.8 lim	191	24	82.8	283	2	T20734	hypothetical prote
119	25	86.2	774	2	T34496	hypothetical prote	192	24	82.8	286	2	A13105	hypothetical prote
120	25	86.2	804	2	G71546	probable DNA gyras	193	24	82.8	287	2	A12038	carboxyphosphoen
121	25	86.2	812	2	H87386	hypothetical prote	194	24	82.8	300	2	F83621	hypothetical prote
122	25	86.2	1119	2	A86340	protein F2D10.24 (	195	24	82.8	301	2	C98181	sitC protein (AF12
123	25	86.2	1147	1	I53165	nitric-oxide synth	196	24	82.8	309	2	T35801	probable polyamine
124	25	86.2	1147	1	I56575	nitric-oxide synth	197	24	82.8	311	2	D64240	methionyl-tRNA for
125	25	86.2	1147	1	S38253	nitric-oxide synth	198	24	82.8	315	2	S59779	probable membrane
126	25	86.2	1147	1	S47647	nitric-oxide synth	199	24	82.8	323	2	AC2119	hypothetical prote
127	25	86.2	1147	2	JC5029	nitric-oxide synth	200	24	82.8	325	1	B40358	NADH2 dehydrogenas
128	25	86.2	1147	2	JC5028	nitric-oxide synth	201	24	82.8	330	2	T29640	mitochondrial carr
129	25	86.2	1147	2	JC5027	nitric-oxide synth	202	24	82.8	331	1	DNOBUL	NADH2 dehydrogenas
130	25	86.2	1147	2	S65440	nitric-oxide synth	203	24	82.8	335	2	A72289	oligopeptide ABC t
131	25	86.2	1324	2	T01508	mismatch repair en	204	24	82.8	337	2	AG0963	hypothetical prote
132	25	86.2	2241	2	T02857	conserved hypotet	205	24	82.8	337	2	T48341	hypothetical prote
133	25	86.2	3623	2	T08618	intrinsic factor-B	206	24	82.8	341	2	S73685	hypothetical prote
134	25	86.2	4152	2	T31105	filamentous hemag	207	24	82.8	342	2	AE2238	methionyl-tRNA for
135	25	86.2	4919	2	T31102	hypothetical prote	208	24	82.8	344	2	E83562	N-acetyl-gamma-glu
136	24	82.8	20	2	JU0330	hypothetical prote	209	24	82.8	345	2	AB1837	hypothetical prote
137	24	82.8	20	2	A99091	hypothetical prote	210	24	82.8	352	2	E90175	NADH dehydrogenase
138	24	82.8	62	2	E64530	hypothetical prote	211	24	82.8	352	2	AB3079	transcription regu
139	24	82.8	68	2	C71970	hypothetical prote	212	24	82.8	352	2	G98207	hypothetical prote
140	24	82.8	77	2	AC1381	preprotein translo	213	24	82.8	363	2	S56273	probable membrane
141	24	82.8	91	2	H82370	conserved hypotet	214	24	82.8	379	2	T23443	hypothetical prote
142	24	82.8	95	2	AG0277	probable phage-rel	215	24	82.8	380	2	T29248	hypothetical prote
143	24	82.8	106	2	AG2113	hypothetical prote	216	24	82.8	380	2	F86038	probable LPS biosy
144	24	82.8	108	2	C64516	hypothetical prote	217	24	82.8	380	2	E91191	probable LPS biosy
145	24	82.8	138	2	I47205	Ig heavy chain var	218	24	82.8	382	2	A11427	efflux proteins ho
146	24	82.8	141	1	B70457	gliding motility p	219	24	82.8	383	2	AF1893	hydrogenase expres
147	24	82.8	141	2	I47177	Ig H-chain - pig (	220	24	82.8	385	2	T31493	hypothetical prote
148	24	82.8	143	1	A44397	cofilin - yeast (S	221	24	82.8	393	2	D86168	hypothetical prote
149	24	82.8	144	2	D72219	conserved hypotet	222	24	82.8	400	2	H69009	hypothetical prote
150	24	82.8	147	2	H82313	hypothetical prote	223	24	82.8	401	2	T44831	probable emulsan r
151	24	82.8	163	2	F86878	hypothetical prote	224	24	82.8	409	2	S29124	membrane glycoprot
152	24	82.8	169	2	AF2630	hypothetical prote	225	24	82.8	415	2	C71467	probable tyrosine
153	24	82.8	171	2	C71244	hypothetical prote	226	24	82.8	416	2	I64039	hypothetical prote
154	24	82.8	174	2	G81349	periplasmic nitrat	227	24	82.8	422	2	E82904	hypothetical prote
155	24	82.8	179	2	AB0652	probable intracell	228	24	82.8	429	2	T28950	hypothetical prote
156	24	82.8	179	2	T45503	hypothetical prote	229	24	82.8	440	1	B29413	ubiquinol-cytochro
157	24	82.8	179	2	S07799	probable membrane	230	24	82.8	442	2	T39683	zuoitin-like protei
158	24	82.8	179	2	B90848	probable membrane	231	24	82.8	448	2	AE6534	integral membrane
159	24	82.8	179	2	A85706	probable membrane	232	24	82.8	448	2	A72089	ABC transporter, p
160	24	82.8	179	2	S70898	intracellular sept	233	24	82.8	451	2	A81581	probable integral
161	24	82.8	184	2	AH3581	alkyl hydroperoxid	234	24	82.8	451	2	G71561	hypothetical prote
162	24	82.8	193	2	A82435	conserved hypotet	235	24	82.8	452	2	H84016	conserved hypotet
163	24	82.8	195	2	T22032	hypothetical prote	236	24	82.8	455	2	H69837	protein imported
164	24	82.8	197	2	G83597	conserved hypotet	237	24	82.8	456	2	D95384	aromatic amino aci
165	24	82.8	210	2	C97260	probable membrane	238	24	82.8	463	2	S52754	hypothetical prote
166	24	82.8	210	2	S67140	probable membrane	239	24	82.8	466	2	A95179	LPS glycosyltransf
167	24	82.8	214	2	B84217	hypothetical prote	240	24	82.8	466	2	B97030	hypothetical prote
168	24	82.8	216	2	B88065	protein T16A1.3 (i	241	24	82.8	466	2	H98045	hypothetical prote
169	24	82.8	219	1	A35617	HDEL receptor ERD2	242	24	82.8	471	2	T41602	hypothetical prote
170	24	82.8	219	2	A75004	glutaredoxin-relat	243	24	82.8	485	2	B84394	argininosuccinate
171	24	82.8	221	2	G72322	hypothetical prote	244	24	82.8	490	2	A35312	potassium channel
172	24	82.8	222	2	T47768	hypothetical prote	245	24	82.8	500	2	B83364	pyoverdine biosynt
173	24	82.8	225	2	A90260	conserved hypotet	246	24	82.8	500	2	F83418	sodium/proton anti
174	24	82.8	238	2	E75169	hypothetical prote	247	24	82.8	503	2	T34694	probable cationic
175	24	82.8	240	2	G70303	cytochrome c - Aqu	248	24	82.8	507	2	F97765	hypothetical prote

249 24 82.8 509 2 S51348  
 250 24 82.8 527 2 G86390  
 251 24 82.8 529 2 C71561  
 252 24 82.8 528 2 C81714  
 253 24 82.8 533 2 S71617  
 254 24 82.8 558 2 S56200  
 255 24 82.8 574 2 S61943  
 256 24 82.8 582 2 I40198  
 257 24 82.8 586 2 T49210  
 258 24 82.8 603 2 T11490  
 259 24 82.8 604 2 T11867  
 260 24 82.8 606 1 OXB05M  
 261 24 82.8 606 2 T11150  
 262 24 82.8 606 2 C39851  
 263 24 82.8 606 2 T41830  
 264 24 82.8 606 2 T45560  
 265 24 82.8 606 2 T11373  
 266 24 82.8 606 2 T10982  
 267 24 82.8 606 2 T11060  
 268 24 82.8 648 2 E85567  
 269 24 82.8 648 2 E90717  
 270 24 82.8 655 2 T31691  
 271 24 82.8 710 2 JC7192  
 272 24 82.8 726 2 T15810  
 273 24 82.8 732 2 T32023  
 274 24 82.8 763 2 T21006  
 275 24 82.8 806 2 T15468  
 276 24 82.8 825 2 T46311  
 277 24 82.8 826 2 JC5153  
 278 24 82.8 912 2 G96830  
 279 24 82.8 935 2 T40715  
 280 24 82.8 1089 2 C70522  
 281 24 82.8 1121 2 T21303  
 282 24 82.8 1133 2 T30302  
 283 24 82.8 1253 2 T40302  
 284 24 82.8 1270 2 T21269  
 285 24 82.8 1291 2 T21267  
 286 24 82.8 1316 2 D87145  
 287 24 82.8 1316 2 S31146  
 288 24 82.8 1316 2 G70535  
 289 24 82.8 1316 2 T50444  
 290 24 82.8 1318 2 T21266  
 291 24 82.8 1327 2 T21268  
 292 24 82.8 1462 2 T00345  
 293 24 82.8 1533 2 F71274  
 294 24 82.8 2009 2 S49764  
 295 24 82.8 2380 2 E71604  
 296 24 82.8 3623 2 T09456  
 297 23 79.3 20 2 C60894  
 298 23 79.3 31 2 S73244  
 299 23 79.3 31 2 A53841  
 300 23 79.3 32 2 T11995

## ALIGNMENTS

## RESULT 1

WRZ19  
 19K globulin precursor - rice  
 N:Alternate names: alpha-globulin  
 C:Species: Oryza sativa (rice)  
 C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text\_change 31-Dec-2004  
 C:Accession: S20024; S25735; FN0497  
 R:Shorrosh, B.S.; Wen, L.; Zen, K.C.; Huang, J.K.; Pan, J.S.; Herndonson, M.A.; Tanaka, K.  
 Plant Mol. Biol. 18, 151-154, 1992  
 A:Title: A novel cereal storage protein: molecular Genetics of the 19 kDa globulin of rice  
 A:Reference number: S20024; MUID:92119226; PMID:1731968  
 A:Accession: S20024  
 A:Molecule type: mRNA  
 A:Residues: 1-186 <SHO>  
 A:Cross-references: UNIPROT:P29835; UNIPARC:UPI000012B4D1; EMBL:X63990; NID:g20158; PIDN  
 A:Accession: S25735

A:Molecule type: protein  
 A:Residues: 68-74;108-133;171-186 <SH2>  
 A:Cross-references: UNIPARC:UPI0000173296; UNIPARC:UPI0000173297; UNIPARC:UPI0000173298  
 R:Krishnan, H.B.; Puepke, S.G.  
 Biochem. Biophys. Res. Commun. 193, 460-466, 1993  
 A:Title: Nucleotide sequence of an abundant rice seed globulin: homology with the high  
 A:Reference number: PN0497; MUID:93277591; PMID:8503935  
 A:Accession: PN0497  
 A:Molecule type: mRNA  
 A:Residues: 6-186 <KRI>  
 A:Cross-references: UNIPARC:UPI0000173299; GB:L12252  
 A:Experimental source: seed  
 C:Superfamily: Alpha amylase inhibitor  
 C:Keywords: storage protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-186/Product: 19K globulin #status predicted <MAT>  
 Query Match 100.0%; Score 29; DB 1; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 13; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;  
 Qy 1 KWVFFA 6  
 Db 4 KWVFFA 9  
 RESULT 2  
 JC4784  
 alpha-globulin precursor - rice  
 C:Species: Oryza sativa (rice)  
 C>Date: 10-May-1996 #sequence\_revision 16-Aug-1996 #text\_change 31-Dec-2004  
 C:Accession: JC4784  
 R:Nakase, M.; Hotta, H.; Adachi, T.; Aoki, N.; Nakamura, R.; Masumura, T.; Tanaka, K.;  
 Gene 170, 223-226, 1996  
 A:Title: Cloning of the rice seed alpha-globulin-encoding gene: Sequence similarity of  
 A:Reference number: JC4784; MUID:96235139; PMID:8666249  
 A:Accession: JC4784  
 A:Molecule type: DNA  
 A:Residues: 1-186 <NAK>  
 A:Cross-references: UNIPROT:P93414; UNIPARC:UPI00000A4C3C; DDBJ:D50643; NID:g840704; PT  
 C:Experimental source: seed  
 C:Genetics:  
 A:Gene: Glb  
 C:Superfamily: Alpha amylase inhibitor  
 C:Keywords: Globulin; seed  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-186/Product: alpha-globulin #status predicted <MAT>  
 Query Match 100.0%; Score 29; DB 2; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 13; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;  
 Qy 1 KWVFFA 6  
 Db 4 KWVFFA 9  
 RESULT 3  
 H81402  
 probable integral membrane protein Cj0560 [imported] - Campylobacter jejuni (strain NC  
 C:Species: Campylobacter jejuni  
 C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C:Accession: H81402  
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barr  
 Nature 403, 665-668, 2000  
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h  
 A:Reference number: A81250; MUID:20150912; PMID:10688204  
 A:Accession: H81402  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-442 <PAR>

A;Cross-references: UNIPROT:Q9PHV5; UNIPARC:UPI000000C217E; GB:AL139075; GB:AL111168; NID:  
A;Experimental source: serotype O2, strain NCTC 11168  
A;Genetics:  
A;Gene: Cj0560

Query Match 100.0%; Score 29; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
Db 313 KVVFFA 318

RESULT 4  
A43271  
nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 05-Oct-2004  
C;Accession: A43271; A42166; JN0458; A46186  
R;Xie, Q.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A.;  
Science 256, 225-228, 1992  
A;Title: Cloning and characterization of inducible nitric oxide synthase from mouse macrophages  
A;Reference number: A43271; MUID:92229444; PMID:1373522  
A;Accession: A43271  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1144 <XIE>  
A;Cross-references: UNIPROT:P29477; UNIPARC:UPI000000D36; GB:M87039; NID:G198406; PIDN:  
R;Lyons, C.R.; Orloff, G.J.; Cunningham, J.M.  
J. Biol. Chem. 267, 6370-6374, 1992  
A;Title: Molecular cloning and functional expression of an inducible nitric oxide synthase  
A;Reference number: A42166; MUID:92210618; PMID:1372907  
A;Accession: A42166  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1144 <LYO>  
A;Cross-references: UNIPARC:UPI000000D36; GB:M84373; NID:G200095; PIDN:AAA39834.1; PID:  
R;Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.  
Biochem. Biophys. Res. Commun. 191, 767-774, 1993  
A;Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxide  
A;Reference number: JN0457; MUID:93221515; PMID:7682072  
A;Accession: JN0458  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-278, 'F', 280-682, 'H', 684-937, 939-1144 <WOO>  
A;Cross-references: UNIPARC:UPI000017223A  
A;Experimental source: liver  
R;Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992  
A;Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the brain  
A;Reference number: A46186; MUID:92357701; PMID:1379716  
A;Accession: A46186  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-190, 'V', 192-765, 'P', 767-843, 'G', 845-1144 <LOW>  
A;Cross-references: UNIPARC:UPI00017223B; GB:M92649; NID:G200109  
A;Experimental source: BALB/c, RAW 264.7 cells, macrophage  
A;Note: sequence extracted from NCBI backbone (NCBI:P113541)  
C;Genetics:  
A;Gene: NOS  
C;Function:  
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH  
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reductase  
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
P;533-1121/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F;535-671/Domain: flavodoxin homology <FLX>  
F;194/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
Db 514 KVVFFA 519

RESULT 5  
F70399  
hydrogenase expression/formation protein HypD - Aquifex aeolicus  
C;Species: Aquifex aeolicus  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C;Accession: F70399  
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A;Reference number: A70300; MUID:98196666; PMID:9537320  
A;Accession: F70399  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-380 <AQF>  
A;Cross-references: UNIPROT:O67225; UNIPARC:UPI0000056543; GB:AE000726; NID:G2983612; P:  
A;Experimental source: strain VF5  
C;Genetics:  
A;Gene: HypD  
C;Superfamily: [NiFe]-hydrogenase maturation factor, HypD type

Query Match 96.6%; Score 28; DB 2; Length 380;  
Best Local Similarity 83.3%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
Db 141 KVVFFA 146

RESULT 6  
F71039  
hypothetical protein PH1606 - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 05-Oct-2004  
C;Accession: F71039  
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch  
DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: F71039  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-447 <KAW>  
A;Cross-references: UNIPROT:O59243; UNIPARC:UPI00000630DB; GB:AP000006; NID:G3236133; P:  
A;Experimental source: strain OT3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C;Genetics:  
A;Gene: PH1606  
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1142

Query Match 93.1%; Score 27; DB 2; Length 447;  
Best Local Similarity 66.7%; Pred. No. 91;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
Db 207 KVVFFA 212

RESULT 7  
S23094  
beta-amyloid protein precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
C;Accession: S23094  
R;Kojima, S.; Omori, M.

FEBS Lett. 304, 57-60, 1992  
 A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
 A;Reference number: S23094; MUID:92316198; PMID:1618299  
 A;Accession: S23094  
 A;Molecule type: protein  
 A;Residues: 1-33 <JOH>  
 A;Cross-references: UNIPARC:UPI00001777FB  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

Query Match 89.7%; Score 26; DB 2; Length 33;  
 Best Local Similarity 83.3%; Pred. No. 14;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:|:|:|

Db 21 KLVFFA 26

## RESULT 8

PN0512  
 beta-amyloid protein - guinea pig (fragment)  
 C;Species: Cavia porcellus (guinea pig)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C;Accession: PN0512  
 R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.  
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
 A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment  
 A;Reference number: PN0512; MUID:93290653; PMID:7685598  
 A;Accession: PN0512  
 A;Molecule type: protein  
 A;Residues: 1-42 <SHI>  
 A;Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

C;Keywords: alternative splicing; amyloid

Query Match 89.7%; Score 26; DB 2; Length 42;  
 Best Local Similarity 83.3%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:|:|:|

Db 16 KLVFFA 21

## RESULT 9

A60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
 C;Species: Canis lupus familiaris (dog)  
 C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C;Accession: A60045  
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A;Reference number: A60045; MUID:92017079; PMID:1656157  
 A;Accession: A60045  
 A;Molecule type: mRNA  
 A;Residues: 1-57 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56125  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
 Best Local Similarity 83.3%; Pred. No. 23;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:|:|:|

Db 21 KLVFFA 26

## RESULT 10

F60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
 C;Accession: F60045  
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A;Reference number: A60045; MUID:92017079; PMID:1656157  
 A;Accession: F60045  
 A;Molecule type: mRNA  
 A;Residues: 1-57 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
 Best Local Similarity 83.3%; Pred. No. 23;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:|:|:|

Db 21 KLVFFA 26

## RESULT 11

D60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C;Accession: D60045  
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A;Reference number: A60045; MUID:92017079; PMID:1656157  
 A;Accession: D60045  
 A;Molecule type: mRNA  
 A;Residues: 1-57 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56124  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
 Best Local Similarity 83.3%; Pred. No. 23;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:|:|:|

Db 21 KLVFFA 26

## RESULT 12

E60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
 C;Species: Ovis sp. (sheep)  
 C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C;Accession: E60045  
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in do,  
 A;Reference number: A60045; MUID:92017079; PMID:1656157  
 A;Accession: E60045  
 A;Molecule type: mRNA  
 A;Residues: 1-57 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56130  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
 Best Local Similarity 83.3%; Pred. No. 23;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:|:|:|

Db 21 KLVFFA 26

RESULT 13  
G60045  
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
C:Species: Cavia porcellus (Guinea pig)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: G60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079; PMID:1656157  
A:Accession: G60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
Best Local Similarity 83.3%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|:||||  
Db 21 KLVFFA 26

RESULT 14  
B60045  
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C:Species: Ursus maritimus (polar bear)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C:Accession: B60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079; PMID:1656157  
A:Accession: B60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; MUID:g2165; PIDN:  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
Best Local Similarity 83.3%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|:||||  
Db 21 KLVFFA 26

RESULT 15  
F90736  
molybdopterin biosynthesis protein D chain [imported] - Escherichia coli (strain O157:H7)  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 16-Aug-2004  
C:Accession: F90736  
R:Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gaasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: F90736  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-81 <HAY>  
A:Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000009BF; GB:BA000007; PIDN:BA834285.1;  
A:Experimental source: strain O157:H7, substrain RMD 050952  
C:Genetics:  
A:Gene: EC60862

C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|:||||  
Db 3 KVLFFA 8

RESULT 16  
A82251  
molybdenum cofactor biosynthesis protein D VC1027 [imported] - Vibrio cholerae (strain 1  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 16-Aug-2004  
C:Accession: A82251  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,  
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: A82251  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-81 <HEI>  
A:Cross-references: UNIPROT:Q9KT78; UNIPARC:UPI00000C2E5B; GB:AE004184; GB:AE003852; NI  
A:Experimental source: serogroup O1, strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC1027  
A:Map position: 1  
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein  
F:81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|:||||  
Db 3 KVLFFA 8

RESULT 17  
G85586  
molybdopterin biosynthesis [imported] - Escherichia coli (strain O157:H7, substrain EDL  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
C:Accession: G85586  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: G85586  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-81 <STO>  
A:Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000009BF; GB:AE005174; MUID:g12513773;  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: moaD  
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|:||||  
Db 3 KVLFFA 8

## RESULT 18

H64814  
molybdopterin biosynthesis protein D chain [validated] - Escherichia coli (strain K-12)  
A;Alternate names: moaD protein; molybdopterin-converting factor 10K chain; molybdopterin C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text\_change 05-Oct-2004  
C;Accession: H64814; S35001; A46585; S31882  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: H64814  
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-81 <BLAT>

A;Cross-references: UNIPROT:P30748; UNIPARC:UPI00001116DF; GB:AE000181; GB:U00096; MID:9

A;Experimental source: strain K-12, substrain MG1655

R;Rivers, S.L.; McNairn, E.; Blasco, F.; Giordano, G.; Boxer, D.H.

Mol. Microbiol. 8, 1071-1081, 1993

A;Title: Molecular genetic analysis of the moa operon of Escherichia coli K-12 required

A;Reference number: S34998; MUID:93368423; PMID:8361352

A;Accession: S35001

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-44, 'R', '46-81 <RIV>

A;Cross-references: UNIPARC:UPI000016F2FD; EMBL:X70420; MID:942007; PIDN:CAA49864.1; PID

A;Experimental source: strain K12

R;Pitterle, D.M.; Rajagopalan, K.V.

J. Biol. Chem. 268, 13499-13505, 1993

A;Title: The biosynthesis of molybdopterin in Escherichia coli. Purification and character

A;Reference number: A46585; MUID:93293873; PMID:8514782

A;Accession: A46585

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8, 'E', 10-15 <PIT>

A;Cross-references: UNIPARC:UPI0000178EC3

A;Note: sequence extracted from NCBI backbone (NCBIP:134491)

C;Genetics:

A;Gene: moaD

A;Map position: 17.7 min

C;Complex: heterodimer with D chain (PIR:S31883) [validated, MUID:93293873]

C;Function:

A;Description: required for the addition of the Mo-binding dithiolene group to a molybd

C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

C;Keywords: heterodimer; molybdopterin biosynthesis

P;81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 81;

Best Local Similarity 83.3%; Pred. No. 32;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

||:||||

Db 3 KVLFFA 8

## RESULT 19

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence revision 19-Oct-1995 #text\_change 19-Oct-1995

C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.B.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor

A;Reference number: PQ0438; MUID:93075180; PMID:1445331

A;Accession: PQ0438

A;Molecule type: DNA

A;Residues: 1-82 <DAV>

A;Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog  
A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: C60045

A;Molecule type: mRNA

A;Residues: 12-68 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56129

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 89.7%; Score 26; DB 2; Length 82;

Best Local Similarity 83.3%; Pred. No. 32;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

||:||||

Db 32 KLVFFA 37

## RESULT 20

AC0598

molybdopterin converting factor, chain 1 [imported] - Salmonella enterica subsp. enteri

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 16-Aug-2004

C;Accession: AC0598

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AC0598

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-83 <PAR>

A;Cross-references: UNIPARC:UPI000005A0EA; GB:AL513382; PIDN:CAD05253.1; PID:G16502022,

C;Genetics:

A;Gene: STY0839

C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 89.7%; Score 26; DB 2; Length 83;

Best Local Similarity 83.3%; Pred. No. 33;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

||:||||

Db 5 KVLFFA 10

## RESULT 21

T06645

hypothetical protein T20K18.220 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C;Accession: T06645

R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mc

submitted to the Protein Sequence Database, April 1999

A;Reference number: Z15790

A;Accession: T06645

A;Molecule type: DNA

A;Residues: 1-152 <BBV>

A;Cross-references: UNIPROT:Q9STZ9; UNIPARC:UPI00000A0722; EMBL:AL049640; GSPDB:GN00062

A;Experimental source: cultivar Columbia; BAC clone T20K18

C;Genetics:

A;Gene: ATSP:T20K18.220

A;Map position: 4

A;Introns: 87/3; 109/3

C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 89.7%; Score 26; DB 2; Length 152;

Best Local Similarity 83.3%; Pred. No. 58;

Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	9	KLVFFA 14							
RESULT 22									
B90157									
hypothetical protein SSO0168 [imported] - Sulfolobus solfataricus									
C:Species: Sulfolobus solfataricus									
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004									
C:Accession: B90157									
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-									
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F									
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.									
submitted to GenBank, April 2001									
A:Description: Sulfolobus solfataricus complete genome.									
A:Reference number: A99139									
A:Accession: B90157									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-193 <KUR>									
A:Cross-references: UNIPROT:Q980V9; UNIPARC:UPI00000641A8; GB:AE006641; NID:g13813299; F									
C:Genetics:									
A:Gene: SSO0168									
Query Match	89.7%;	Score 26;	DB 2;	Length 193;					
Best Local Similarity	83.3%;	Pred. No. 72;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	117	KVFFYA 122							
RESULT 23									
B81256									
phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3									
C:Species: Campylobacter jejuni									
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004									
C:Accession: B81256									
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin									
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell									
Nature 403, 665-668, 2000									
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp									
A:Reference number: A81250; MUID:20150912; PMID:10688204									
A:Accession: B81256									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-207 <PAR>									
A:Cross-references: UNIPROT:Q9PM71; UNIPARC:UPI000012C76D; GB:AL139079; GB:AL1111168; NID									
A:Experimental source: serotype O2, strain NCTC 11168									
C:Genetics:									
A:Gene: hisI; Cj1604									
C:Superfamily: hisI bifunctional enzyme; hisI bifunctional enzyme homology; hisI protein									
C:Keywords: hydrolase									
Query Match	89.7%;	Score 26;	DB 2;	Length 207;					
Best Local Similarity	83.3%;	Pred. No. 77;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	51	KVFFS 56							
RESULT 24									
H85138									
hypothetical protein AT4g12900 [imported] - Arabidopsis thaliana									
C:Species: Arabidopsis thaliana (mouse-ear cress)									
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004									
C:Accession: H85138									

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin									
Nature 402, 769-777, 1999									
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.									
A:Reference number: A85001; MUID:20083488; PMID:10617198									
A:Accession: H85138									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-231 <STO>									
A:Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI00000A7E0E; GB:NC_001368; NID:g7267992; i									
C:Genetics:									
A:Gene: AT4g12900									
A:Map position: 4									
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100									
Query Match	89.7%;	Score 26;	DB 2;	Length 231;					
Best Local Similarity	83.3%;	Pred. No. 85;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	12	KLVFFA 17							
RESULT 25									
D69355									
hypothetical protein AF0844 - Archaeoglobus fulgidus									
C:Species: Archaeoglobus fulgidus									
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004									
C:Accession: D69355									
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson									
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F									
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.									
Nature 390, 364-370, 1997									
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S									
Smith, H.O.; Woese, C.R.; Venter, J.C.									
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae									
A:Reference number: A69250; MUID:98049343; PMID:9389475									
A:Accession: D69355									
A:Status: preliminary; nucleic acid sequence not shown; translation not shown									
A:Molecule type: DNA									
A:Residues: 1-293 <KLE>									
A:Cross-references: UNIPROT:Q29414; UNIPARC:UPI0000056F64; GB:AE001046; GB:AE000782; NI									
Query Match	89.7%;	Score 26;	DB 2;	Length 293;					
Best Local Similarity	83.3%;	Pred. No. 1.1e+02;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	140	KVLFFA 145							
RESULT 26									
H90318									
Glycerol kinase (glpK-1) [imported] - Sulfolobus solfataricus									
C:Species: Sulfolobus solfataricus									
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004									
C:Accession: H90318									
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan									
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, i									
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.									
submitted to GenBank, April 2001									
A:Description: Sulfolobus solfataricus complete genome.									
A:Reference number: A99139									
A:Accession: H90318									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-294 <KUR>									
A:Cross-references: UNIPROT:Q97XW2; UNIPARC:UPI00000644B6; GB:AE006641; NID:g13814829;									
C:Genetics:									
A:Gene: glpK-1									
Query Match	89.7%;	Score 26;	DB 2;	Length 294;					



Best Local Similarity 83.3%; Pred. No. 1.1e+02; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|||:  
Db 184 KVVYTA 189  
|||:  
RESULT 27  
T26245  
hypothetical protein W06G6.6 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26245  
R:McMurray, A.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z20180  
A:Accession: T26245  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-300 <WIL>  
A:Cross-references: UNIPROT:Q9XU61; UNIPARC:UPI0000061208; EMBL:Z83129; PIDN: CAB05641.1;  
A:Experimental source: clone W06G6  
C:Genetics:  
A:Gene: CESP:W06G6.6  
A:Map position: 5  
A:Introns: 171/2; 204/2

Query Match 89.7%; Score 26; DB 2; Length 300;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||:  
Db 281 KVVFFA 286  
|||:

RESULT 28  
B82822  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 [similarity] - *Xylella fastidiosa*  
C:Species: *Xylella fastidiosa*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: B82822  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: B82822  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-330 <SIN>  
A:Cross-references: UNIPROT:Q9PGI8; UNIPARC:UPI00000C2381; GB:AE003884; GB:AE003849; NID  
R:Simpton, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrier, H  
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facinani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XP0312  
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-c  
C:Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match 89.7%; Score 26; DB 2; Length 330;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|||:  
Db 275 KVVFFA 280  
|||:  
RESULT 29  
B72402  
UDP-N-acetylglucosamine-N-acetyluramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-a  
C:Species: *Thermotoga maritima*  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: B72402  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke  
Garttett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: B72402  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-339 <ARN>  
A:Cross-references: UNIPROT:Q9WY74; UNIPARC:UPI0000012P9EB; GB:AE001707; GB:AE000512; NI  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM0232  
C:Superfamily: murG protein

Query Match 89.7%; Score 26; DB 2; Length 339;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||:  
Db 32 KVVFFA 37  
|||:

RESULT 30  
T26247  
hypothetical protein W06G6.8 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26247  
R:McMurray, A.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z20180  
A:Accession: T26247  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-349 <WIL>  
A:Cross-references: UNIPROT:Q9XU59; UNIPARC:UPI0000061209; EMBL:Z83129; PIDN: CAB05643.1;  
A:Experimental source: clone W06G6  
C:Genetics:  
A:Gene: CESP:W06G6.8  
A:Map position: 5  
A:Introns: 172/2; 210/3; 247/2

Query Match 89.7%; Score 26; DB 2; Length 349;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||:  
Db 324 KVVFFA 329  
|||:

RESULT 31  
T48903  
wax synthase [imported] - *Simmondsia chinensis*  
C:Species: *Simmondsia chinensis*



```
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T48903
R;Lardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W.
Plant Physiol. 122, 645-655, 2000
A;Title: Purification of a jojoba embryo wax synthase, cloning of its cDNA and production
of a complementary DNA
A;Reference number: Z25002
A;Accession: T48903
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <LAR>
A;Cross-references: UNIPROT:Q9XGY6; UNIPARC:UPI00000A1C81; EMBL:AF149919; PIDN:RAD38041.

Query Match      89.7%; Score 26; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
Db      135 KLVFFFA 140

RESULT 32
T48008
hypothetical protein T17J13.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: T48008
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24482
A;Accession: T48008
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-428 <RIE>
A;Cross-references: UNIPROT:Q9M108; UNIPARC:UPI00000488B7; EMBL:AL138651
A;Experimental source: cultivar Columbia; BAC clone F17J13
C;Genetics:
A;Map position: 3
A;Introns: 137/3
A;Note: T17J13.120
C;Superfamily: N-hydroxycinnamoyl/benzoyl transferase

Query Match      89.7%; Score 26; DB 2; Length 428;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
Db      271 KLVFFFA 276

RESULT 33
B28988
hypothetical protein F1696 (photosynthetic gene cluster) - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
C;Accession: B28988
R;Youvan, D.C.; Bylina, E.J.; Alberti, M.; Begusch, H.; Hearst, J.E.
Cell 37, 949-957, 1984
A;Title: Nucleotide and deduced polypeptide sequences of the photosynthetic reaction-cent
er
A;Reference number: A90850; MUID:84259352; PMID:6744416
A;Accession: B28988
A;Molecule type: DNA
A;Residues: 1-477 <YOU>
A;Cross-references: UNIPROT:P26176; UNIPARC:UPI000013BE54; GB:K01183

Query Match      89.7%; Score 26; DB 2; Length 477;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
Db      349 KLVFFFA 354
```

```
RESULT 34
A81548
hypothetical protein CP0705 [imported] - Chlamydophila pneumoniae (strain AR39)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: A81548
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
, R.; Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: A81548
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-520 <REA>
A;Cross-references: UNIPROT:Q9K207; UNIPARC:UPI00000CCCC9E; GB:AE002229; GB:AE002161; NI
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0705

Query Match      89.7%; Score 26; DB 2; Length 520;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
Db      381 RVVFFFA 386

RESULT 35
F86499
hypothetical protein CPj0069 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86499
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: F86499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-594 <STO>
A;Cross-references: UNIPROT:Q9JSK0; UNIPARC:UPI00000CCCCBF; GB:BA000008; NID:g8978443; P
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0069

Query Match      89.7%; Score 26; DB 2; Length 594;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
Db      455 RVVFFFA 460

RESULT 36
F72237
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72237
R;Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72237
A;Status: preliminary
```

A;Molecule type: DNA  
A;Residues: 1-603 <ARN>  
A;Cross-references: UNIPROT:Q9X1Q9; UNIPARC:UPI000000C125F; GB:AE001802; GB:AE000512; NID  
A;Experimental source: strain MSB8  
C;Genetics:  
A;Gene: TM1573

Query Match 89.7%; Score 26; DB 2; Length 603;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||: 198  
Db 193 KVVFFS 198

RESULT 37  
A72123  
hypothetical protein CT326 homolog - Chlamydomophila pneumoniae (strain CWL029)  
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: A72123  
R;Kallman, S.; Mitchell, W.; Maxatthe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21: 385-389, 1999  
A;Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.  
A;Reference number: A72000; MUID:99206606; PMID:10192398  
A;Accession: A72123  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-617 <ARN>  
A;Cross-references: UNIPROT:Q929B2; UNIPARC:UPI000000C11C1; GB:AE001592; GB:AE001363; NID  
A;Experimental source: strain CWL029  
C;Genetics:  
A;Gene: CPn0609

Query Match 89.7%; Score 26; DB 2; Length 617;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||: 483  
Db 478 RVVFFA 483

RESULT 38  
A49795  
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
C;Species: Macaca fascicularis (crab-eating macaque)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: A49795  
R;Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.  
Am. J. Pathol. 138: 1423-1435, 1991  
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a p  
A;Reference number: A49795; MUID:91273117; PMID:1905108  
A;Accession: A49795  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-695 <POD>  
A;Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:g342062; PIDN:AAA36829.1; PID  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;Keywords: alternative splicing

Query Match 89.7%; Score 26; DB 1; Length 695;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||: 617  
Db 612 KLVFFA 617

RESULT 39  
A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
N;Alternate names: proteinase nexin II  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
C;Accession: A27485; S19727; I49485  
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
Biochem. Biophys. Res. Commun. 149: 665-671, 1987  
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein prec  
A;Reference number: A27485; MUID:88106489; PMID:3322280  
A;Accession: A27485  
A;Molecule type: mRNA  
A;Residues: 1-695 <YAM>  
A;Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN  
A;Experimental source: brain  
R;de Strooper, B.; van Leeuwen, F.; van den Berghe, H.  
Biochim. Biophys. Acta 1129: 141-143, 1991  
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
A;Reference number: S19727; MUID:92096458; PMID:1756177  
A;Accession: S19727  
A;Molecule type: mRNA  
A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
A;Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379  
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
Gene 112: 189-195, 1992  
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer'  
A;Reference number: I49485; MUID:92209998; PMID:1555768  
A;Accession: I49485  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-19 <RES>  
A;Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BAA01456.1; PID  
C;Genetics:  
A;Map position: 16C3  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 89.7%; Score 26; DB 2; Length 695;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||: 617  
Db 612 KLVFFA 617

RESULT 40  
S00550  
Alzheimer's disease amyloid beta protein precursor - rat  
N;Alternate names: beta-A4 amyloid protein  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: S00550; A41245; A39820; S46251  
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
EMBO J. 7: 1365-1370, 1988  
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brai  
A;Reference number: S00550; MUID:88312583; PMID:2900758  
A;Accession: S00550  
A;Molecule type: mRNA  
A;Residues: 1-695 <SHI>  
A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648; NID:g55616; PII  
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saich, T.; Cole, G.  
Science 241: 223-226, 1988  
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan cor  
A;Reference number: A41245; MUID:88264430; PMID:2968652  
A;Accession: A41245  
A;Molecule type: protein  
A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
A;Cross-references: UNIPARC:UPI0000177FD  
A;Note: evidence for heparan sulfate attachment  
R;Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.  
FEBS Lett. 349: 109-116, 1994  
A;Title: The beta-A4 amyloid precursor protein binding to copper.  
A;Reference number: S46251; MUID:94320627; PMID:7913895

A;Contents: annotation; copper binding sites  
A;Note: rat peptides were isolated but not sequenced  
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
J. Biol. Chem. 266, 8464-8469, 1991  
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
A;Reference number: A39820; MUID:91217087; PMID:1673681  
A;Accession: A39820  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 18-32 <POT>  
A;Cross-references: UNIPARC:UPI00001777PE  
A;Experimental source: brain  
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor; alternative splicing; amyloid; glycoprotein; transmembrane protein  
F;625-648/Domain: transmembrane #status predicted <TM>

Query Match 89.7%; Score 26; DB 2; Length 695;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
DB 612 KLVFFA 617

RESULT 41  
JH0773  
Alzheimer's disease amyloid beta protein precursor - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
C;Accession: JH0773  
R;Okado, H.; Okamoto, H.  
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental  
A;Reference number: JH0773; MUID:93129227; PMID:1282805  
A;Accession: JH0773  
A;Molecule type: mRNA  
A;Residues: 1-747 <OKA>  
A;Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:G263150; PIDN:AAB24853.1; PID:  
A;Experimental source: larva  
A;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor  
C;Keywords: alternative splicing; amyloid  
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 89.7%; Score 26; DB 2; Length 747;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
DB 664 KLVFFA 669

RESULT 42  
QRHUA4  
Alzheimer's disease amyloid beta protein precursor [validated] - human  
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibitor  
N;Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
protein precursor splice form APP (770)  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
C;Accession: S02260; S05194; A32277; A33260; I39452; I39451; I39453; I59562; A44  
466B; A28583; A29302; A60805; JLO038; S06121; A60355; A59011; A38384; S29076; S38252; S3  
R;Lemaire, H.G.; Salbaum, J.M.; Malthaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey  
Nucleic Acids Res. 17, 517-522, 1989  
A;Title: The PreA4 (695) precursor protein of Alzheimer's disease A4 amyloid is encoded by  
A;Reference number: S02260; MUID:89128427; PMID:2783775  
A;Accession: S02260  
A;Molecule type: DNA  
A;Residues: 1-288, 'V', 365-770 <LEM1>  
A;Cross-references: UNIPARC:UPI00000A2A2F2; EMBL:X13466  
A;Note: alternative splice form APP (695)

R;Lemaire, H.G.  
submitted to the EMBL Data Library, November 1988  
A;Reference number: S05194  
A;Accession: S05194  
A;Molecule type: DNA  
A;Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
A;Cross-references: UNIPARC:UPI000016AEFC; EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PI:  
A;Note: alternative splice form APP (695)  
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prot  
A;Reference number: A32277; MUID:89165870; PMID:2538123  
A;Accession: A32277  
A;Molecule type: DNA  
A;Residues: 1-75 <LAF>  
A;Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:G341202; PIDN:AAAC1  
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, P.H.; Little, S.P.  
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similar  
A;Reference number: A33260; MUID:89392030; PMID:2675837  
A;Accession: A33260  
A;Molecule type: DNA  
A;Residues: 656-737 <JOH>  
A;Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:G178863; PIDN:AAA51768.1; PID:  
R;Pirelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
A;Reference number: A35486; MUID:90321244; PMID:2196878  
A;Accession: A35486  
A;Molecule type: DNA  
A;Residues: 672-710 <PRE1>  
A;Cross-references: UNIPARC:UPI0000148176  
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 87, 257-263, 1990  
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.  
A;Reference number: I39451; MUID:90236318; PMID:2110105  
A;Accession: I39451  
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM  
A;Molecule type: DNA  
A;Residues: 1-770 <YOS1>  
A;Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:  
A;Accession: I39451  
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM  
A;Molecule type: DNA  
A;Residues: 1-530, 'QWLMPVTPAFWEAKVGR' <YOS2>  
A;Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:  
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 102, 291-292, 1991  
A;Reference number: A59020; MUID:91340168; PMID:1908403  
A;Contents: annotation; erratum  
A;Note: revised physical map for reference I39451  
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duin  
Science 248, 1124-1126, 1990  
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorr  
A;Reference number: I39453; MUID:90260663; PMID:2111584  
A;Accession: I39453  
A;Status: translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 656-737 <LEV>  
A;Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:G178618; PIDN:AAA51727.1; PID:  
A;Note: a mutation with 693-Gln is presented  
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
Science 254, 97-99, 1991  
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer  
A;Reference number: I59562; MUID:92022553; PMID:1925564  
A;Accession: I59562  
A;Status: translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 689-716, 'F', 718-737 <MUR>  
A;Cross-references: UNIPARC:UPI000011F7EA; GB:S57665; NID:G236720; PIDN:AAB19991.1; PID:  
R;Kamino, K.; Orr, H.T.; Payami, H.; Wajsbman, M.E.; Alonso, M.E.; Pulst, S.M.; Anderson, R.  
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heaton, L.L.; Martin,

Am. J. Hum. Genet. 51, 998-1014, 1992  
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the  
A;Reference number: A44017; MUID:93035397; PMID:1415269  
A;Accession: A44017  
A;Molecule type: DNA  
A;Residues: 687-692, 'G', 694-718 <KAM1>  
A;Cross-references: UNIPARC:UPI000011F7EB; GB:S45135; NID:9257377; PIDN:AAB23645.1; PID:  
A;Experimental source: familial Alzheimer disease family SB  
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)  
A;Accession: B44017  
A;Molecule type: DNA  
A;Residues: 687-718 <KAM2>  
A;Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:9257379; PIDN:AAB23646.1; PID:  
A;Experimental source: familial Alzheimer disease family LIT  
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)  
A;Note: this sequence has a silent mutation  
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
Nature 325, 733-736, 1987  
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
A;Reference number: A03134; MUID:87144572; PMID:2881207  
A;Accession: A03134  
A;Molecule type: mRNA  
A;Residues: 1-288, 'V', 365-770 <KAN>  
A;Cross-references: UNIPARC:UPI00002A2P2; GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:9  
A;Note: alternative splice form APP(695)  
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a  
A;Reference number: A29030; MUID:87231971; PMID:3035574  
A;Accession: A29030  
A;Molecule type: mRNA  
A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
A;Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:9178539; PIDN:AAA51722.1; PID:  
A;Note: the authors translated the codon GAG for residue 647 as Asp  
R;Goldhaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.  
Science 235, 877-880, 1987  
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
A;Reference number: A47584; MUID:87120328; PMID:3810169  
A;Accession: A47584  
A;Molecule type: mRNA  
A;Residues: 674-756, 'S', 758-770 <GOL>  
A;Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:9178706; PIDN:AAA35540.1; PID:  
A;Experimental source: brain  
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
Science 235, 880-884, 1987  
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
A;Reference number: A47585; MUID:87120329; PMID:2949367  
A;Accession: A47585  
A;Molecule type: mRNA  
A;Residues: 674-703 <TANI>  
A;Cross-references: UNIPARC:UPI000016A46P; GB:M15532; NID:9177957; PIDN:AAA51564.1; PID:  
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
EMBO J. 7, 949-957, 1988  
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
A;Reference number: S02638; MUID:86296437; PMID:2900137  
A;Accession: S02638  
A;Molecule type: mRNA  
A;Residues: 672-678 <DYR>  
A;Cross-references: UNIPARC:UPI0000035AB0  
R;Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
Nature 331, 528-530, 1988  
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
A;Reference number: S00707; MUID:88122640; PMID:2893290  
A;Accession: S00707  
A;Molecule type: mRNA  
A;Residues: 286-344, 'I', 365-366 <TAN2>  
A;Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:  
A;Experimental source: promyelocytic leukemia cell line HL60  
A;Note: alternative splice form APP(751)  
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De  
Nature 331, 525-527, 1988  
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi  
A;Reference number: S00925; MUID:88122639; PMID:2893289

A;Accession: S00925  
A;Molecule type: mRNA  
A;Residues: 1-344, 'I', 365-770 <PO2>  
A;Cross-references: UNIPARC:UPI000002A2P6; GB:X06989; EMBL:X00297; NID:928720; PIDN:CAA  
A;Note: alternative splice form APP(751)  
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
Nature 331, 530-532, 1988  
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito  
A;Reference number: A38949; MUID:88122641; PMID:2893291  
A;Accession: A38949  
A;Molecule type: mRNA  
A;Residues: 287-367 <KIT>  
A;Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:928816; PIDN:CAA30041.1; PID:  
A;Experimental source: glioblastoma cell line  
A;Note: alternative splice form APP(770)  
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashto  
Brain Res. Mol. Brain Res. 4, 121-131, 1988  
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three  
A;Reference number: A30320  
A;Accession: A30320  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 284-288, 'V', 365-770 <VIT1>  
A;Cross-references: UNIPARC:UPI0000174094  
A;Accession: B30320  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 122-288, 'V', 365-770 <VIT2>  
A;Cross-references: UNIPARC:UPI0000174094  
A;Accession: C30320  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 606-770 <VIT3>  
A;Cross-references: UNIPARC:UPI0000174094  
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.  
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b  
A;Reference number: A31087; MUID:88124954; PMID:2893379  
A;Accession: A31087  
A;Molecule type: mRNA

Query Match 89.7%; Score 26; DB 1; Length 770;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KVVFFA 6  
|:|:|:|  
Db 687 KLVFFA 692

RESULT 43  
A82511  
glycogen phosphorylase (EC 2.4.1.1) [similarity] - Vibrio cholerae (strain N16961 serog  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 18-Aug-2003  
C;Accession: A82511  
R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,  
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 405, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: A82511  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-817 <HEI>  
A;Cross-references: UNIPARC:UPI00000C33CA; GB:AE004345; GB:AE003853; NID:92657390; PID:  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VCA0013  
A;Map position: 2  
C;Superfamily: glucan phosphorylase  
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphat

F:664/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 817;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
:|||||  
Db 585 RVVFFA 590

## RESULT 44

S30236  
genome polyprotein - zucchini yellow mosaic virus (strain Singapore) (fragment)  
N;Contains: coat protein; nuclear inclusion protein a; RNA-directed RNA polymerase (EC 2.7.7.48)  
C;Species: zucchini yellow mosaic virus, ZYMV  
A;Variety: strain Singapore  
C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: S30236  
R;Wu, M.; Yeong, C.Y.; Lee, S.C.; Wong, S.M.  
Nucleic Acids Res. 21, 1317, 1993  
A;Title: Nucleotide sequence of the 3' half of zucchini yellow mosaic virus (Singapore isolate)  
A;Reference number: S30236; MUID:93219099; PMID:8464715  
A;Accession: S30236  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-1016 <WUM>  
A;Cross-references: UNIPROT:Q05912; UNIPARC:UPI000008CC69; EMBL:X68509; NID:g288233; PIR:G10000  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992  
C;Superfamily: tobacco etch virus genome polyprotein  
C;Keywords: coat protein; genome-linked protein; nucleotidyltransferase; phosphoprotein;  
F;9-61/Product: VPg protein #status predicted <VPG>  
F;62-494/Product: nuclear inclusion protein a #status predicted <NIA>  
F;495-1010/Product: RNA-directed RNA polymerase #status predicted <POL>  
F;1011-1016/Product: coat protein (fragment) #status predicted <COP>  
F;125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 1016;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
:|||||  
Db 837 KLVFFA 842

## RESULT 45

E64214  
hypothetical protein homolog MG131 - Mycoplasma genitalium  
C;Species: Mycoplasma genitalium  
C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: E64214  
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;  
M.; Fuhmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
C.A.; Venter, J.C.  
Science 270, 397-403, 1995  
A;Title: The minimal gene complement of Mycoplasma genitalium.  
A;Reference number: A64200; MUID:96026346; PMID:7569993  
A;Accession: E64214  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-74 <TIGR>  
A;Cross-references: UNIPROT:P47377; UNIPARC:UPI000013931D; GB:U39691; GB:I43967; NID:g10000  
A;Experimental source: strain G-37  
C;Genetics:  
A;Genetic code: SGC3

Query Match 86.2%; Score 25; DB 2; Length 74;  
Best Local Similarity 66.7%; Pred. No. 51;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
:|||||

Db 34 KILFFA 39

## RESULT 46

B72213  
conserved hypothetical protein - Thermotoga maritima (strain MSB8)  
C;Species: Thermotoga maritima  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: B72213  
R;Nelson, K.R.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing  
A;Reference number: A72200; MUID:99287316; PMID:10360571  
A;Accession: B72213  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-109 <ARN>  
A;Cross-references: UNIPROT:Q9X292; UNIPARC:UPI000000C120B; GB:AE001815; GB:AE000512; NFI  
A;Experimental source: strain MSB8  
C;Genetics:  
A;Gene: TM1771  
C;Superfamily: Bacillus subtilis conserved hypothetical protein yqhY

Query Match 86.2%; Score 25; DB 2; Length 109;  
Best Local Similarity 66.7%; Pred. No. 73;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
:|||||  
Db 19 KIVFFA 24

## RESULT 47

T19479  
hypothetical protein C26C6.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T19479  
R;McMurray, A.  
submitted to the EMBL Data Library, May 1996  
A;Reference number: Z19128  
A;Accession: T19479  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-136 <WIL>  
A;Cross-references: UNIPROT:Q18208; UNIPARC:UPI000007BES9; EMBL:Z72503; PIR:CAA96598.1  
A;Experimental source: clone C26C6  
C;Genetics:  
A;Gene: CESP:C26C6.6  
A;Map position: 1  
A;Introns: 22/3; 44/3; 78/1

Query Match 86.2%; Score 25; DB 2; Length 136;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
:|||||  
Db 24 KVVFF 28

## RESULT 48

E75134  
hypothetical protein PAB1779 - Pyrococcus abyssi (strain Orsay)  
C;Species: Pyrococcus abyssi  
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Dec-2002  
C;Accession: E75134  
R;anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure  
A;Reference number: A75001

A:Accession: E75134  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-146 <KAW>  
 A:Cross-references: UNIPARC:UPI000063351; GB:AJ248285; GB:AL096836; NID:G5458067; PIDN:  
 C:Genetics:  
 A:Gene: PAB1779  
 C:Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 146;  
 Best Local Similarity 66.7%; Pred. No. 96;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 ||:|:  
 Db 39 KVIFFA 44

RESULT 49  
 T32362  
 hypothetical protein C08E3.11 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T32362  
 R:Miller, N.; Kramer, J.; Keppler, D.  
 A:Description: The sequence of C. elegans cosmid C08E3.  
 A:Reference number: Z21155  
 A:Accession: T32362  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-148 <MIL>  
 A:Cross-references: UNIPROT:O17202; UNIPARC:UPI0000076D24; EMBL:AF025457; PIDN:AAE70972.  
 A:Experimental source: strain Bristol N2; clone C08E3  
 C:Genetics:  
 A:Gene: CESP:C08E3.11  
 A:Map position: 2  
 A:Introns: 66/2

Query Match 86.2%; Score 25; DB 2; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
 |||||  
 Db 126 KVVFF 130

RESULT 50  
 H95252  
 PTS system, IIB component [imported] - Streptococcus pneumoniae (strain TIGR4)  
 C:Species: Streptococcus pneumoniae  
 C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
 C:Accession: H95252  
 R:Tettein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
 on, J.D.; Unay, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
 nson, T.; Hickey, E.K.; Holt, I.E.  
 Science 293 498-506, 2001  
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
 A:Reference number: A95000; MUID:21357209; PMID:11463916  
 A:Accession: H95252  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-156 <KUR>  
 A:Cross-references: UNIPROT:Q97N92; UNIPARC:UPI0000051B4E; GB:AE005672; PIDN:AAK76217.1;  
 A:Experimental source: strain TIGR4  
 C:Genetics:  
 A:Gene: SP2163  
 C:Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 86.2%; Score 25; DB 2; Length 156;

Best Local Similarity 66.7%; Pred. No. 1e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 ||:|:  
 Db 56 KIVFFS 61

RESULT 51  
 F98117  
 hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)  
 C:Species: Streptococcus pneumoniae  
 C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
 C:Accession: F98117  
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;  
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;  
 Y, P.; Sun, P.M.; Winkler, M.E.  
 J. Bacteriol. 183, 5709-5717, 2001  
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R  
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
 A:Reference number: A97872; MUID:21429245; PMID:11544234  
 A:Accession: F98117  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-156 <KUR>  
 A:Cross-references: UNIPROT:Q8DN20; UNIPARC:UPI00000E3754; GB:AE007317; PIDN:RAL00771.1  
 C:Genetics:  
 A:Gene: PTS-EII  
 C:Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 86.2%; Score 25; DB 2; Length 156;  
 Best Local Similarity 66.7%; Pred. No. 1e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 ||:|:  
 Db 56 KIVFFS 61

RESULT 52  
 C71080  
 hypothetical protein PH0907 - Pyrococcus horikoshii  
 C:Species: Pyrococcus horikoshii  
 C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 16-Aug-2004  
 C:Accession: C71080  
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki  
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogut  
 DNA Res. 5, 55-76, 1998  
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
 A:Reference number: A71000; MUID:98344137; PMID:9679194  
 A:Accession: C71080  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-159 <KAW>  
 A:Cross-references: UNIPARC:UPI0000062F34; GB:AF000004; NID:G3236131; PIDN:BA030001.1;  
 A:Experimental source: strain OT3  
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBan  
 C:Genetics:  
 A:Gene: PH0907  
 C:Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 159;  
 Best Local Similarity 66.7%; Pred. No. 1e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 ||:|:  
 Db 54 KVIFFA 59

RESULT 53  
 T13659  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia sagittata chloroplast

C:Species: chloroplast Pontederia sagittata  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13659  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Syst. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13659  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <GRA>  
A:Cross-references: UNIPROT:Q32915; UNIPARC:UPI0000096540; EMBL:U41621; NID:g1174015; PT13656  
C:Genetics:  
A:Genome: chloroplast  
A:Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
DB 13 KVIFFS 18  
|||:

RESULT 54  
T13656  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia rotundifolia chloroplast  
C:Species: chloroplast Pontederia rotundifolia  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13656  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Syst. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13656  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <GRA>  
A:Cross-references: UNIPROT:Q32892; UNIPARC:UPI000008CB4C; EMBL:U41620; NID:g1174011; PT13653  
C:Genetics:  
A:Genome: chloroplast  
A:Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
DB 13 KVIFFS 18  
|||:

RESULT 55  
T13653  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia cordata chloroplast  
C:Species: chloroplast Pontederia cordata  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13563  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Syst. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13563  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <GRA>  
A:Cross-references: UNIPROT:Q32802; UNIPARC:UPI000008F006; EMBL:U41619; NID:g1174003; PT13562  
A:Experimental source: var. ovalle

C:Genetics:  
A:Genome: chloroplast  
A:Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
DB 13 KVIFFS 18  
|||:

RESULT 56  
T13487  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Monochoria vaginalis chloroplast  
C:Species: chloroplast Monochoria vaginalis  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13487  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Syst. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13487  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <GRA>  
A:Cross-references: UNIPROT:Q32648; UNIPARC:UPI00000976F4; EMBL:U41616; NID:g1173991; PT13562  
C:Genetics:  
A:Genome: chloroplast  
A:Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
DB 13 KVIFFS 18  
|||:

RESULT 57  
T13562  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia cordata chloroplast  
C:Species: chloroplast Pontederia cordata  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13562  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Syst. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13562  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-164 <GRA>  
A:Cross-references: UNIPROT:Q37011; UNIPARC:UPI000016D3B6; EMBL:U41617; NID:g1173999; PT13563  
A:Experimental source: var. cordata  
C:Genetics:  
A:Genome: chloroplast  
A:Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 164;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
DB 13 KVIFFS 18  
|||:







```

A;Cross-references: UNIPROT:O84601; UNIPARC:UPI00000D336C; GB:AE001330; GB:AE001273; NID
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: exbB
C;Superfamily: biopolymer transport protein

Query Match      86.2%; Score 25; DB 2; Length 232;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      ||:||:
Db      21 KVVFFS 26

RESULT 63
T23466
hypothetical protein K08E4.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23466
R;Percy, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19744
A;Accession: T23466
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-234 <WIL>
A;Cross-references: UNIPROT:Q21336; UNIPARC:UPI00000765B4; EMBL:Z68316; PIDN:CAA92683.1;
A;Experimental source: clone K08E4
C;Genetics:
A;Gene: CESP:K08E4.6
A;Map position: 4
A;Introns: 54/3; 154/3

Query Match      86.2%; Score 25; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVVFF 5
      |||||
Db     109 KVVVFF 113

RESULT 64
T32514
hypothetical protein C44B12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T32514
R;Tin-Wollam, A.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C44B12.
A;Reference number: Z21183
A;Accession: T32514
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-247 <TIN>
A;Cross-references: UNIPROT:O44145; UNIPARC:UPI00001793B3; EMBL:AF036692; PIDN:AAB88324.
A;Experimental source: strain Bristol N2; clone C44B12
C;Genetics:
A;Gene: CESP:C44B12.1
A;Map position: 4
A;Introns: 28/3; 82/1; 164/1; 192/1

Query Match      86.2%; Score 25; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      ||:||:
Db     224 KVVFFS 229

```

## RESULT 65

```

D82405
transcription regulator LuxR family VCA0888 [imported] - Vibrio cholerae (strain N16961)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82405
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Esmolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.
L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <HEI>
A;Cross-references: UNIPROT:Q9KL60; UNIPARC:UPI00000C36AA; GB:AE004416; GB:AE003853; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0888
A;Map position: 2

```

```

Query Match      86.2%; Score 25; DB 2; Length 253;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 KVVFFA 6

```

      ||:||:
Db     51 KVVFFS 56

```

## RESULT 66

```

C87434
2-deoxy-D-gluconate 3-dehydrogenase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C;Accession: C87434
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87434
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-255 <STO>
A;Cross-references: UNIPROT:Q9A872; UNIPARC:UPI00000C73DC; GB:AE005673; NID:gl3422867;
C;Genetics:
A;Gene: CC1492
C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology

```

```

Query Match      86.2%; Score 25; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 KVVVFF 5

```

      |||||
Db    117 KVVVFF 121

```

## RESULT 67

```

C83982
hypothetical protein BH2659 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83982
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83982

```

```

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <STO>
A:Cross-references: UNIPROT:Q9K9I8; UNIPARC:UPI00000C3F80; GB:AP001516; GB:BA0000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2659

Query Match      86.2%; Score 25; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
      |||||
Db      4 KVVFF 8

RESULT 68
D64166
hypothetical protein HI1086 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: D64166
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.F.; Glodek, A.; Kelley, J.M.; Weidman, J.;
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: D64166
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <TIGR>
A:Cross-references: UNIPROT:P45030; UNIPARC:UPI000013BFAD; GB:U32788; GB:L42023; NID:g18
A:Note: best homolog was a hypothetical protein from Escherichia coli
C:Superfamily: conserved hypothetical protein HI1086

Query Match      86.2%; Score 25; DB 2; Length 261;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |||||
Db     205 KAVFFA 210

RESULT 69
T31855
hypothetical protein C02E7.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31855
R:Fulton, B.; Wohlmann, P.
submitted to the EMBL Data Library, June 1998
A:Description: The sequence of C. elegans cosmid C02E7.
A:Reference number: Z21093
A:Accession: T31855
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-277 <FUL>
A:Cross-references: UNIPARC:UPI000017B71A; EMBL:AF016446; PIDN:AAC24170.1; GSPDB:GN00023
A:Experimental source: strain Bristol N2; clone C02E7
C:Genetics:
A:Gene: CESP:C02E7.12
A:Map position: 5
A:Introns: 45/2; 146/3

Query Match      86.2%; Score 25; DB 2; Length 277;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6

```

```

Db     112 KIVFFA 117
      ||:|:|

RESULT 70
C84857
hypothetical protein At2g42710 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84857
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <STO>
A:Cross-references: UNIPROT:Q9SJ15; UNIPARC:UPI00000A82D6; GB:AE002093; NID:g4512681; P
C:Genetics:
A:Gene: At2g42710
A:Map position: 2
C:Superfamily: ribosomal protein Llp/L10e

Query Match      86.2%; Score 25; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |||||
Db     241 KAVFFA 246

RESULT 71
JC4744
NAD-dinitrogen-reductase ADP-D-ribosyltransferase (EC 2.4.2.37) - rice
C:Species: Oryza sativa (rice)
C>Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 02-Aug-2002
C:Accession: JC4744
R:Inoue, A.; Shigematsu, T.; Hidaka, M.; Maseki, H.; Uozumi, T.
Gene 170, 101-106, 1996
A:Title: Cloning, sequencing and transcriptional regulation of the drat and drag genes
A:Reference number: JC4744; MUID:96200864; PMID:8621068
A:Accession: JC4744
A:Molecule type: DNA
A:Residues: 1-295 <INO>
A:Cross-references: UNIPARC:UPI00000BDA45; DDBJ:D55631; NID:g862322; PID:g862323
C:Comment: This enzyme is responsible for the post-translation regulation of nitroge
C:Genetics:
A:Gene: drat
C:Superfamily: Azospirillum NAD+-nitrogenase ADP-D-ribosyltransferase
C:Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match      86.2%; Score 25; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
      |||||
Db     262 KVVFF 266

RESULT 72
I39751
NAD-dinitrogen-reductase ADP-D-ribosyltransferase (EC 2.4.2.37) - Azospirillum brasil
C:Species: Azospirillum brasilense
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39751
R:Zhang, Y.; Burris, R.H.; Roberts, G.P.
J. Bacteriol. 174, 3364-3369, 1992
A:Title: Cloning, sequencing, mutagenesis, and functional characterization of drat and

```

A;Reference number: I39751; MUID:92250433; PMID:1577701  
 A;Accession: I39751  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-295 <RES>  
 A;Cross-references: UNIPROT:Q43903; UNIPARC:UPI00000B0CDB; GB:M87319; NID:g142411; PIDN:  
 C;Genetics:

A;Gene: drat  
 C;Superfamily: Azospirillum NAD+-nitrogenase ADP-D-ribosyltransferase  
 C;Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 86.2%; Score 25; DB 2; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
 |||||  
 Db 262 KVVFF 266

## RESULT 73

C70736  
 hypothetical protein Rv3406 - Mycobacterium tuberculosis (strain H37RV)  
 C;Species: Mycobacterium tuberculosis  
 C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 C;Accession: C70736

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.T.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
 A;Authors: Sqaes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: C70736  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA

A;Residues: 1-295 <COL>  
 A;Cross-references: UNIPROT:Q50719; UNIPARC:UPI000013C263; GB:Z77165; GB:AL123456; NID:9  
 A;Experimental source: strain H37RV  
 C;Genetics:  
 A;Gene: Rv3406

Query Match 86.2%; Score 25; DB 2; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
 |||||  
 Db 43 KVVFF 47

## RESULT 74

A99074  
 hypothetical protein ABC-MSP [imported] - Streptococcus pneumoniae (strain R6)  
 C;Species: Streptococcus pneumoniae  
 C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
 C;Accession: A99074

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B  
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
 y, P.; Sun, P.M.; Winkler, M.E.  
 J. Bacteriol. 183, 5709-5717, 2001  
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
 A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: A99074  
 A;Status: preliminary  
 A;Molecule type: DNA

A;Residues: 1-302 <KUR>  
 A;Cross-references: UNIPROT:Q8DNN9; UNIPARC:UPI00000E36B3; GB:AE007317; PIDN:AAL00422.1;  
 C;Genetics:  
 A;Gene: ABC-MSP  
 C;Superfamily: inner membrane protein uga

Query Match 86.2%; Score 25; DB 2; Length 302;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFF 6  
 |||||  
 Db 118 KVAFPA 123

## RESULT 75

B35961  
 hypothetical 21K protein - Pseudomonas syringae pv. savastanoi  
 C;Species: Pseudomonas syringae pv. savastanoi  
 C;Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 09-Jul-2004  
 C;Accession: B35961

R;Roberto, F.F.; Klee, H.; White, F.; Nordeen, R.; Kosuge, T.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 5797-5801, 1990  
 A;Title: Expression and fine structure of the gene encoding N(epsilon)-((indole-3-acetyl)-  
 A;Reference number: A35961; MUID:90332869; PMID:2377619

A;Accession: B35961  
 A;Status: preliminary  
 A;Molecule type: DNA

A;Residues: 1-302 <ROB>  
 A;Cross-references: UNIPROT:P18205; UNIPARC:UPI000013B36E; GB:M35373; NID:g151286; PIDN:

Query Match 86.2%; Score 25; DB 2; Length 302;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 6  
 :|||  
 Db 197 QVFFFA 202

Search completed: December 29, 2005, 17:49:20

Job time : 13.9677 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds  
(without alignments)  
13.656 Million cell updates/sec

Title: US-10-009-122-17

Perfect score: 29

Sequence: 1 KVPFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 300 summaries

Database : Published Applications AA\_New.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	89.7	19	6	US-10-923-605-5
2	26	89.7	19	6	US-10-934-818-5
3	26	89.7	40	7	US-11-016-706-36
4	26	89.7	40	7	US-11-098-674-12
5	26	89.7	42	6	US-10-923-605-1
6	26	89.7	42	6	US-10-934-818-1
7	26	89.7	42	6	US-11-016-706-37
8	26	89.7	43	6	US-10-934-818-6
9	26	89.7	43	6	US-10-250-581-1
10	26	89.7	43	6	US-10-250-581-1
11	26	89.7	770	6	US-10-982-545-15
12	26	89.7	770	6	US-10-789-273-38
13	25	86.2	660	7	US-11-186-284-125
14	25	86.2	708	6	US-10-821-234-917
15	24	82.8	229	6	US-10-131-826A-410
16	24	82.8	269	6	US-10-467-657-330
17	24	82.8	311	6	US-10-793-626-2450
18	24	82.8	400	6	US-10-793-626-1056
19	24	82.8	3623	6	US-10-995-561-593
20	23	79.3	50	6	US-10-467-657-7892
21	23	79.3	167	7	US-11-210-316-18
22	23	79.3	239	6	US-10-467-657-432
23	23	79.3	265	6	US-10-793-626-2500
24	23	79.3	347	6	US-10-467-657-2014
25	23	79.3	402	6	US-10-467-657-9070
26	23	79.3	402	6	US-10-467-657-9070
27	23	79.3	402	6	US-10-467-657-9070
28	23	79.3	402	6	US-10-467-657-9070
29	23	79.3	402	6	US-10-467-657-9070
30	23	79.3	402	6	US-10-467-657-9070
31	23	79.3	402	6	US-10-467-657-9070
32	23	79.3	402	6	US-10-467-657-9070
33	23	79.3	402	6	US-10-467-657-9070
34	23	79.3	402	6	US-10-467-657-9070
35	23	79.3	402	6	US-10-467-657-9070
36	23	79.3	402	6	US-10-467-657-9070
37	23	79.3	402	6	US-10-467-657-9070
38	23	79.3	402	6	US-10-467-657-9070
39	23	79.3	402	6	US-10-467-657-9070
40	23	79.3	402	6	US-10-467-657-9070
41	23	79.3	402	6	US-10-467-657-9070
42	23	79.3	402	6	US-10-467-657-9070
43	23	79.3	402	6	US-10-467-657-9070
44	23	79.3	402	6	US-10-467-657-9070
45	23	79.3	402	6	US-10-467-657-9070
46	23	79.3	402	6	US-10-467-657-9070
47	23	79.3	402	6	US-10-467-657-9070
48	23	79.3	402	6	US-10-467-657-9070
49	23	79.3	402	6	US-10-467-657-9070
50	23	79.3	402	6	US-10-467-657-9070
51	23	79.3	402	6	US-10-467-657-9070
52	23	79.3	402	6	US-10-467-657-9070
53	23	79.3	402	6	US-10-467-657-9070
54	23	79.3	402	6	US-10-467-657-9070
55	23	79.3	402	6	US-10-467-657-9070
56	23	79.3	402	6	US-10-467-657-9070
57	23	79.3	402	6	US-10-467-657-9070
58	23	79.3	402	6	US-10-467-657-9070
59	23	79.3	402	6	US-10-467-657-9070
60	23	79.3	402	6	US-10-467-657-9070
61	23	79.3	402	6	US-10-467-657-9070
62	23	79.3	402	6	US-10-467-657-9070
63	23	79.3	402	6	US-10-467-657-9070
64	23	79.3	402	6	US-10-467-657-9070
65	23	79.3	402	6	US-10-467-657-9070
66	23	79.3	402	6	US-10-467-657-9070
67	23	79.3	402	6	US-10-467-657-9070
68	23	79.3	402	6	US-10-467-657-9070
69	23	79.3	402	6	US-10-467-657-9070
70	23	79.3	402	6	US-10-467-657-9070
71	23	79.3	402	6	US-10-467-657-9070
72	23	79.3	402	6	US-10-467-657-9070
73	23	79.3	402	6	US-10-467-657-9070
74	23	79.3	402	6	US-10-467-657-9070
75	23	79.3	402	6	US-10-467-657-9070
76	23	79.3	402	6	US-10-467-657-9070
77	23	79.3	402	6	US-10-467-657-9070
78	23	79.3	402	6	US-10-467-657-9070
79	23	79.3	402	6	US-10-467-657-9070
80	23	79.3	402	6	US-10-467-657-9070
81	23	79.3	402	6	US-10-467-657-9070
82	23	79.3	402	6	US-10-467-657-9070
83	23	79.3	402	6	US-10-467-657-9070
84	23	79.3	402	6	US-10-467-657-9070
85	23	79.3	402	6	US-10-467-657-9070
86	23	79.3	402	6	US-10-467-657-9070
87	23	79.3	402	6	US-10-467-657-9070
88	23	79.3	402	6	US-10-467-657-9070
89	23	79.3	402	6	US-10-467-657-9070
90	23	79.3	402	6	US-10-467-657-9070
91	23	79.3	402	6	US-10-467-657-9070
92	23	79.3	402	6	US-10-467-657-9070
93	23	79.3	402	6	US-10-467-657-9070
94	23	79.3	402	6	US-10-467-657-9070
95	23	79.3	402	6	US-10-467-657-9070
96	23	79.3	402	6	US-10-467-657-9070
97	23	79.3	402	6	US-10-467-657-9070
98	23	79.3	402	6	US-10-467-657-9070

Sequence 2120, Ap  
Sequence 959, App  
Sequence 22, Appl  
Sequence 13, Appl  
Sequence 230, Appl  
Sequence 26, Appl  
Sequence 2, Appl  
Sequence 1, Appl  
Sequence 786, Ap  
Sequence 5436, Ap  
Sequence 2836, Ap  
Sequence 3436, Ap  
Sequence 1372, Ap  
Sequence 45, Appl  
Sequence 106, App  
Sequence 104, App  
Sequence 1930, App  
Sequence 2868, Ap  
Sequence 104, App  
Sequence 347, App  
Sequence 348, App  
Sequence 7, Appl  
Sequence 114, App  
Sequence 4746, Ap  
Sequence 9209, Ap  
Sequence 1701, Ap  
Sequence 2486, Ap  
Sequence 2420, Ap  
Sequence 2232, Ap  
Sequence 6318, Ap  
Sequence 6932, Ap  
Sequence 4, Appl  
Sequence 568, App  
Sequence 4838, Ap  
Sequence 1322, Ap  
Sequence 544, App  
Sequence 543, App  
Sequence 16, Appl  
Sequence 2476, Ap  
Sequence 2734, Ap  
Sequence 234, App  
Sequence 19, Appl  
Sequence 376, App  
Sequence 7996, Ap  
Sequence 572, App  
Sequence 836, App  
Sequence 7420, Ap  
Sequence 1, Appl  
Sequence 308, App  
Sequence 69, Appl  
Sequence 112, App  
Sequence 1075, Ap  
Sequence 678, App  
Sequence 7094, Ap  
Sequence 8028, Ap  
Sequence 76, Appl  
Sequence 7104, Ap  
Sequence 198, App  
Sequence 178, App  
Sequence 350, App  
Sequence 225, App  
Sequence 1067, Ap  
Sequence 7120, Ap  
Sequence 1673, Ap  
Sequence 94, Appl  
Sequence 2948, Ap  
Sequence 6, Appl  
Sequence 3, Appl  
Sequence 64, Appl  
Sequence 4, Appl  
Sequence 9, Appl

99	21	72.4	1165	7	US-11-192-219-2	Sequence 2, Appl	172	20	69.0	329	6	US-10-524-647-80	Sequence 80, Appl
100	21	72.4	1217	7	US-11-074-176-252	Sequence 252, App	173	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap
101	21	72.4	7968	7	US-11-186-731-5	Sequence 5, Appl	174	20	69.0	341	6	US-10-524-647-27	Sequence 27, Appl
102	20	69.0		6	US-10-250-581-14	Sequence 14, Appl	175	20	69.0	348	6	US-10-821-234-1402	Sequence 1402, Ap
103	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	176	20	69.0	355	6	US-10-454-437-102	Sequence 102, App
104	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	177	20	69.0	356	7	US-11-012-762-46	Sequence 46, Appl
105	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	178	20	69.0	362	7	US-11-012-762-62	Sequence 62, Appl
106	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	179	20	69.0	364	6	US-10-131-826A-186	Sequence 186, App
107	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	180	20	69.0	370	6	US-10-821-234-1105	Sequence 1105, App
108	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	181	20	69.0	370	7	US-11-073-605-2	Sequence 2, Appl
109	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	182	20	69.0	386	7	US-11-075-400-14	Sequence 14, Appl
110	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	183	20	69.0	386	7	US-11-012-762-44	Sequence 44, Appl
111	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	184	20	69.0	395	6	US-11-069-642-18	Sequence 18, Appl
112	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	185	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
113	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	186	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
114	20	69.0	43	7	US-11-075-400-28	Sequence 28, Appl	187	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
115	20	69.0	52	6	US-10-467-657-2216	Sequence 2216, Ap	188	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
116	20	69.0	54	6	US-10-467-657-4978	Sequence 4978, Ap	189	20	69.0	418	6	US-10-467-657-5788	Sequence 5788, Ap
117	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	190	20	69.0	423	6	US-10-525-710-44	Sequence 44, Appl
118	20	69.0	76	6	US-10-467-657-5690	Sequence 5690, Ap	191	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, Ap
119	20	69.0	80	6	US-10-986-501-200	Sequence 200, App	192	20	69.0	443	6	US-10-793-626-1860	Sequence 1860, Ap
120	20	69.0	86	6	US-10-467-657-3962	Sequence 3962, Ap	193	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
121	20	69.0	91	6	US-10-821-234-1703	Sequence 1703, Ap	194	20	69.0	445	6	US-10-454-437-312	Sequence 312, App
122	20	69.0	98	6	US-10-467-657-3376	Sequence 3376, Ap	195	20	69.0	445	7	US-11-082-389-376	Sequence 376, App
123	20	69.0	107	6	US-10-467-657-2102	Sequence 2102, Ap	196	20	69.0	445	7	US-11-082-389-376	Sequence 376, App
124	20	69.0	115	6	US-10-793-626-1554	Sequence 1554, Ap	197	20	69.0	456	6	US-10-467-657-4150	Sequence 4150, Ap
125	20	69.0	115	6	US-10-432-483-10	Sequence 10, Appl	198	20	69.0	456	6	US-10-467-657-6352	Sequence 6352, Ap
126	20	69.0	123	6	US-10-793-626-430	Sequence 430, App	199	20	69.0	463	6	US-10-467-657-7604	Sequence 7604, Ap
127	20	69.0	133	6	US-10-467-657-5166	Sequence 5166, Ap	200	20	69.0	465	6	US-10-793-626-2928	Sequence 2928, Ap
128	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	201	20	69.0	475	7	US-11-180-997-4	Sequence 4, Appl
129	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appl	202	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appl
130	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appl	203	20	69.0	489	6	US-10-467-657-7846	Sequence 7846, Ap
131	20	69.0	134	6	US-10-793-626-2374	Sequence 2374, Ap	204	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
132	20	69.0	137	6	US-10-793-626-530	Sequence 530, App	205	20	69.0	492	6	US-10-793-626-770	Sequence 770, App
133	20	69.0	139	6	US-10-467-657-5728	Sequence 5728, Ap	206	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appl
134	20	69.0	164	6	US-10-793-626-2478	Sequence 2478, Ap	207	20	69.0	496	7	US-11-067-121-12	Sequence 12, Appl
135	20	69.0	165	6	US-10-467-657-4990	Sequence 4990, Ap	208	20	69.0	508	7	US-11-075-185-26	Sequence 26, Appl
136	20	69.0	175	6	US-10-965-694-23	Sequence 23, Appl	209	20	69.0	522	6	US-10-995-561-1030	Sequence 1030, Ap
137	20	69.0	182	6	US-10-467-657-3510	Sequence 3510, Ap	210	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
138	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	211	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
139	20	69.0	183	6	US-10-467-657-8138	Sequence 8138, Ap	212	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
140	20	69.0	186	6	US-10-793-626-630	Sequence 630, App	213	20	69.0	582	7	US-11-090-439-58	Sequence 58, Appl
141	20	69.0	200	6	US-10-524-198-2	Sequence 2, Appl	214	20	69.0	585	7	US-11-012-762-6	Sequence 6, Appl
142	20	69.0	204	6	US-11-073-605-3	Sequence 3, Appl	215	20	69.0	592	6	US-10-467-657-4888	Sequence 3, Appl
143	20	69.0	204	6	US-10-467-657-5874	Sequence 5874, Ap	216	20	69.0	601	7	US-11-103-957-3	Sequence 3, Appl
144	20	69.0	210	6	US-10-986-501-126	Sequence 126, App	217	20	69.0	615	6	US-10-995-561-940	Sequence 940, App
145	20	69.0	216	6	US-10-467-657-8102	Sequence 8102, Ap	218	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
146	20	69.0	220	6	US-10-467-657-3184	Sequence 3184, Ap	219	20	69.0	637	7	US-11-080-991-48	Sequence 48, Appl
147	20	69.0	221	6	US-10-467-657-290	Sequence 290, App	220	20	69.0	662	6	US-10-995-561-943	Sequence 943, App
148	20	69.0	221	6	US-10-467-657-5750	Sequence 5750, App	221	20	69.0	690	6	US-10-131-826A-306	Sequence 306, App
149	20	69.0	231	6	US-10-689-742-132	Sequence 132, App	222	20	69.0	702	6	US-10-995-561-942	Sequence 942, App
150	20	69.0	234	6	US-10-467-657-6144	Sequence 6144, Ap	223	20	69.0	721	6	US-10-467-9628-49	Sequence 49, Appl
151	20	69.0	272	6	US-10-632-150-46	Sequence 46, Appl	224	20	69.0	738	7	US-11-147-047-48	Sequence 48, Appl
152	20	69.0	272	6	US-11-073-457-46	Sequence 46, Appl	225	20	69.0	741	6	US-10-467-657-6266	Sequence 6266, Ap
153	20	69.0	272	7	US-11-073-460-46	Sequence 46, Appl	226	20	69.0	747	7	US-11-018-018-1	Sequence 1, Appl
154	20	69.0	288	6	US-10-467-657-1272	Sequence 1272, Ap	227	20	69.0	747	6	US-11-047-757-1	Sequence 1, Appl
155	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appl	228	20	69.0	754	6	US-10-995-561-941	Sequence 941, App
156	20	69.0	292	6	US-11-102-883-24	Sequence 24, Appl	229	20	69.0	797	6	US-10-995-561-802	Sequence 802, App
157	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	230	20	69.0	852	6	US-10-467-657-5004	Sequence 5004, Ap
158	20	69.0	296	6	US-10-965-972-8	Sequence 8, Appl	231	20	69.0	916	6	US-10-467-657-4242	Sequence 4242, Ap
159	20	69.0	296	6	US-11-012-978-7	Sequence 7, Appl	232	20	69.0	926	6	US-10-841-129-2	Sequence 2, Appl
160	20	69.0	314	7	US-11-018-018-4	Sequence 4, Appl	233	20	69.0	928	6	US-10-841-129-4	Sequence 4, Appl
161	20	69.0	314	7	US-11-047-757-4	Sequence 4, Appl	234	20	69.0	984	7	US-11-055-822-508	Sequence 508, App
162	20	69.0	315	6	US-10-524-647-25	Sequence 25, Appl	235	20	69.0	984	7	US-11-055-822-594	Sequence 594, App
163	20	69.0	317	6	US-10-995-561-798	Sequence 798, App	236	20	69.0	989	6	US-10-821-234-975	Sequence 975, App
164	20	69.0	319	6	US-10-467-657-640	Sequence 640, App	237	20	69.0	1070	6	US-11-147-047-49	Sequence 49, Appl
165	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	238	20	69.0	1278	6	US-10-995-561-952	Sequence 952, App
166	20	69.0	322	6	US-11-073-605-4	Sequence 4, Appl	239	20	69.0	1451	7	US-11-046-346-1	Sequence 1, Appl
167	20	69.0	324	6	US-10-467-657-7692	Sequence 7692, Ap	240	20	69.0	1857	7	US-11-102-217-2	Sequence 2, Appl
168	20	69.0	324	6	US-10-467-657-8440	Sequence 8440, Ap	241	20	69.0	2261	6	US-10-995-561-600	Sequence 600, App
169	20	69.0	325	6	US-10-454-437-142	Sequence 142, App	242	20	69.0	2261	7	US-11-055-309A-9	Sequence 9, Appl
170	20	69.0	329	6	US-10-524-647-2	Sequence 2, Appl	243	20	69.0	2261	7	US-11-055-309A-10	Sequence 10, Appl
171	20	69.0	329	6	US-10-524-647-23	Sequence 23, Appl	244	20	69.0	2504	6	US-10-647-956A-8	Sequence 8, Appl

```

245 19 65.5 9 6 US-10-982-891-44 Sequence 44, Appl
246 19 65.5 13 6 US-10-511-559-836 Sequence 836, App
247 19 65.5 13 6 US-10-511-559-837 Sequence 837, App
248 19 65.5 13 6 US-10-511-559-838 Sequence 838, App
249 19 65.5 13 6 US-10-511-559-839 Sequence 839, App
250 19 65.5 13 6 US-10-511-559-840 Sequence 840, App
251 19 65.5 13 6 US-10-511-559-841 Sequence 841, App
252 19 65.5 13 6 US-10-511-559-842 Sequence 842, App
253 19 65.5 19 6 US-10-467-657-8712 Sequence 8712, App
254 19 65.5 27 6 US-10-986-501-347 Sequence 347, App
255 19 65.5 28 6 US-10-250-581-2 Sequence 2, Appli
256 19 65.5 30 6 US-10-250-581-2 Sequence 2, Appli
257 19 65.5 30 6 US-10-467-657-1296 Sequence 1296, App
258 19 65.5 38 6 US-10-467-657-1296 Sequence 1296, App
259 19 65.5 40 6 US-10-250-581-3 Sequence 3, Appli
260 19 65.5 40 6 US-10-250-581-3 Sequence 3, Appli
261 19 65.5 42 6 US-10-467-657-8811 Sequence 8811, App
262 19 65.5 42 6 US-10-250-581-4 Sequence 4, Appli
263 19 65.5 42 6 US-10-250-581-4 Sequence 4, Appli
264 19 65.5 76 7 US-11-000-463-318 Sequence 318, App
265 19 65.5 76 7 US-11-000-463-318 Sequence 318, App
266 19 65.5 83 6 US-10-467-657-5366 Sequence 5366, App
267 19 65.5 95 6 US-10-467-657-2518 Sequence 2518, App
268 19 65.5 98 6 US-10-467-657-6988 Sequence 6988, App
269 19 65.5 100 7 US-11-123-896-137 Sequence 137, App
270 19 65.5 102 6 US-10-793-626-2592 Sequence 2592, App
271 19 65.5 102 6 US-10-485-788A-650 Sequence 650, App
272 19 65.5 102 7 US-11-053-076-132 Sequence 12, App
273 19 65.5 105 6 US-10-131-826A-470 Sequence 470, App
274 19 65.5 107 6 US-10-793-626-1586 Sequence 1586, App
275 19 65.5 107 6 US-10-467-657-1018 Sequence 1018, App
276 19 65.5 108 6 US-10-467-657-4266 Sequence 4266, App
277 19 65.5 114 6 US-10-821-234-1140 Sequence 1140, App
278 19 65.5 114 6 US-10-467-657-1414 Sequence 1414, App
279 19 65.5 114 6 US-10-467-657-3162 Sequence 3162, App
280 19 65.5 114 6 US-10-467-657-3754 Sequence 3754, App
281 19 65.5 114 6 US-10-467-657-5012 Sequence 5012, App
282 19 65.5 114 6 US-10-467-657-8674 Sequence 8674, App
283 19 65.5 116 6 US-10-467-657-5514 Sequence 5514, App
284 19 65.5 131 6 US-10-467-657-5308 Sequence 5308, App
285 19 65.5 137 7 US-11-193-512-31 Sequence 31, Appl
286 19 65.5 138 6 US-10-793-626-1254 Sequence 1254, App
287 19 65.5 138 7 US-11-137-465-37 Sequence 37, Appl
288 19 65.5 139 6 US-10-467-657-28 Sequence 28, Appl
289 19 65.5 139 6 US-10-467-657-8188 Sequence 8188, App
290 19 65.5 140 7 US-11-083-800-7 Sequence 7, Appli
291 19 65.5 144 6 US-10-793-626-1640 Sequence 1640, App
292 19 65.5 144 6 US-10-793-626-1358 Sequence 1358, App
293 19 65.5 156 6 US-10-467-657-1280 Sequence 1280, App
294 19 65.5 157 7 US-11-116-144-167 Sequence 167, App
295 19 65.5 160 6 US-10-793-626-750 Sequence 750, App
296 19 65.5 162 6 US-10-980-388-89 Sequence 89, Appl
297 19 65.5 186 6 US-10-467-657-3918 Sequence 3918, App
298 19 65.5 192 6 US-10-467-657-5388 Sequence 5388, App
299 19 65.5 193 7 US-11-102-240-142 Sequence 142, App
300 19 65.5

```

# ALIGNMENTS

```

RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923, 605
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322, 289

```

```

; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

```

```

Query Match 89.7%; Score 26; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

```

```

RESULT 2
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934, 818
; CURRENT FILING DATE: 2004-09-02
; PRIOR FILING DATE: 1997-12-02
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

```

```

Query Match 89.7%; Score 26; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

```

```

RESULT 3
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.

```

; APPLICANT: NGUYEN, BETH P.  
; APPLICANT: SANDERS, VIRGINIA J.  
; APPLICANT: SNOW, ALAN D.  
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS  
; FILE REFERENCE: PROTEO.P03C13  
; CURRENT APPLICATION NUMBER: US/11/016,706  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 09/962,955  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 36  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-016-706-36

Query Match 89.7%; Score 26; DB 7; Length 40;  
Best Local Similarity 83.3%; Pred. No. 5.5;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

RESULT 4  
US-11-098-674-12  
; Sequence 12, Application US/11098674  
; Publication No. US20050267029A1  
; GENERAL INFORMATION:  
; APPLICANT: Ancsin, John B.  
; APPLICANT: Elimova, Elena  
; APPLICANT: Kisilevsky, Robert  
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their  
; TITLE OF INVENTION: Identification and Use  
; FILE REFERENCE: PTQ-0066  
; CURRENT APPLICATION NUMBER: US/11/098,674  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 60/559,122  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-098-674-12

Query Match 89.7%; Score 26; DB 7; Length 40;  
Best Local Similarity 83.3%; Pred. No. 5.5;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

RESULT 5  
US-10-923-605-1  
; Sequence 1, Application US/10923605  
; Publication No. US20050249727A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004740US  
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: US/09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide  
US-10-923-605-1

Query Match 89.7%; Score 26; DB 6; Length 42;  
Best Local Similarity 83.3%; Pred. No. 5.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

RESULT 6  
US-10-934-818-1  
; Sequence 1, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide  
US-10-934-818-1

Query Match 89.7%; Score 26; DB 6; Length 42;  
Best Local Similarity 83.3%; Pred. No. 5.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

RESULT 7  
US-11-016-706-37  
; Sequence 37, Application US/11016706  
; Publication No. US20050244334A1  
; GENERAL INFORMATION:  
; APPLICANT: CASTILLO, GERARDO  
; APPLICANT: LAKE, THOMAS P.  
; APPLICANT: NGUYEN, BETH P.  
; APPLICANT: SANDERS, VIRGINIA J.  
; APPLICANT: SNOW, ALAN D.  
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS  
; FILE REFERENCE: PROTEO.P03C13  
; CURRENT APPLICATION NUMBER: US/11/016,706  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 09/962,955  
; PRIOR FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 37  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-016-706-37

Query Match 89.7%; Score 26; DB 7; Length 42;  
Best Local Similarity 83.3%; Pred. No. 5.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

RESULT 8  
US-10-934-818-6  
; Sequence 6, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide  
US-10-934-818-6

Query Match 89.7%; Score 26; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 5.9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

RESULT 9  
US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs...  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 89.7%; Score 26; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 5.9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21  
RESULT 10  
US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs...  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 89.7%; Score 26; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 5.9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

RESULT 11  
US-10-982-545-15  
; Sequence 15, Application US/10982545  
; Publication No. US20050244890A1  
; GENERAL INFORMATION:  
; APPLICANT: Davies, Huw Alun  
; APPLICANT: McGuire, James  
; APPLICANT: Simonsen, Anja Hvild  
; APPLICANT: Blennow, Kaj  
; APPLICANT: Podust, Vladimir  
; APPLICANT: CIPHERGEN Biosystems, Inc.  
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease  
; FILE REFERENCE: 016866-011550US  
; CURRENT APPLICATION NUMBER: US/10/982,545  
; CURRENT FILING DATE: 2004-11-06  
; PRIOR APPLICATION NUMBER: US 60/518,360  
; PRIOR FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US 60/526,753  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: US 60/546,423  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/547,250  
; PRIOR FILING DATE: 2004-02-23  
; PRIOR APPLICATION NUMBER: US 60/558,896  
; PRIOR FILING DATE: 2004-04-02  
; PRIOR APPLICATION NUMBER: US 60/572,617  
; PRIOR FILING DATE: 2004-05-18  
; PRIOR APPLICATION NUMBER: US 60/586,503  
; PRIOR FILING DATE: 2004-07-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease



```
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; OTHER INFORMATION: C31
US-10-982-545-15
```

```
Query Match      89.7%; Score 26; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
        |:||||
Db      687 KLVFFA 692
```

RESULT 12

```
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-38
```

```
Query Match      89.7%; Score 26; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
        |:||||
Db      687 KLVFFA 692
```

RESULT 13

```
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125
```

```
Query Match      86.2%; Score 25; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 13e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 KVVFFA 6  
 Db 531 KAVFFA 536

## RESULT 14

US-10-821-234-917  
 ; Sequence 917, Application US/10821234  
 ; Publication No. US20050255114A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Labat, Ivan  
 ; APPLICANT: Stache-Crain, Birgit  
 ; APPLICANT: Andarmani, Susan  
 ; APPLICANT: Tang, Y. Tom  
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 ; FILE REFERENCE: 821A  
 ; CURRENT APPLICATION NUMBER: US/10/821,234  
 ; CURRENT FILING DATE: 2004-04-07  
 ; PRIOR APPLICATION NUMBER: US 60/462,047  
 ; PRIOR FILING DATE: 2003-04-07  
 ; NUMBER OF SEQ ID NOS: 1704  
 ; SOFTWARE: pt\_seq\_genes Version 1.0  
 ; SEQ ID NO 917  
 ; LENGTH: 708  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-821-234-917

Query Match 86.2%; Score 25; DB 6; Length 708;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 Db 579 KAVFFA 584

## RESULT 15

US-10-131-826A-410  
 ; Sequence 410, Application US/10131826A  
 ; Publication No. US20050245730A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DePorge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C128  
 ; CURRENT APPLICATION NUMBER: US/10/131,826A  
 ; CURRENT FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: 60/049911  
 ; PRIOR FILING DATE: 1997-06-18  
 ; PRIOR APPLICATION NUMBER: 60/056974  
 ; PRIOR FILING DATE: 1997-08-26  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059115  
 ; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059122  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059184  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059263  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 60/059352  
 ; PRIOR FILING DATE: 1997-09-19  
 ; PRIOR APPLICATION NUMBER: 60/059588  
 ; PRIOR FILING DATE: 1997-09-19  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 410  
 ; LENGTH: 229  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-131-826A-410

Query Match 82.8%; Score 24; DB 6; Length 229;  
 Best Local Similarity 80.0%; Pred. No. 79;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5  
 Db 118 KVIFF 122

## RESULT 16

US-10-467-657-330  
 ; Sequence 330, Application US/10467657  
 ; Publication No. US20050260581A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SpA  
 ; APPLICANT: FONTANA Maria Rita  
 ; APPLICANT: PIZZA Mariagrazia  
 ; APPLICANT: MASNANI Vega  
 ; APPLICANT: MONACI Elisabetta  
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/467,657  
 ; CURRENT FILING DATE: 2003-08-11  
 ; PRIOR APPLICATION NUMBER: GB-0103424.8  
 ; PRIOR FILING DATE: 2001-02-12  
 ; NUMBER OF SEQ ID NOS: 9218  
 ; SOFTWARE: SeqWin99, version 1.04  
 ; SEQ ID NO 330  
 ; LENGTH: 269  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria gonorrhoeae  
 US-10-467-657-330

Query Match 82.8%; Score 24; DB 6; Length 269;  
 Best Local Similarity 80.0%; Pred. No. 92;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5  
 Db 11 KVIFF 15

## RESULT 17

US-10-793-626-2450  
 ; Sequence 2450, Application US/10793626  
 ; Publication No. US20050255478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PU3480US  
 ; CURRENT APPLICATION NUMBER: US/10/793,626  
 ; CURRENT FILING DATE: 2004-03-04  
 ; PRIOR APPLICATION NUMBER: 60/164,258

```
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2450
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2450

Query Match      82.8%; Score 24; DB 6; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VVFFA 6
Db      296 VVFFA 300

RESULT 18
US-10-793-626-1056
; Sequence 1056, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1056

Query Match      82.8%; Score 24; DB 6; Length 400;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVF 5
Db      7 KVVF 11

RESULT 19
US-10-995-561-593
; Sequence 593, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 593
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-593

Query Match      82.8%; Score 24; DB 6; Length 3623;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVF 5
Db      2544 KVIF 2548

RESULT 20
US-10-467-657-7892
; Sequence 7892, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7892
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7892

Query Match      79.3%; Score 23; DB 6; Length 50;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVF 5
Db      33 KVIF 37

RESULT 21
US-11-210-316-18
; Sequence 18, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
```

```
; NAME/KEY: UNSURE
; LOCATION: (98)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-18
```

```
Query Match 79.3%; Score 23; DB 7; Length 167;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 KVFFA 6
Db 105 VIFFA 109
```

```
RESULT 22
US-10-467-657-432
; Sequence 432, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; TITLE OF INVENTION: MONACI Elisabetta
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 432
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-432
```

```
Query Match 79.3%; Score 23; DB 6; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 KVFFA 6
Db 128 KVIFA 133
```

```
RESULT 23
US-10-793-626-2500
; Sequence 2500, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2500
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2500
```

```
Query Match 79.3%; Score 23; DB 6; Length 265;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 KVFFA 6
Db 230 KVFFMA 235
```

```
RESULT 24
US-10-467-657-2014
; Sequence 2014, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2014
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2014
```

```
Query Match 79.3%; Score 23; DB 6; Length 347;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 VFFFA 6
Db 73 IVFFA 77
```

```
RESULT 25
US-10-467-657-9070
; Sequence 9070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9070
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9070
```

```
Query Match 79.3%; Score 23; DB 6; Length 402;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
```

```
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 264 IVFFA 268

RESULT 26
US-10-467-657-2120
; Sequence 2120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2120
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2120

Query Match 79.3%; Score 23; DB 6; Length 426;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 414 IVFFA 418

RESULT 27
US-10-995-561-959
; Sequence 959, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 959
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-959

Query Match 79.3%; Score 23; DB 6; Length 481;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 275 KVVFA 280

RESULT 28
US-11-210-316-22
; Sequence 22, Application US/11210316
; Publication No. US20050282278A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (102)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-22

Query Match 79.3%; Score 23; DB 7; Length 510;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 96 VIFFA 100

RESULT 29
US-10-689-742-13
; Sequence 13, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: McCoy, John M
; APPLICANT: Lavalie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-13

Query Match 79.3%; Score 23; DB 6; Length 524;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 404 IVFFA 408

RESULT 30
US-11-210-316-26
; Sequence 26, Application US/11210316
; Publication No. US20050282278A1
```

; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; TITLE OF INVENTION: Plant Sugar Transport Proteins  
; FILE REFERENCE: B81163USDIV  
; CURRENT APPLICATION NUMBER: US/11/210,316  
; PRIOR FILING DATE: 2005-08-24  
; PRIOR APPLICATION NUMBER: US/10/051,902  
; PRIOR FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 60/083,044  
; PRIOR FILING DATE: 1998-04-24  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 26  
; LENGTH: 539  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-11-210-316-26

Query Match 79.3%; Score 23; DB 7; Length 539;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6  
Db 121 VVFFA 125

RESULT 31  
US-10-131-826A-230  
; Sequence 230, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330RIC128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 230  
; LENGTH: 677  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-230

Query Match 79.3%; Score 23; DB 6; Length 677;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6  
Db 557 VVFFA 561

RESULT 32  
US-10-873-528-2  
; Sequence 2, Application US/10873528  
; Publication No. US20050276814A1  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; CURRENT FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2233  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-2

Query Match 79.3%; Score 23; DB 6; Length 2233;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFFFA 6  
Db 1895 KVFFFA 1900

RESULT 33  
US-11-098-674-1  
; Sequence 1, Application US/11098674  
; Publication No. US20050267029A1  
; GENERAL INFORMATION:  
; APPLICANT: Ancsin, John B.  
; APPLICANT: Elimova, Elena  
; APPLICANT: Kisilevsky, Robert  
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their  
; TITLE OF INVENTION: Identification and Use  
; FILE REFERENCE: PTQ-0066  
; CURRENT APPLICATION NUMBER: US/11/098,674  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 60/559,122  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1

```
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match      75.9%; Score 22; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
Db      1 KLVFF 5

RESULT 34
US-10-467-657-7886
; Sequence 7886, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7886
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7886

Query Match      75.9%; Score 22; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      14 KVVFFA 19

RESULT 35
US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match      75.9%; Score 22; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 47;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
Db      36 KVVFF 40

RESULT 36
US-10-793-626-2836
; Sequence 2836, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2836
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2836

Query Match      75.9%; Score 22; DB 6; Length 182;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      14 KVVFFS 19

RESULT 37
US-10-467-657-3436
; Sequence 3436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3436
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3436

Query Match      75.9%; Score 22; DB 6; Length 190;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      46 KTVFFA 51
```

```

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: EGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 106
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-11-082-389-106

Query Match 75.9%; Score 22; DB 7; Length 440;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
Db 333 RVVFF 337

RESULT 41
US-10-793-626-24
; Sequence 24, Application US/10793626
; Publication No. US2005025478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-24

Query Match 75.9%; Score 22; DB 6; Length 482;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
Db 388 KVLFF 393

; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF PRE-ECLAMPSIA
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pf SEQ_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1372

Query Match 75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
Db 33 KTVFF 38

RESULT 39
US-10-957-569-45
; Sequence 45, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
; APPLICANT: COOK, Zhihong et al.
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; TITLE OF INVENTION: THEROP
; FILE REFERENCE: 2750-1577PUS3
; CURRENT APPLICATION NUMBER: US/10/957,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/950,321
; PRIOR FILING DATE: 2004-09-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-957-569-45

Query Match 75.9%; Score 22; DB 6; Length 278;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
Db 55 KVLFF 59

RESULT 40
US-11-082-389-106
; Sequence 106, Application US/11082389
; Publication No. US2005024935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
```



RESULT 42  
US-11-080-991-104  
; Sequence 104, Application US/11080991  
; Publication No. US20050266437A1  
; GENERAL INFORMATION:  
; APPLICANT: Veiby, Petter Ole  
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR  
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST  
; AND OVARIAN CANCER  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST  
; AND OVARIAN CANCER  
; FILE REFERENCE: MRI-039  
; CURRENT APPLICATION NUMBER: US/11/080,991  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: US/10/176,847  
; PRIOR FILING DATE: 2002-06-21  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 104  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-080-991-104

Query Match 75.9%; Score 22; DB 7; Length 522;  
Best Local Similarity 60.0%; Pred. No. 4.7e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6  
:|||||  
Db 260 IIFFA 264

RESULT 43  
US-10-793-626-1930  
; Sequence 1930, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PUB480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1930  
; LENGTH: 528  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1930

Query Match 75.9%; Score 22; DB 6; Length 528;  
Best Local Similarity 80.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
:|||||  
Db 477 KLVFF 481

RESULT 44  
US-10-467-657-2868  
; Sequence 2868, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2868  
; LENGTH: 533  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2868

Query Match 75.9%; Score 22; DB 6; Length 533;  
Best Local Similarity 60.0%; Pred. No. 4.8e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6  
:|||||  
Db 371 IIFFA 375

RESULT 45  
US-11-082-389-104  
; Sequence 104, Application US/11082389  
; Publication No. US20050244935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; FILE REFERENCE: BGI-131CPCN  
; CURRENT APPLICATION NUMBER: US/11/082,389  
; CURRENT FILING DATE: 2005-03-16  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 104  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-082-389-104

Query Match 75.9%; Score 22; DB 7; Length 569;  
Best Local Similarity 80.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 KVWFF 5
Db 462 RVWFF 466

RESULT 46
US-11-000-463-347
; Sequence 347, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1061
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-347

Query Match 75.9%; Score 22; DB 7; Length 1061;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVWFF 6
Db 131 KVDFFA 136

RESULT 48
US-11-075-185-7
; Sequence 7, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 3507
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-11-075-185-7

Query Match 75.9%; Score 22; DB 7; Length 3507;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVWFF 6
Db 565 KVFEFA 570

RESULT 49
US-10-510-386-114
; Sequence 114, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
```

```
/ APPLICANT: Clausen, Ib Groth
/ APPLICANT: Jorgensen, Steen Troels
/ APPLICANT: Olsen, Peter Bjarke
/ APPLICANT: Rasmussen, Michael Dolberg
/ TITLE OF INVENTION: Improved Bacillus Host Cell
/ FILE REFERENCE: 10294.204-US
/ CURRENT APPLICATION NUMBER: US/10/510,386
/ CURRENT FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 248
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 114
/ LENGTH: 83
/ TYPE: PRT
/ ORGANISM: Bacillus licheniformis
US-10-510-386-114

Query Match          72.4%; Score 21; DB 6; Length 83;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 VVFFA 6
      |:|
Db      17 VLFFA 21

RESULT 50
US-10-467-657-4746
/ Sequence 4746, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 4746
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4746

Query Match          72.4%; Score 21; DB 6; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |:|
Db      62 KIVFY 66

RESULT 51
US-10-467-657-9209
/ Sequence 9209, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 2486
/ LENGTH: 140
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9209

/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 1701
/ LENGTH: 137
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1701

Query Match          72.4%; Score 21; DB 6; Length 137;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |:|
Db      28 KVTFP 32

RESULT 53
US-10-467-657-2486
/ Sequence 2486, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 2486
/ LENGTH: 140
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2486
```

Query Match 72.4%; Score 21; DB 6; Length 140;  
Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5  
Db 89 KVIYF 93

RESULT 54  
US-10-467-657-2420  
; Sequence 2420, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2420  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2420

Query Match 72.4%; Score 21; DB 6; Length 155;  
Best Local Similarity 80.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6  
Db 18 MVFFA 22

RESULT 55  
US-10-467-657-2232  
; Sequence 2232, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2232  
; LENGTH: 179  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2232

Query Match 72.4%; Score 21; DB 6; Length 179;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
||| |

Db 107 KVVSPA 112

RESULT 56  
US-10-467-657-6318  
; Sequence 6318, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6318  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6318

Query Match 72.4%; Score 21; DB 6; Length 210;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 5  
| |||  
Db 116 KAVFF 120

RESULT 57  
US-10-467-657-6932  
; Sequence 6932, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6932  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6932

Query Match 72.4%; Score 21; DB 6; Length 211;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6  
: |||  
Db 19 LVFFA 23

RESULT 58  
US-10-131-826A-4  
; Sequence 4, Application US/10131826A  
; Publication No. US20050245730A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria A.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3330R1C128
/ CURRENT APPLICATION NUMBER: US/10/131,826A
/ CURRENT FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 4
/ LENGTH: 215
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match 72.4%; Score 21; DB 6; Length 215;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 166 LVFFA 170

RESULT 59
US-10-467-657-568
/ Sequence 568, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON Spa
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 4838
/ LENGTH: 228
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae

Query Match 72.4%; Score 21; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 156 LVFFA 160

RESULT 60
US-10-467-657-4838
/ Sequence 4838, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON Spa
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 4838
/ LENGTH: 228
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae

US-10-467-657-4838

Query Match 72.4%; Score 21; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 156 LVFFA 160

RESULT 61
US-10-821-234-1322
/ Sequence 1322, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 1322
/ LENGTH: 233
/ TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match      72.4%; Score 21; DB 6; Length 233;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VVFFA 6
Db      166 LVFFA 170

RESULT 62
US-10-995-561-544
; Sequence 544, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(266)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-995-561-544

Query Match      72.4%; Score 21; DB 6; Length 266;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVPF 5
Db      152 KVTFF 156

RESULT 63
US-10-995-561-543
; Sequence 543, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 543
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(267)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-995-561-543

Query Match      72.4%; Score 21; DB 6; Length 267;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KVVPF 5
Db      153 KVTFF 157

RESULT 64
US-11-055-822-16
; Sequence 16, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 16
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-16

Query Match      72.4%; Score 21; DB 7; Length 312;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVPF 5
Db      133 EVVFF 137

RESULT 65
US-10-793-626-2476
; Sequence 2476, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P13480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2476
; LENGTH: 330
```

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2476

Query Match 72.4%; Score 21; DB 6; Length 330;  
Best Local Similarity 60.0%; Pred. No. 5e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
|::||  
Db 3 KIMFF 7

RESULT 66  
US-10-793-626-2734  
; Sequence 2734, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: F034800S  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2734  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2734

Query Match 72.4%; Score 21; DB 6; Length 330;  
Best Local Similarity 60.0%; Pred. No. 5e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
|::||  
Db 3 KIMFF 7

RESULT 67  
US-10-485-517-234  
; Sequence 234, Application US/10485517  
; Publication No. US20050256299A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Sheffield  
; APPLICANT: Biosynexus Incorporated  
; APPLICANT: Foster, Simon  
; APPLICANT: Mond, James  
; TITLE OF INVENTION: Antigenic Polypeptides  
; FILE REFERENCE: P100629W0  
; CURRENT APPLICATION NUMBER: US/10/485,517  
; CURRENT FILING DATE: 2004-02-02  
; PRIOR APPLICATION NUMBER: GB 0118825.9  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: GB 0200349.9  
; PRIOR FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 424  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 234  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-485-517-234

Query Match 72.4%; Score 21; DB 6; Length 337;  
Best Local Similarity 80.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFF 5  
|::||  
Db 175 KVAFF 179

RESULT 68  
US-10-878-556A-19  
; Sequence 19, Application US/10878556A  
; Publication No. US20050266399A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoffmann La-Roche Inc.  
; TITLE OF INVENTION: HCV regulated protein expression  
; FILE REFERENCE: 21762  
; CURRENT APPLICATION NUMBER: US/10/878,556A  
; CURRENT FILING DATE: 2004-06-28  
; NUMBER OF SEQ ID NOS: 199  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: sw\_hum/cn03\_human  
; DATABASE ENTRY DATE: 2001-10-16  
US-10-878-556A-19

Query Match 72.4%; Score 21; DB 6; Length 338;  
Best Local Similarity 60.0%; Pred. No. 5.1e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
|::||  
Db 76 KLIFF 80

RESULT 69  
US-10-131-826A-376  
; Sequence 376, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115



```

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match      72.4%; Score 21; DB 6; Length 344;
Best Local Similarity 60.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
Db 279 KLIPF 283

RESULT 70
US-10-467-657-7996
; Sequence 7996, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 7996
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7996

Query Match      72.4%; Score 21; DB 6; Length 355;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 5 KTTFFA 10

RESULT 71
US-11-055-822-572
; Sequence 572, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor

```

```

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 572
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-572

Query Match      72.4%; Score 21; DB 7; Length 358;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 61 KIVVFA 66

RESULT 72
US-11-055-822-836
; Sequence 836, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08

```

```
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 836
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-836

Query Match          72.4%; Score 21; DB 7; Length 358;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      61 KIVVFA 66

RESULT 73
US-10-467-657-7420
; Sequence 7420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7420
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7420

Query Match          72.4%; Score 21; DB 6; Length 406;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      310 KTAFFA 315

RESULT 74
US-10-878-556A-1
; Sequence 1, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (307)..(307)
```

```
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: hsupg:006101-3-0
; DATABASE ENTRY DATE: 2003-02-16
US-10-878-556A-1

Query Match          72.4%; Score 21; DB 6; Length 414;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 VVFFA 6
Db      59 VMFFA 63

RESULT 75
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND ME
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308

Query Match          72.4%; Score 21; DB 7; Length 432;
Best Local Similarity 60.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
Db      4 KILFF 8

Search completed: December 29, 2005, 18:50:21
Job time : 4.29032 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds  
(without alignments)  
37.818 Million cell updates/sec

Title: US-10-009-122-17  
Perfected score: 29  
Sequence: 1 KVPFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29	100.0	6	3	US-09-867-847-18
2	29	100.0	6	3	US-09-867-847-26
3	29	100.0	6	3	US-09-915-092-8
4	29	100.0	6	3	US-09-915-092-16
5	29	100.0	6	3	US-09-747-408-9
6	29	100.0	6	3	US-09-747-408-17
7	29	100.0	6	5	US-10-728-028-8
8	29	100.0	6	5	US-10-728-028-16
9	29	100.0	6	5	US-10-825-958-16
10	29	100.0	6	5	US-10-825-958-24
11	29	100.0	37	4	US-10-641-924-7
12	29	100.0	37	4	US-10-642-255-7
13	29	100.0	60	4	US-10-437-963-173619
14	29	100.0	87	4	US-10-437-963-133986
15	29	100.0	109	4	US-10-437-963-105773
16	29	100.0	135	4	US-10-437-963-141578
17	29	100.0	175	4	US-10-437-963-122124
18	29	100.0	186	5	US-10-481-032A-214
19	29	100.0	186	5	US-10-481-032A-228
20	29	100.0	188	4	US-10-437-963-172476
21	29	100.0	198	4	US-10-437-963-172452
22	29	100.0	416	6	US-11-042-922-14
23	29	100.0	416	6	US-11-042-922-14
24	29	100.0	514	4	US-10-055-475-13
25	29	100.0	514	6	US-11-042-922-13
26	29	100.0	925	4	US-10-408-765A-2031
27	29	100.0	925	4	US-10-755-889-234

28	29	100.0	925	5	US-10-370-715B-8	Sequence 8, Appli
29	29	100.0	925	5	US-10-631-467-680	Sequence 680, App
30	29	100.0	925	5	US-10-631-467-747	Sequence 747, App
31	29	100.0	1144	3	US-09-870-759-124	Sequence 124, App
32	29	100.0	1144	3	US-09-751-708A-124	Sequence 124, App
33	29	100.0	1144	4	US-10-428-817A-120	Sequence 120, App
34	29	100.0	1144	5	US-10-937-758A-101	Sequence 101, App
35	29	100.0	1144	5	US-10-631-467-1388	Sequence 1388, Ap
36	29	100.0	1144	5	US-10-631-467-1464	Sequence 1464, Ap
37	29	100.0	1640	4	US-10-437-963-109646	Sequence 109646,
38	28	96.6	6	3	US-09-867-847-11	Sequence 11, Appli
39	28	96.6	6	3	US-09-867-847-19	Sequence 19, Appli
40	28	96.6	6	3	US-09-915-092-1	Sequence 1, Appli
41	28	96.6	6	3	US-09-915-092-9	Sequence 9, Appli
42	28	96.6	6	3	US-09-747-408-1	Sequence 1, Appli
43	28	96.6	6	3	US-09-747-408-10	Sequence 10, Appli
44	28	96.6	6	5	US-10-728-028-1	Sequence 1, Appli
45	28	96.6	6	5	US-10-728-028-9	Sequence 9, Appli
46	28	96.6	6	5	US-10-825-958-9	Sequence 9, Appli
47	28	96.6	6	5	US-10-825-958-17	Sequence 17, Appli
48	28	96.6	58	4	US-10-425-115-280164	Sequence 280164,
49	28	96.6	90	4	US-10-424-599-165325	Sequence 165325,
50	28	96.6	93	4	US-10-424-599-240310	Sequence 240310,
51	28	96.6	99	5	US-10-450-763-56957	Sequence 56957, A
52	27	93.1	564	6	US-11-097-143-12723	Sequence 12723, A
53	27	93.1	1443	6	US-11-097-143-32208	Sequence 32208, A
54	26	89.7	6	3	US-09-867-847-7	Sequence 7, Appli
55	26	89.7	6	3	US-09-867-847-20	Sequence 20, Appli
56	26	89.7	6	3	US-09-972-475-9	Sequence 9, Appli
57	26	89.7	6	3	US-09-915-092-10	Sequence 10, Appli
58	26	89.7	6	3	US-09-915-092-28	Sequence 28, Appli
59	26	89.7	6	3	US-09-956-825-25	Sequence 25, Appli
60	26	89.7	6	3	US-09-747-408-3	Sequence 3, Appli
61	26	89.7	6	3	US-09-747-408-11	Sequence 11, Appli
62	26	89.7	6	4	US-10-463-729-9	Sequence 9, Appli
63	26	89.7	6	5	US-10-728-028-10	Sequence 10, Appli
64	26	89.7	6	5	US-10-728-028-27	Sequence 27, Appli
65	26	89.7	6	5	US-10-728-028-28	Sequence 28, Appli
66	26	89.7	6	5	US-10-825-958-7	Sequence 7, Appli
67	26	89.7	6	5	US-10-825-958-18	Sequence 18, Appli
68	26	89.7	6	5	US-10-666-095-3	Sequence 3, Appli
69	26	89.7	7	3	US-09-867-847-12	Sequence 12, Appli
70	26	89.7	7	3	US-09-867-847-27	Sequence 27, Appli
71	26	89.7	7	3	US-09-867-847-28	Sequence 28, Appli
72	26	89.7	7	3	US-09-972-475-7	Sequence 7, Appli
73	26	89.7	7	3	US-09-915-092-2	Sequence 2, Appli
74	26	89.7	7	3	US-09-915-092-17	Sequence 17, Appli
75	26	89.7	7	3	US-09-915-092-18	Sequence 18, Appli
76	26	89.7	7	3	US-09-915-092-18	Sequence 18, Appli
77	26	89.7	7	3	US-09-747-408-18	Sequence 18, Appli
78	26	89.7	7	3	US-09-747-408-19	Sequence 19, Appli
79	26	89.7	7	4	US-10-463-729-7	Sequence 7, Appli
80	26	89.7	7	5	US-10-728-028-2	Sequence 2, Appli
81	26	89.7	7	5	US-10-728-028-17	Sequence 17, Appli
82	26	89.7	7	5	US-10-728-028-18	Sequence 18, Appli
83	26	89.7	7	5	US-10-825-958-10	Sequence 10, Appli
84	26	89.7	7	5	US-10-825-958-25	Sequence 25, Appli
85	26	89.7	7	5	US-10-825-958-26	Sequence 26, Appli
86	26	89.7	7	5	US-10-810-881A-128	Sequence 128, App
87	26	89.7	7	5	US-10-505-313-269	Sequence 269, App
88	26	89.7	8	3	US-09-850-061A-44	Sequence 44, Appli
89	26	89.7	8	3	US-09-972-475-5	Sequence 5, Appli
90	26	89.7	8	4	US-10-235-483-1	Sequence 1, Appli
91	26	89.7	8	4	US-10-463-729-5	Sequence 5, Appli
92	26	89.7	8	4	US-10-281-092-42	Sequence 42, Appli
93	26	89.7	8	4	US-10-721-774-44	Sequence 44, Appli
94	26	89.7	8	5	US-10-810-881A-125	Sequence 125, App
95	26	89.7	8	5	US-10-817-979-73	Sequence 73, Appli
96	26	89.7	9	3	US-09-867-847-9	Sequence 9, Appli
97	26	89.7	9	3	US-09-899-815-2	Sequence 2, Appli
98	26	89.7	9	3	US-09-747-408-20	Sequence 20, Appli
99	26	89.7	9	4	US-10-235-483-64	Sequence 64, Appli
100	26	89.7	9	4	US-10-619-454-3	Sequence 3, Appli

101	26	89.7	9	4	US-10-619-454-25	Sequence 25, Appl	174	26	89.7	12	6	US-11-012-797A-33	Sequence 33, Appl
102	26	89.7	9	4	US-10-619-454-28	Sequence 28, Appl	175	26	89.7	13	4	US-10-281-458-1	Sequence 1, Appl
103	26	89.7	9	4	US-10-619-454-57	Sequence 57, Appl	176	26	89.7	13	5	US-10-625-854-127	Sequence 127, App
104	26	89.7	9	4	US-10-619-454-157	Sequence 157, App	177	26	89.7	13	5	US-10-625-854-140	Sequence 140, App
105	26	89.7	10	3	US-09-867-847-29	Sequence 29, Appl	178	26	89.7	14	3	US-09-992-800-5	Sequence 5, Appl
106	26	89.7	10	3	US-09-915-092-19	Sequence 19, Appl	179	26	89.7	14	3	US-09-992-994-5	Sequence 5, Appl
107	26	89.7	10	3	US-10-889-999-20	Sequence 20, Appl	180	26	89.7	14	3	US-10-385-065-5	Sequence 5, Appl
108	26	89.7	10	5	US-10-889-999-21	Sequence 21, Appl	181	26	89.7	14	5	US-10-810-881A-114	Sequence 114, App
109	26	89.7	10	5	US-10-889-999-22	Sequence 22, Appl	182	26	89.7	14	5	US-10-505-313-2	Sequence 2, Appl
110	26	89.7	10	5	US-10-889-999-23	Sequence 23, Appl	183	26	89.7	14	5	US-10-625-854-115	Sequence 115, App
111	26	89.7	10	5	US-10-889-999-24	Sequence 24, Appl	184	26	89.7	14	5	US-10-625-854-128	Sequence 128, App
112	26	89.7	10	5	US-10-890-070-20	Sequence 20, Appl	185	26	89.7	14	5	US-10-625-854-141	Sequence 141, App
113	26	89.7	10	5	US-10-890-070-21	Sequence 21, Appl	186	26	89.7	14	6	US-11-063-350-5	Sequence 5, Appl
114	26	89.7	10	5	US-10-890-070-22	Sequence 22, Appl	187	26	89.7	14	6	US-09-972-475-14	Sequence 14, Appl
115	26	89.7	10	5	US-10-890-070-23	Sequence 23, Appl	188	26	89.7	15	3	US-09-996-357-9	Sequence 9, Appl
116	26	89.7	10	5	US-10-890-070-24	Sequence 24, Appl	189	26	89.7	15	4	US-10-235-483-56	Sequence 56, Appl
117	26	89.7	10	5	US-10-890-000-20	Sequence 20, Appl	190	26	89.7	15	4	US-10-235-483-57	Sequence 57, Appl
118	26	89.7	10	5	US-10-890-000-21	Sequence 21, Appl	191	26	89.7	15	4	US-10-235-483-58	Sequence 58, Appl
119	26	89.7	10	5	US-10-890-000-22	Sequence 22, Appl	192	26	89.7	15	4	US-10-235-483-60	Sequence 60, Appl
120	26	89.7	10	5	US-10-890-000-23	Sequence 23, Appl	193	26	89.7	15	4	US-10-235-483-61	Sequence 61, Appl
121	26	89.7	10	5	US-10-890-000-24	Sequence 24, Appl	194	26	89.7	15	4	US-10-235-483-62	Sequence 62, Appl
122	26	89.7	10	5	US-10-823-463-20	Sequence 20, Appl	195	26	89.7	15	4	US-10-235-483-63	Sequence 63, Appl
123	26	89.7	10	5	US-10-823-463-21	Sequence 21, Appl	196	26	89.7	15	4	US-10-235-483-65	Sequence 65, Appl
124	26	89.7	10	5	US-10-823-463-22	Sequence 22, Appl	197	26	89.7	15	4	US-10-463-729-14	Sequence 14, Appl
125	26	89.7	10	5	US-10-823-463-23	Sequence 23, Appl	198	26	89.7	15	5	US-10-625-854-103	Sequence 103, App
126	26	89.7	10	5	US-10-823-463-24	Sequence 24, Appl	199	26	89.7	15	5	US-10-625-854-116	Sequence 116, App
127	26	89.7	10	5	US-10-728-028-19	Sequence 19, Appl	200	26	89.7	15	5	US-10-625-854-129	Sequence 129, App
128	26	89.7	10	5	US-10-822-968-20	Sequence 20, Appl	201	26	89.7	15	5	US-10-625-854-142	Sequence 142, App
129	26	89.7	10	5	US-10-822-968-21	Sequence 21, Appl	202	26	89.7	16	5	US-10-625-854-91	Sequence 91, Appl
130	26	89.7	10	5	US-10-822-968-22	Sequence 22, Appl	203	26	89.7	16	5	US-10-625-854-104	Sequence 104, App
131	26	89.7	10	5	US-10-822-968-23	Sequence 23, Appl	204	26	89.7	16	5	US-10-625-854-117	Sequence 117, App
132	26	89.7	10	5	US-10-822-968-24	Sequence 24, Appl	205	26	89.7	16	5	US-10-625-854-130	Sequence 130, App
133	26	89.7	10	5	US-10-777-792-20	Sequence 20, Appl	206	26	89.7	16	5	US-10-625-854-143	Sequence 143, App
134	26	89.7	10	5	US-10-777-792-21	Sequence 21, Appl	207	26	89.7	17	3	US-09-992-800-3	Sequence 3, Appl
135	26	89.7	10	5	US-10-777-792-22	Sequence 22, Appl	208	26	89.7	17	3	US-09-992-994-3	Sequence 3, Appl
136	26	89.7	10	5	US-10-777-792-23	Sequence 23, Appl	209	26	89.7	17	3	US-09-998-491-8	Sequence 8, Appl
137	26	89.7	10	5	US-10-777-792-24	Sequence 24, Appl	210	26	89.7	17	4	US-10-385-065-3	Sequence 3, Appl
138	26	89.7	10	5	US-10-825-958-27	Sequence 27, Appl	211	26	89.7	17	4	US-10-451-367-26	Sequence 26, Appl
139	26	89.7	10	5	US-10-890-071-20	Sequence 20, Appl	212	26	89.7	17	4	US-10-475-281-8	Sequence 8, Appl
140	26	89.7	10	5	US-10-890-071-21	Sequence 21, Appl	213	26	89.7	17	4	US-10-810-919-3	Sequence 3, Appl
141	26	89.7	10	5	US-10-890-071-22	Sequence 22, Appl	214	26	89.7	17	5	US-10-684-346-24	Sequence 24, Appl
142	26	89.7	10	5	US-10-890-071-23	Sequence 23, Appl	215	26	89.7	17	5	US-10-997-078-46	Sequence 46, Appl
143	26	89.7	10	5	US-10-890-071-24	Sequence 24, Appl	216	26	89.7	17	5	US-10-997-700-19	Sequence 19, Appl
144	26	89.7	10	5	US-10-890-024-20	Sequence 20, Appl	217	26	89.7	17	6	US-11-063-350-3	Sequence 3, Appl
145	26	89.7	10	5	US-10-890-024-21	Sequence 21, Appl	218	26	89.7	17	6	US-11-066-697-950	Sequence 950, App
146	26	89.7	10	5	US-10-890-024-22	Sequence 22, Appl	219	26	89.7	17	6	US-11-066-697-983	Sequence 983, App
147	26	89.7	10	5	US-10-890-024-23	Sequence 23, Appl	220	26	89.7	19	3	US-09-825-242-5	Sequence 5, Appl
148	26	89.7	10	5	US-10-890-024-24	Sequence 24, Appl	221	26	89.7	19	4	US-10-429-216-5	Sequence 5, Appl
149	26	89.7	10	5	US-10-928-926-20	Sequence 20, Appl	222	26	89.7	19	4	US-10-816-022-5	Sequence 5, Appl
150	26	89.7	10	5	US-10-928-926-21	Sequence 21, Appl	223	26	89.7	19	4	US-10-816-529-5	Sequence 5, Appl
151	26	89.7	10	5	US-10-928-926-22	Sequence 22, Appl	224	26	89.7	19	4	US-10-815-353-5	Sequence 5, Appl
152	26	89.7	10	5	US-10-928-926-23	Sequence 23, Appl	225	26	89.7	19	4	US-10-815-391-5	Sequence 5, Appl
153	26	89.7	10	5	US-10-928-926-24	Sequence 24, Appl	226	26	89.7	19	5	US-10-828-548-5	Sequence 5, Appl
154	26	89.7	10	6	US-11-058-757-20	Sequence 20, Appl	227	26	89.7	19	5	US-10-816-380-5	Sequence 5, Appl
155	26	89.7	10	6	US-11-058-757-21	Sequence 21, Appl	228	26	89.7	19	5	US-10-889-999-75	Sequence 75, Appl
156	26	89.7	10	6	US-11-058-757-22	Sequence 22, Appl	229	26	89.7	19	5	US-10-890-070-75	Sequence 75, Appl
157	26	89.7	10	6	US-11-058-757-23	Sequence 23, Appl	230	26	89.7	19	5	US-10-890-000-75	Sequence 75, Appl
158	26	89.7	10	6	US-11-058-757-24	Sequence 24, Appl	231	26	89.7	19	5	US-10-788-666-5	Sequence 5, Appl
159	26	89.7	11	3	US-09-988-842-9	Sequence 9, Appl	232	26	89.7	19	5	US-10-923-471-5	Sequence 5, Appl
160	26	89.7	11	3	US-09-988-842-25	Sequence 25, Appl	233	26	89.7	19	5	US-10-823-463-75	Sequence 75, Appl
161	26	89.7	11	4	US-10-235-483-14	Sequence 14, Appl	234	26	89.7	19	5	US-10-923-469-5	Sequence 5, Appl
162	26	89.7	11	4	US-10-050-200-33	Sequence 33, Appl	235	26	89.7	19	5	US-10-933-559-5	Sequence 5, Appl
163	26	89.7	11	4	US-10-237-673-20	Sequence 20, Appl	236	26	89.7	19	5	US-10-815-404-5	Sequence 5, Appl
164	26	89.7	11	5	US-10-464-117-13	Sequence 13, Appl	237	26	89.7	19	5	US-10-934-609-5	Sequence 5, Appl
165	26	89.7	11	5	US-10-772-230-9	Sequence 9, Appl	238	26	89.7	19	5	US-10-923-474-5	Sequence 5, Appl
166	26	89.7	11	3	US-10-772-230-25	Sequence 25, Appl	239	26	89.7	19	5	US-10-884-892-5	Sequence 5, Appl
167	26	89.7	12	3	US-09-867-847-8	Sequence 8, Appl	240	26	89.7	19	5	US-10-822-968-75	Sequence 75, Appl
168	26	89.7	12	4	US-10-481-180-671	Sequence 671, App	241	26	89.7	19	5	US-10-777-792-75	Sequence 75, Appl
169	26	89.7	12	5	US-10-810-881A-115	Sequence 115, App	242	26	89.7	19	5	US-10-890-071-75	Sequence 75, Appl
170	26	89.7	12	5	US-10-810-881A-117	Sequence 117, App	243	26	89.7	19	5	US-10-890-024-75	Sequence 75, Appl
171	26	89.7	12	5	US-10-508-586-2	Sequence 2, Appl	244	26	89.7	19	5	US-10-934-818-5	Sequence 5, Appl
172	26	89.7	12	5	US-10-508-586-3	Sequence 3, Appl	245	26	89.7	19	5	US-10-923-267-5	Sequence 5, Appl
173	26	89.7	12	5	US-10-625-854-139	Sequence 139, App	246	26	89.7	19	5	US-10-928-926-75	Sequence 75, Appl

247 Sequence 75, Appl  
248 Sequence 5, Appl  
249 Sequence 25, Appl  
250 Sequence 710, Appl  
251 Sequence 25, Appl  
252 Sequence 25, Appl  
253 Sequence 25, Appl  
254 Sequence 25, Appl  
255 Sequence 25, Appl  
256 Sequence 25, Appl  
257 Sequence 6, Appl  
258 Sequence 724, Appl  
259 Sequence 11, Appl  
260 Sequence 11, Appl  
261 Sequence 4, Appl  
262 Sequence 66, Appl  
263 Sequence 5, Appl  
264 Sequence 5, Appl  
265 Sequence 2, Appl  
266 Sequence 7, Appl  
267 Sequence 4, Appl  
268 Sequence 36, Appl  
269 Sequence 7, Appl  
270 Sequence 735, Appl  
271 Sequence 4, Appl  
272 Sequence 4, Appl  
273 Sequence 66, Appl  
274 Sequence 4, Appl  
275 Sequence 3, Appl  
276 Sequence 959, Appl  
277 Sequence 965, Appl  
278 Sequence 976, Appl  
279 Sequence 992, Appl  
280 Sequence 1003, Appl  
281 Sequence 1, Appl  
282 Sequence 1, Appl  
283 Sequence 1, Appl  
284 Sequence 5, Appl  
285 Sequence 24, Appl  
286 Sequence 1, Appl  
287 Sequence 5, Appl  
288 Sequence 99, Appl  
289 Sequence 295, Appl  
290 Sequence 84, Appl  
291 Sequence 85, Appl  
292 Sequence 98, Appl  
293 Sequence 95, Appl  
294 Sequence 85, Appl  
295 Sequence 295, Appl  
296 Sequence 746, Appl  
297 Sequence 3, Appl  
298 Sequence 16, Appl  
299 Sequence 16, Appl  
300 Sequence 3, Appl

## ALIGNMENTS

RESULT-1  
US-09-867-847-18  
; Sequence 18, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867, 847  
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-09-867-847-18

Query Match 100.0%; Score 29; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 1 KVVFFA 6

## RESULT 2

US-09-867-847-26  
; Sequence 26, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; NAME/KEY: MOD\_RBS  
; LOCATION: (6)  
; OTHER INFORMATION: AMIDATION  
US-09-867-847-26

Query Match 100.0%; Score 29; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 1 KVVFFA 6

## RESULT 3

US-09-915-092-8  
; Sequence 8, Application US/09915092  
; Publication No. US20020115717A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Chalfour, Robert

```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-8

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      1 KVVFFA 6

RESULT 4
US-09-915-092-16
; Sequence 16, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-16

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      1 KVVFFA 6

RESULT 5
US-09-747-408-9
; Sequence 9, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      1 KVVFFA 6

RESULT 6
US-09-747-408-17
; Sequence 17, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      1 KVVFFA 6

RESULT 7
US-10-728-028-8
; Sequence 8, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-8

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |||||
Db 1 KVVFFA 6

RESULT 8
US-10-728-028-16
; Sequence 16, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6.
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-16

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |||||
Db 1 KVVFFA 6

RESULT 9
US-10-825-958-16
; Sequence 16, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6.
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-16

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |||||
Db 1 KVVFFA 6

RESULT 11
US-10-641-924-7
; Sequence 7, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE OF INVENTION: 5303SAUSM1
; FILE REFERENCE: 5303SAUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
; SEQ ID NO 16
```

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-16

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |||||
Db 1 KVVFFA 6

RESULT 10
US-10-825-958-24
; Sequence 24, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-24

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |||||
Db 1 KVVFFA 6

RESULT 11
US-10-641-924-7
; Sequence 7, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE OF INVENTION: 5303SAUSM1
; FILE REFERENCE: 5303SAUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
; SEQ ID NO 16
```



```
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-924-7

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
    |||||
Db 18 KVVFFA 23

RESULT 12
US-10-642-255-7
; Sequence 7, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyi, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-255-7

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
    |||||
Db 18 KVVFFA 23

RESULT 13
US-10-437-963-173619
; Sequence 173619, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173619
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
```

```
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71639C.1.pep
US-10-437-963-173619

Query Match      100.0%; Score 29; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
    |||||
Db 4 KVVFFA 9

RESULT 14
US-10-437-963-133986
; Sequence 133986, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133986
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35803C.1.pep
US-10-437-963-133986

Query Match      100.0%; Score 29; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
    |||||
Db 6 KVVFFA 11

RESULT 15
US-10-437-963-105773
; Sequence 105773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105773
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
```

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102988C.1.pep  
US-10-437-963-105773

Query Match 100.0%; Score 29; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
| | | | |  
Db 4 KVVFFA 9

## RESULT 16

US-10-437-963-141578

; Sequence 141578, Application US/10437963  
; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 141578

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_42668C.1.pep

US-10-437-963-141578

Query Match 100.0%; Score 29; DB 4; Length 135;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
| | | | |  
Db 4 KVVFFA 9

## RESULT 17

US-10-437-963-122124

; Sequence 122124, Application US/10437963  
; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 122124

; LENGTH: 175

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(175)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_25081C.1.pep  
US-10-437-963-122124

Query Match 100.0%; Score 29; DB 4; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
| | | | |  
Db 4 KVVFFA 9

## RESULT 18

US-10-481-032A-214

; Sequence 214, Application US/10481032A  
; Publication No. US20050177901A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Cheng, Wenqiong

; APPLICANT: Briggs, Steven

; APPLICANT: Cooper, Bret

; APPLICANT: Goff, Stephen A.

; APPLICANT: Moughamer, Todd

; APPLICANT: Glazebrook, Jane

; APPLICANT: Katagiri, Fumiaki

; APPLICANT: Kreps, Joel

; APPLICANT: Provart, Nicolas

; APPLICANT: Ricke, Darrell

; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES  
; FILE REFERENCE: 60148USPCT

; CURRENT APPLICATION NUMBER: US/10/481.032A

; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 60/300,112

; PRIOR FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: US 60/325,277

; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: US 60/342,327

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: PCT/IB02/02450

; PRIOR FILING DATE: 2002-06-21

; NUMBER OF SEQ ID NOS: 1201

; SOFTWARE: PatentIn Ver. 2.2

; SEQ ID NO 214

; LENGTH: 186

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-481-032A-214

Query Match 100.0%; Score 29; DB 5; Length 186;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
| | | | |  
Db 4 KVVFFA 9

## RESULT 19

US-10-481-032A-228

; Sequence 228, Application US/10481032A  
; Publication No. US20050177901A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Cheng, Wenqiong

; APPLICANT: Briggs, Steven

; APPLICANT: Cooper, Bret

; APPLICANT: Goff, Stephen A.

; APPLICANT: Moughamer, Todd

; APPLICANT: Glazebrook, Jane

; APPLICANT: Katagiri, Fumiaki

```
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-228
```

```
Query Match 100.0%; Score 29; DB 5; Length 186;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
Db 4 KVVFFA 9
```

```
RESULT 20
US-10-437-963-172476
; Sequence 172476, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172476
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(188)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70608C.1.pap
US-10-437-963-172476
```

```
Query Match 100.0%; Score 29; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
Db 4 KVVFFA 9
```

RESULT 21

```
US-10-437-963-172452
; Sequence 172452, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172452
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70587C.1.pap
US-10-437-963-172452
```

```
Query Match 100.0%; Score 29; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
Db 4 KVVFFA 9
```

```
RESULT 22
US-10-055-475-14
; Sequence 14, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopaikrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-055-475-14
```

```
Query Match 100.0%; Score 29; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
Db 57 KVVFFA 62
```



```
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 234
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-234

Query Match          100.0%; Score 29; DB 4; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 28
US-10-370-715B-8
; Sequence 8, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patent Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: F1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 8
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-8

Query Match          100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 29
US-10-631-467-680
; Sequence 680, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive P
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
```

```
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-680

Query Match          100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 30
US-10-631-467-747
; Sequence 747, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive ;
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 747
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-747

Query Match          100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 31
US-09-870-759-124
; Sequence 124, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-124

Query Match          100.0%; Score 29; DB 3; Length 1144;
```

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 32  
US-09-751-708A-124  
; Sequence 124, Application US/09751708A  
; Publication No. US20030157113A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 751708  
; CURRENT APPLICATION NUMBER: US/09/751,708A  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 60/173,371  
; PRIOR FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 124  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-751-708A-124

Query Match 100.0%; Score 29; DB 3; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 33  
US-10-428-817A-120  
; Sequence 120, Application US/10428817A  
; Publication No. US20040214783A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 38373-189118  
; CURRENT APPLICATION NUMBER: US/10/428,817A  
; CURRENT FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: US 60/378,988  
; PRIOR FILING DATE: 2002-05-08  
; PRIOR APPLICATION NUMBER: US 60/389,366  
; PRIOR FILING DATE: 2002-06-15  
; PRIOR APPLICATION NUMBER: US 60/406,697  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: US 60/406,750  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/415,310  
; PRIOR FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: US 60/415,400  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: US 60/438,686  
; PRIOR FILING DATE: 2003-01-09  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 120  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-428-817A-120

Query Match 100.0%; Score 29; DB 4; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 34  
US-10-937-758A-101  
; Sequence 101, Application US/10937758A  
; Publication No. US20050112141A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 650884  
; CURRENT APPLICATION NUMBER: US/10/937,758A  
; CURRENT FILING DATE: 2004-09-08  
; PRIOR APPLICATION NUMBER: 09/650,884  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 101  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-937-758A-101

Query Match 100.0%; Score 29; DB 5; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 35  
US-10-631-467-1388  
; Sequence 1388, Application US/10631467  
; Publication No. US20050208496A1  
; GENERAL INFORMATION:  
; APPLICANT: Genox Research Inc.  
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive  
; FILE REFERENCE: 3462.1005-000  
; CURRENT APPLICATION NUMBER: US/10/631,467  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: JP 2003-077212  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: JP 2002-229312  
; PRIOR FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 2086  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1388  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-631-467-1388

Query Match 100.0%; Score 29; DB 5; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 36  
US-10-631-467-1464  
; Sequence 1464, Application US/10631467  
; Publication No. US20050208496A1  
; GENERAL INFORMATION:  
; APPLICANT: Genox Research Inc.  
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive

```
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1464
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1464

Query Match          100.0%; Score 29; DB 5; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      514 KVVFFA 519

RESULT 37
US-10-437-963-109646
; Sequence 109646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109646
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13784C.1.pep
US-10-437-963-109646

Query Match          100.0%; Score 29; DB 4; Length 1640;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      1596 KVVFFA 1601

RESULT 38
US-09-867-847-11
; Sequence 11, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP

; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 39
US-09-867-847-19
; Sequence 19, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 40
US-09-915-092-1
; Sequence 1, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
```



; APPLICANT: Kong, Xianqi  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: NBI-139  
; CURRENT APPLICATION NUMBER: US/09/915,092  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220,808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-092-1

Query Match 96.6%; Score 28; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6  
|:||||  
Db 1 KIVFFA 6

## RESULT 41

US-09-915-092-9  
; Sequence 9, Application US/09915092  
; Publication No. US2002011571A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: NBI-139  
; CURRENT APPLICATION NUMBER: US/09/915,092  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220,808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-092-9

Query Match 96.6%; Score 28; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6  
|:||||  
Db 1 KIVFFA 6

## RESULT 42

US-09-747-408-1  
; Sequence 1, Application US/09747408  
; Publication No. US2003003141A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877

; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-408-1

Query Match 96.6%; Score 28; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6  
|:||||  
Db 1 KIVFFA 6

## RESULT 43

US-09-747-408-10  
; Sequence 10, Application US/09747408  
; Publication No. US2003003141A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-408-10

Query Match 96.6%; Score 28; DB 3; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6  
|:||||  
Db 1 KIVFFA 6

## RESULT 44

US-10-728-028-1  
; Sequence 1, Application US/10728028  
; Publication No. US2005004800A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: NBI-139CP  
; CURRENT APPLICATION NUMBER: US/10/728,028  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: 60/443291  
; PRIOR FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: 09/915092  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 6

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1
```

```
Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:|||||
Db      1 KIVFFA 6
```

```
RESULT 45
US-10-728-028-9
; Sequence 9, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR FILING DATE: 2003-01-29
; PRIOR FILING DATE: 2001-07-24
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9
```

```
Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:|||||
Db      1 KIVFFA 6
```

```
RESULT 46
US-10-825-958-9
; Sequence 9, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-9
```

```
Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:|||||
Db      1 KIVFFA 6
```

```
RESULT 47
US-10-825-958-17
; Sequence 17, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-17
```

```
Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:|||||
Db      1 KIVFFA 6
```

```
RESULT 48
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
```

```
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280164
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_187087C.1.pep
US-10-425-115-280164

Query Match          96.6%; Score 28; DB 4; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 28 KIVFFA 33

RESULT 49
US-10-424-599-165325
; Sequence 165325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424.599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pep
US-10-424-599-165325

Query Match          96.6%; Score 28; DB 4; Length 90;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 21 KIVFFA 26

RESULT 50
US-10-424-599-240310
; Sequence 240310, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424.599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep
```

```
US-10-424-599-240310

Query Match          96.6%; Score 28; DB 4; Length 93;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 34 KIVFFA 39

RESULT 51
US-10-450-763-56957
; Sequence 56957, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450.763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-56957

Query Match          96.6%; Score 28; DB 5; Length 99;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 63 KIVFFA 68

RESULT 52
US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
```

```
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match      93.1%; Score 27; DB 6; Length 564;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
        |::|||
DB      53 KIIFFA 58
```

```
RESULT 53
US-11-097-143-32208
; Sequence 32208, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32208
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32208
```

```
Query Match      93.1%; Score 27; DB 6; Length 1443;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
        |::|||
DB     1204 KIIFFA 1209
```

```
RESULT 54
US-09-867-847-7
; Sequence 7, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-7
```

```
Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
        |::|||
DB      1 KLVFFA 6
```

```
RESULT 55
US-09-867-847-20
; Sequence 20, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-20
```

```
Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:|||||
Db      1 KLVFFA 6

RESULT 56
US-09-972-475-9
; Sequence 9, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-972-475-9

      Query Match      89.7%; Score 26; DB 3; Length 6;
      Best Local Similarity 83.3%; Pred. No. 1.7e+06;
      Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      1 KLVFFA 6

RESULT 57
US-09-915-092-10
; Sequence 10, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
```

```
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-10

      Query Match      89.7%; Score 26; DB 3; Length 6;
      Best Local Similarity 83.3%; Pred. No. 1.7e+06;
      Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      1 KLVFFA 6

RESULT 58
US-09-915-092-28
; Sequence 28, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(6)
; OTHER INFORMATION: D-amino acids
US-09-915-092-28

      Query Match      89.7%; Score 26; DB 3; Length 6;
      Best Local Similarity 83.3%; Pred. No. 1.7e+06;
      Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      1 KLVFFA 6

RESULT 59
US-09-956-625-25
; Sequence 25, Application US/09956625
; Patent No. US2002011926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
```

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Antifibrillogenic agents
US-09-956-625-25

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 60
US-09-747-408-3
; Sequence 3, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 61
US-09-747-408-11
; Sequence 11, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 62
US-10-463-729-9
; Sequence 9, Application US/10463729
; Publication No. US20040005307A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,729
; FILING DATE: 17-JUNE-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-463-729-9

Query Match      89.7%; Score 26; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 63
US-10-728-028-10
; Sequence 10, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
```

; APPLICANT: MIGNEAULT, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; FILE REFERENCE: NBI-139CP  
; CURRENT APPLICATION NUMBER: US/10/728,028  
; PRIOR FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: 60/443291  
; PRIOR FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: 09/915092  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-728-028-10

Query Match 89.7%; Score 26; DB 5; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 1 KLVFFA 6

## RESULT 64

US-10-728-028-27  
; Sequence 27, Application US/10728028  
; Publication No. US20050048000A1  
; GENERAL INFORMATION:  
; APPLICANT: GERVAIS, Francine  
; APPLICANT: KONG, Xianqi  
; APPLICANT: CHALIFOUR, Robert  
; APPLICANT: MIGNEAULT, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; FILE REFERENCE: NBI-139CP  
; CURRENT APPLICATION NUMBER: US/10/728,028  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: 60/443291  
; PRIOR FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: 09/915092  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-728-028-27

Query Match 89.7%; Score 26; DB 5; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 1 KLVFFA 6

## RESULT 65

US-10-728-028-28  
; Sequence 28, Application US/10728028

; Publication No. US20050048000A1  
; GENERAL INFORMATION:  
; APPLICANT: GERVAIS, Francine  
; APPLICANT: KONG, Xianqi  
; APPLICANT: CHALIFOUR, Robert  
; APPLICANT: MIGNEAULT, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; FILE REFERENCE: NBI-139CP  
; CURRENT APPLICATION NUMBER: US/10/728,028  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: 60/443291  
; PRIOR FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: 09/915092  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-728-028-28

Query Match 89.7%; Score 26; DB 5; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 1 KLVFFA 6

## RESULT 66

US-10-825-958-7  
; Sequence 7, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
US-10-825-958-7

Query Match 89.7%; Score 26; DB 5; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 1 KLVFFA 6



```
RESULT 67
US-10-825-958-18
; Sequence 18, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-18

Query Match      89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      1 KLVFFA 6

RESULT 68
US-10-666-095-3
; Sequence 3, Application US/10666095
; Publication No. US20050119187A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Robert P.
; APPLICANT: Fu, Yanwen
; APPLICANT: Aucoin, Jed P.
; APPLICANT: Miller, Tod J.
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: McCauley, Robin L.
; TITLE OF INVENTION: Anti-fibril Peptides
; FILE REFERENCE: 0212.1 Hammer
; CURRENT APPLICATION NUMBER: US/10/666,095
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,081
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-666-095-3

Query Match      89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
```

```
Db      1 KLVFFA 6
       |:||||

RESULT 69
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-12

Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      2 KLVFFA 7

RESULT 70
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      2 KLVFFA 7
```

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

## RESULT 71

US-09-867-847-28  
; Sequence 28, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; NAME/KEY: MOD\_RES  
; LOCATION: (7)  
; OTHER INFORMATION: AMIDATION  
US-09-867-847-28

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

## RESULT 72

US-09-972-475-7  
; Sequence 7, Application US/09972475  
; Patent No. US20020098173A1  
; GENERAL INFORMATION:  
; APPLICANT: Pondeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/972,475  
; FILING DATE: 04-Oct-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/617,267

; FILING DATE: <Unknown>  
; APPLICATION NUMBER: USN 08/475,579  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: USN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-972-475-7

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 2 KLVFFA 7

## RESULT 73

US-09-915-092-2  
; Sequence 2, Application US/09915092  
; Publication No. US20020115717A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: NBI-139  
; CURRENT APPLICATION NUMBER: US/09/915,092  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220,808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-092-2

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 2 KLVFFA 7

## RESULT 74

US-09-915-092-17  
; Sequence 17, Application US/09915092  
; Publication No. US20020115717A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND

```

; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-17

```

```

Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

```

```

RESULT 75
US-09-915-092-18
; Sequence 18, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-18

```

```

Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

```

```

Search completed: December 29, 2005, 18:49:48
Job time : 67.2903 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds  
(without alignments)  
24.763 Million cell updates/sec

Title: US-10-009-122-17

Perfect score: 29

Sequence: 1 KVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	2	US-09-747-408-9
2	29	100.0	6	2	US-09-747-408-17
3	29	100.0	77	2	US-09-513-999C-6921
4	29	100.0	1144	1	US-08-147-812-5
5	29	100.0	1144	1	US-08-319-866-12
6	29	100.0	1144	2	US-09-123-708-2
7	29	100.0	1144	2	US-09-123-624-2
8	29	100.0	1144	2	US-09-661-258-5
9	29	100.0	1144	2	US-08-809-917-12
10	29	100.0	1144	2	US-09-419-371-12
11	28	96.6	6	2	US-09-747-408-1
12	28	96.6	6	2	US-09-747-408-10
13	28	96.6	123	2	US-09-902-540-13513
14	26	89.7	6	1	US-08-612-785B-9
15	26	89.7	6	2	US-08-703-675C-32
16	26	89.7	6	2	US-08-617-267C-9
17	26	89.7	6	2	US-09-747-408-3
18	26	89.7	6	2	US-09-747-408-11
19	26	89.7	7	1	US-08-127-904-14
20	26	89.7	7	1	US-08-612-785B-7
21	26	89.7	7	2	US-08-703-675C-30
22	26	89.7	7	2	US-08-617-267C-7
23	26	89.7	7	2	US-08-264-709A-13
24	26	89.7	7	2	US-09-747-408-2
25	26	89.7	7	2	US-09-747-408-18
26	26	89.7	7	2	US-09-747-408-19
27	26	89.7	7	4	PCT-US94-10475-14

28	89.7	8	1	US-08-612-785B-5	Sequence 5, Appli
29	89.7	8	1	US-08-630-645-1	Sequence 1, Appli
30	89.7	8	2	US-08-703-675C-28	Sequence 28, Appli
31	89.7	8	2	US-08-617-267C-5	Sequence 5, Appli
32	89.7	8	2	US-09-095-106A-44	Sequence 44, Appli
33	89.7	8	2	US-08-766-596A-1	Sequence 1, Appli
34	89.7	8	2	US-09-668-314C-73	Sequence 73, Appli
35	89.7	8	4	PCT-US96-10220-1	Sequence 1, Appli
36	89.7	9	2	US-08-766-596A-64	Sequence 64, Appli
37	89.7	9	2	US-09-747-408-20	Sequence 20, Appli
38	89.7	10	2	US-08-970-833-3	Sequence 3, Appli
39	89.7	10	2	US-09-724-961-20	Sequence 20, Appli
40	89.7	10	2	US-09-724-961-21	Sequence 21, Appli
41	89.7	10	2	US-09-724-961-22	Sequence 22, Appli
42	89.7	10	2	US-09-724-961-23	Sequence 23, Appli
43	89.7	10	2	US-09-724-961-24	Sequence 24, Appli
44	89.7	10	2	US-09-580-018-20	Sequence 20, Appli
45	89.7	10	2	US-09-580-018-21	Sequence 21, Appli
46	89.7	10	2	US-09-580-018-22	Sequence 22, Appli
47	89.7	10	2	US-09-580-018-23	Sequence 23, Appli
48	89.7	10	2	US-09-580-018-24	Sequence 24, Appli
49	89.7	10	2	US-09-724-551-20	Sequence 20, Appli
50	89.7	10	2	US-09-724-551-21	Sequence 21, Appli
51	89.7	10	2	US-09-724-551-22	Sequence 22, Appli
52	89.7	10	2	US-09-724-551-23	Sequence 23, Appli
53	89.7	10	2	US-09-724-551-24	Sequence 24, Appli
54	89.7	10	2	US-09-724-940-20	Sequence 20, Appli
55	89.7	10	2	US-09-724-940-21	Sequence 21, Appli
56	89.7	10	2	US-09-724-940-22	Sequence 22, Appli
57	89.7	10	2	US-09-724-940-23	Sequence 23, Appli
58	89.7	10	2	US-09-724-940-24	Sequence 24, Appli
59	89.7	11	1	US-08-630-645-14	Sequence 14, Appli
60	89.7	11	2	US-08-766-596A-14	Sequence 14, Appli
61	89.7	11	2	US-09-988-842-9	Sequence 9, Appli
62	89.7	11	2	US-09-988-842-25	Sequence 25, Appli
63	89.7	11	4	PCT-US96-10220-14	Sequence 14, Appli
64	89.7	14	2	US-09-594-366-5	Sequence 5, Appli
65	89.7	14	2	US-09-992-800-5	Sequence 5, Appli
66	89.7	15	1	US-08-612-785B-14	Sequence 14, Appli
67	89.7	15	1	US-08-612-785B-37	Sequence 37, Appli
68	89.7	15	2	US-08-617-267C-14	Sequence 14, Appli
69	89.7	15	2	US-08-766-596A-56	Sequence 56, Appli
70	89.7	15	2	US-08-766-596A-57	Sequence 57, Appli
71	89.7	15	2	US-08-766-596A-58	Sequence 58, Appli
72	89.7	15	2	US-08-766-596A-60	Sequence 60, Appli
73	89.7	15	2	US-08-766-596A-61	Sequence 61, Appli
74	89.7	15	2	US-08-766-596A-62	Sequence 62, Appli
75	89.7	15	2	US-08-766-596A-63	Sequence 63, Appli
76	89.7	15	2	US-08-766-596A-65	Sequence 65, Appli
77	89.7	17	2	US-09-264-709A-2	Sequence 2, Appli
78	89.7	17	2	US-09-594-366-3	Sequence 3, Appli
79	89.7	17	2	US-09-623-548A-950	Sequence 950, App
80	89.7	17	2	US-09-623-548A-983	Sequence 983, App
81	89.7	17	2	US-09-992-800-3	Sequence 3, Appli
82	89.7	17	2	US-09-657-276-950	Sequence 950, App
83	89.7	17	2	US-09-657-276-983	Sequence 983, App
84	89.7	19	2	US-08-970-833-11	Sequence 11, Appli
85	89.7	19	2	US-09-723-384-5	Sequence 5, Appli
86	89.7	19	2	US-09-724-961-75	Sequence 75, Appli
87	89.7	19	2	US-09-724-552-5	Sequence 5, Appli
88	89.7	19	2	US-09-580-018-75	Sequence 75, Appli
89	89.7	19	2	US-09-723-927-5	Sequence 5, Appli
90	89.7	19	2	US-09-724-489-5	Sequence 5, Appli
91	89.7	19	2	US-09-724-477-5	Sequence 5, Appli
92	89.7	19	2	US-09-723-762-5	Sequence 5, Appli
93	89.7	19	2	US-09-201-430-5	Sequence 5, Appli
94	89.7	19	2	US-09-724-551-75	Sequence 75, Appli
95	89.7	19	2	US-10-815-353-5	Sequence 5, Appli
96	89.7	19	2	US-10-816-529-5	Sequence 5, Appli
97	89.7	19	2	US-10-815-391-5	Sequence 5, Appli
98	89.7	19	2	US-10-816-022-5	Sequence 5, Appli
99	89.7	19	2	US-09-724-940-75	Sequence 75, Appli
100	89.7	19	2	US-10-934-609-5	Sequence 5, Appli

101	26	89.7	19	2	US-10-884-892-5	Sequence 5, Appl	174	26	89.7	38	2	US-09-623-548A-1002	Sequence 1002, Ap
102	26	89.7	20	2	US-08-970-833-10	Sequence 10, Appl	175	26	89.7	38	2	US-09-657-276-975	Sequence 975, App
103	26	89.7	20	2	US-09-724-953-33	Sequence 33, Appl	176	26	89.7	38	2	US-09-657-276-1002	Sequence 1002, Ap
104	26	89.7	20	2	US-09-724-567-33	Sequence 33, Appl	177	26	89.7	39	1	US-08-304-585-5	Sequence 5, Appl1
105	26	89.7	20	2	US-09-979-952-33	Sequence 33, Appl	178	26	89.7	39	1	US-08-302-808-2	Sequence 2, Appl1
106	26	89.7	20	2	US-09-585-817-33	Sequence 33, Appl	179	26	89.7	39	1	US-08-609-090-7	Sequence 7, Appl1
107	26	89.7	26	1	US-08-304-585-7	Sequence 7, Appl1	180	26	89.7	39	1	US-08-682-245A-1	Sequence 1, Appl1
108	26	89.7	28	1	US-08-346-849-4	Sequence 4, Appl1	181	26	89.7	39	1	US-08-986-948-2	Sequence 2, Appl1
109	26	89.7	28	1	US-08-302-808-7	Sequence 7, Appl1	182	26	89.7	40	1	US-07-744-767A-1	Sequence 1, Appl1
110	26	89.7	28	1	US-08-609-090-2	Sequence 2, Appl1	183	26	89.7	40	1	US-08-235-400-2	Sequence 2, Appl1
111	26	89.7	28	1	US-08-586-948-7	Sequence 7, Appl1	184	26	89.7	40	1	US-08-476-464A-2	Sequence 2, Appl1
112	26	89.7	28	1	US-08-293-284A-4	Sequence 4, Appl1	185	26	89.7	40	1	US-08-304-585-1	Sequence 1, Appl1
113	26	89.7	28	1	US-08-461-216-2	Sequence 2, Appl1	186	26	89.7	40	1	US-08-304-585-8	Sequence 8, Appl1
114	26	89.7	28	2	US-09-388-890-2	Sequence 2, Appl1	187	26	89.7	40	1	US-08-302-808-3	Sequence 3, Appl1
115	26	89.7	28	2	US-09-388-890-3	Sequence 3, Appl1	188	26	89.7	40	1	US-08-433-734-1	Sequence 1, Appl1
116	26	89.7	28	2	US-09-388-890-4	Sequence 4, Appl1	189	26	89.7	40	1	US-08-609-090-8	Sequence 8, Appl1
117	26	89.7	28	2	US-09-388-890-5	Sequence 5, Appl1	190	26	89.7	40	1	US-07-737-371E-69	Sequence 69, Appl
118	26	89.7	28	2	US-09-388-890-6	Sequence 6, Appl1	191	26	89.7	40	1	US-08-682-245A-2	Sequence 2, Appl1
119	26	89.7	28	2	US-09-388-890-7	Sequence 7, Appl1	192	26	89.7	40	1	US-08-986-948-3	Sequence 3, Appl1
120	26	89.7	28	2	US-09-388-890-8	Sequence 8, Appl1	193	26	89.7	40	1	US-08-461-216-1	Sequence 1, Appl1
121	26	89.7	28	2	US-09-388-890-9	Sequence 9, Appl1	194	26	89.7	40	2	US-08-959-148-1	Sequence 1, Appl1
122	26	89.7	28	2	US-09-388-890-10	Sequence 10, Appl	195	26	89.7	40	2	US-09-242-724-22	Sequence 22, Appl
123	26	89.7	28	2	US-09-388-890-12	Sequence 12, Appl	196	26	89.7	40	2	US-08-723-661B-1	Sequence 1, Appl1
124	26	89.7	28	2	US-09-388-890-13	Sequence 13, Appl	197	26	89.7	40	2	US-09-062-365-3	Sequence 3, Appl1
125	26	89.7	28	2	US-09-388-890-14	Sequence 14, Appl	198	26	89.7	40	2	US-09-133-866-1	Sequence 1, Appl1
126	26	89.7	28	2	US-09-264-709A-1	Sequence 1, Appl1	199	26	89.7	40	2	US-09-861-847A-7	Sequence 7, Appl1
127	26	89.7	28	2	US-08-723-661B-2	Sequence 2, Appl1	200	26	89.7	40	2	US-09-861-847A-8	Sequence 8, Appl1
128	26	89.7	28	2	US-09-660-954-2	Sequence 2, Appl1	201	26	89.7	40	2	US-09-988-842-3	Sequence 3, Appl1
129	26	89.7	28	2	US-08-660-954-3	Sequence 3, Appl1	202	26	89.7	40	2	US-10-455-218-1	Sequence 1, Appl1
130	26	89.7	28	2	US-09-660-954-4	Sequence 4, Appl1	203	26	89.7	40	2	US-10-151-614-1	Sequence 1, Appl1
131	26	89.7	28	2	US-09-660-954-5	Sequence 5, Appl1	204	26	89.7	40	2	US-09-623-548A-956	Sequence 956, App
132	26	89.7	28	2	US-09-660-954-6	Sequence 6, Appl1	205	26	89.7	40	2	US-09-623-548A-962	Sequence 962, App
133	26	89.7	28	2	US-09-660-954-7	Sequence 7, Appl1	206	26	89.7	40	2	US-09-623-548A-968	Sequence 968, App
134	26	89.7	28	2	US-09-660-954-8	Sequence 8, Appl1	207	26	89.7	40	2	US-09-623-548A-978	Sequence 978, App
135	26	89.7	28	2	US-09-660-954-9	Sequence 9, Appl1	208	26	89.7	40	2	US-09-623-548A-989	Sequence 989, App
136	26	89.7	28	2	US-09-660-954-10	Sequence 10, Appl	209	26	89.7	40	2	US-09-623-548A-995	Sequence 995, App
137	26	89.7	28	2	US-09-660-954-12	Sequence 12, Appl	210	26	89.7	40	2	US-09-623-548A-1005	Sequence 1005, Ap
138	26	89.7	28	2	US-09-660-954-13	Sequence 13, Appl	211	26	89.7	40	2	US-09-657-276-956	Sequence 956, App
139	26	89.7	28	2	US-09-660-954-14	Sequence 14, Appl	212	26	89.7	40	2	US-09-657-276-962	Sequence 962, App
140	26	89.7	28	2	US-08-898-100-4	Sequence 4, Appl1	213	26	89.7	40	2	US-09-657-276-968	Sequence 968, App
141	26	89.7	28	2	US-08-824-513-4	Sequence 4, Appl1	214	26	89.7	40	2	US-09-657-276-978	Sequence 978, App
142	26	89.7	28	2	US-09-623-548A-959	Sequence 959, App	215	26	89.7	40	2	US-09-657-276-989	Sequence 989, App
143	26	89.7	28	2	US-09-623-548A-965	Sequence 965, App	216	26	89.7	40	2	US-09-657-276-995	Sequence 995, App
144	26	89.7	28	2	US-09-623-548A-976	Sequence 976, App	217	26	89.7	40	2	US-09-657-276-1005	Sequence 1005, Ap
145	26	89.7	28	2	US-09-623-548A-992	Sequence 992, App	218	26	89.7	40	2	US-09-962-955D-36	Sequence 36, Appl
146	26	89.7	28	2	US-09-623-548A-1003	Sequence 1003, Ap	219	26	89.7	40	4	PCT-US92-06700-1	Sequence 1, Appl1
147	26	89.7	28	2	US-09-657-276-959	Sequence 959, App	220	26	89.7	41	1	US-07-819-361-1	Sequence 1, Appl1
148	26	89.7	28	2	US-09-657-276-965	Sequence 965, App	221	26	89.7	41	1	US-08-302-808-4	Sequence 4, Appl1
149	26	89.7	28	2	US-09-657-276-976	Sequence 976, App	222	26	89.7	41	1	US-08-682-245A-3	Sequence 3, Appl1
150	26	89.7	28	2	US-09-657-276-992	Sequence 992, App	223	26	89.7	41	1	US-08-986-948-4	Sequence 4, Appl1
151	26	89.7	28	2	US-09-657-276-1003	Sequence 1003, Ap	224	26	89.7	42	1	US-07-744-767A-2	Sequence 2, Appl1
152	26	89.7	28	2	US-09-865-294A-66	Sequence 66, Appl	225	26	89.7	42	1	US-08-179-574-1	Sequence 1, Appl1
153	26	89.7	30	1	US-08-609-090-3	Sequence 3, Appl1	226	26	89.7	42	1	US-08-271-162-5	Sequence 5, Appl1
154	26	89.7	30	2	US-09-861-847A-1	Sequence 1, Appl1	227	26	89.7	42	1	US-08-347-144-1	Sequence 1, Appl1
155	26	89.7	33	1	US-08-609-090-4	Sequence 4, Appl1	228	26	89.7	42	1	US-08-462-859A-19	Sequence 19, Appl
156	26	89.7	34	1	US-08-475-579A-4	Sequence 4, Appl1	229	26	89.7	42	1	US-08-123-659A-19	Sequence 19, Appl
157	26	89.7	35	1	US-08-304-585-6	Sequence 6, Appl1	230	26	89.7	42	1	US-08-464-247A-19	Sequence 19, Appl
158	26	89.7	35	1	US-08-612-785B-16	Sequence 16, Appl	231	26	89.7	42	1	US-08-464-248A-19	Sequence 19, Appl
159	26	89.7	35	1	US-08-612-785B-36	Sequence 36, Appl	232	26	89.7	42	1	US-08-476-464A-1	Sequence 1, Appl1
160	26	89.7	35	1	US-08-612-785B-38	Sequence 38, Appl	233	26	89.7	42	1	US-08-304-585-2	Sequence 2, Appl1
161	26	89.7	35	1	US-08-612-785B-40	Sequence 40, Appl	234	26	89.7	42	1	US-08-302-808-5	Sequence 5, Appl1
162	26	89.7	35	2	US-08-617-267C-16	Sequence 16, Appl	235	26	89.7	42	1	US-08-268-348A-1	Sequence 1, Appl1
163	26	89.7	35	2	US-09-623-548A-979	Sequence 979, App	236	26	89.7	42	1	US-08-268-348A-2	Sequence 2, Appl1
164	26	89.7	35	2	US-09-623-548A-1006	Sequence 1006, App	237	26	89.7	42	1	US-08-268-348A-3	Sequence 3, Appl1
165	26	89.7	35	2	US-09-657-276-979	Sequence 979, App	238	26	89.7	42	1	US-08-268-348A-4	Sequence 4, Appl1
166	26	89.7	35	2	US-09-657-276-1006	Sequence 1006, App	239	26	89.7	42	1	US-08-268-348A-5	Sequence 5, Appl1
167	26	89.7	36	1	US-08-609-090-6	Sequence 6, Appl1	240	26	89.7	42	1	US-08-268-348A-6	Sequence 6, Appl1
168	26	89.7	36	2	US-09-861-847A-6	Sequence 6, Appl1	241	26	89.7	42	1	US-08-433-734-2	Sequence 2, Appl1
169	26	89.7	36	2	US-09-861-847A-11	Sequence 11, Appl	242	26	89.7	42	1	US-08-609-090-9	Sequence 9, Appl1
170	26	89.7	38	1	US-08-302-808-1	Sequence 1, Appl1	243	26	89.7	42	1	US-07-737-371E-72	Sequence 72, Appl
171	26	89.7	38	1	US-07-737-371E-68	Sequence 68, Appl	244	26	89.7	42	1	US-08-422-333-4	Sequence 4, Appl1
172	26	89.7	38	1	US-08-986-948-1	Sequence 1, Appl1	245	26	89.7	42	1	US-08-682-245A-4	Sequence 4, Appl1
173	26	89.7	38	2	US-09-623-548A-975	Sequence 975, App	246	26	89.7	42	1	US-08-986-948-5	Sequence 5, Appl1



Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
Db 38 KVVFFA 43

## RESULT 4

US-08-147-812-5  
; Sequence 5, Application US/08147812  
; Patent No. 5766909  
; GENERAL INFORMATION:  
; APPLICANT: Xie, Qiao-wen  
; APPLICANT: Nathan, Carl F.  
; APPLICANT: Mumford, Richard A.  
; APPLICANT: Calaycay, Jimmy Ramos  
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: 126 East Lincoln Avenue  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07065

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: Macintosh Centris650  
; OPERATING SYSTEM: Macintosh 7.0.1  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,812  
; FILING DATE: No. 5766909 Available  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/841,641  
; FILING DATE: 02-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wallen, John W III  
; REGISTRATION NUMBER: 35,403  
; REFERENCE/DOCKET NUMBER: 186581A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-3905  
; TELEFAX: (908) 594-4720  
; TELEX: 138825  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1144 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

Query Match 100.0%; Score 29; DB 1; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
Db 514 KVVFFA 519

## RESULT 5

US-08-319-866-12  
; Sequence 12, Application US/08319866  
; Patent No. 5929223  
; GENERAL INFORMATION:  
; APPLICANT: Tully, Timothy P.  
; APPLICANT: Yin, Jerry C.  
; APPLICANT: Regulski, Michael  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES  
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/319,866  
; FILING DATE: 7-OCT-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL94-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1144 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-319-866-12

Query Match 100.0%; Score 29; DB 1; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
Db 514 KVVFFA 519

## RESULT 6

US-09-123-708-2  
; Sequence 2, Application US/09123708  
; Patent No. 6146887  
; GENERAL INFORMATION:  
; APPLICANT: SCHRADER, Juergen  
; APPLICANT: GOEDECKE, Axel  
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC  
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
; FILE REFERENCE: 51169-2003  
; CURRENT APPLICATION NUMBER: US/09/123,708  
; CURRENT FILING DATE: 1998-07-28  
; EARLIER APPLICATION NUMBER: 08/553,503  
; EARLIER FILING DATE: 1996-03-01  
; EARLIER APPLICATION NUMBER: P4411402.8  
; EARLIER FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Cytomegalovirus  
US-09-123-708-2

Query Match 100.0%; Score 29; DB 2; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||

Db 514 KVVFFA 519

RESULT 7

US-09-123-624-2

; Sequence 2, Application US/09123624

; Patent No. 6149936

; GENERAL INFORMATION:

; APPLICANT: SCHRADER, Jurgen

; APPLICANT: GODECKE, Axel

; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

; FILE REFERENCE: 511169-2004

; CURRENT APPLICATION NUMBER: US/09/123.624

; CURRENT FILING DATE: 1998-07-28

; PRIOR APPLICATION NUMBER: 08/553,503

; PRIOR FILING DATE: 1996-03-01

; PRIOR APPLICATION NUMBER: 4411402.8

; PRIOR FILING DATE: 1994-03-31

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 1144

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-123-624-2

Query Match 100.0%; Score 29; DB 2; Length 1144;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

|||||

Db 514 KVVFFA 519

RESULT 8

US-09-661-258-5

; Sequence 5, Application US/09661258

; Patent No. 6620616

; GENERAL INFORMATION:

; APPLICANT: Stuehr, Dennis J.

; APPLICANT: Adak, Subrata

; TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants

; FILE REFERENCE: 26473/04028

; CURRENT APPLICATION NUMBER: US/09/661.258

; CURRENT FILING DATE: 2000-09-13

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 1144

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-661-258-5

Query Match 100.0%; Score 29; DB 2; Length 1144;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

|||||

Db 514 KVVFFA 519

RESULT 9

US-08-809-917-12

; Sequence 12, Application US/08809917

; Patent No. 6689557

; GENERAL INFORMATION:

; APPLICANT: APPLICANT

; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES

; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY

US-08-809-917-12

Query Match 100.0%; Score 29; DB 2; Length 1144;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

|||||

Db 514 KVVFFA 519

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/809,917

APPLICATION NUMBER: US/08/809,917

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13198

FILING DATE:

APPLICATION NUMBER: US 08/361,063

FILING DATE: 21-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/319,866

FILING DATE: 07-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240

TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1144 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-809-917-12

Query Match 100.0%; Score 29; DB 2; Length 1144;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

|||||

Db 514 KVVFFA 519

RESULT 10

US-09-419-371-12

; Sequence 12, Application US/09419371

; Patent No. 6890516

; GENERAL INFORMATION:

; APPLICANT: Tully, Timothy P.

; APPLICANT: Yin, Jerry Chi-Ping

; TITLE OF INVENTION: Cloning and Characterizing of Genes

; TITLE OF INVENTION: Associated With Long-Term Memory

; FILE REFERENCE: CSHL94-03A32

; CURRENT APPLICATION NUMBER: US/09/419,371

; CURRENT FILING DATE: 1999-10-14

; PRIOR APPLICATION NUMBER: 08/809,917

; PRIOR FILING DATE: 1997-07-07

; PRIOR APPLICATION NUMBER: PCT/US95/13198

; PRIOR FILING DATE: 1995-10-06

; PRIOR APPLICATION NUMBER: 08/361,063

; PRIOR FILING DATE: 1994-12-21

; PRIOR APPLICATION NUMBER: 08/319,866

; PRIOR FILING DATE: 1994-10-07

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 12



```

; LENGTH: 1144
; TYPE: PRT
; ORGANISM: mouse
US-09-419-371-12

Query Match      100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFFA 6
Db      514 KVVFFFA 519

RESULT 11
US-09-747-408-1
; Sequence 1, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match      96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFFA 6
Db      1 KIVFFFA 6

RESULT 12
US-09-747-408-10
; Sequence 10, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match      96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFFA 6
Db      1 KIVFFFA 6

RESULT 13
US-09-902-540-13513
; Sequence 13513, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13513
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13513

Query Match      96.6%; Score 28; DB 2; Length 123;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFFA 6
Db      52 KVVFFFA 57

RESULT 14
US-08-612-785B-9
; Sequence 9, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: S14
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-612-785B-9

Query Match 89.7%; Score 26; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 15  
US-08-703-675C-32  
Sequence 32, Application US/08703675C  
Patent No. 6303567  
GENERAL INFORMATION:  
APPLICANT: Findexis, Mark A. et al.  
TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/703,675C  
FILING DATE: 27-AUG-1996  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/616,081  
FILING DATE: 14-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kara, Catherine J.  
REGISTRATION NUMBER: 41,106  
REFERENCE/DOCKET NUMBER: PPI-016CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-703-675C-32

Query Match 89.7%; Score 26; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 16  
US-08-617-267C-9  
Sequence 9, Application US/08617267C  
Patent No. 6319498  
GENERAL INFORMATION:  
APPLICANT: Findexis, Mark A. et al.  
TITLE OF INVENTION: Modulators of Amyloid Aggregation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C  
FILING DATE: 14-MAR-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-617-267C-9

Query Match 89.7%; Score 26; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 17  
US-09-747-408-3  
Sequence 3, Application US/09747408  
Patent No. 6670399  
GENERAL INFORMATION:  
APPLICANT: Green, Allan M.  
TITLE OF INVENTION: Compounds And Methods For Modulating  
TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
FILE REFERENCE: NBI-088  
CURRENT APPLICATION NUMBER: US/09/747,408

```
/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/171,877
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-747-408-3

Query Match      89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 18
US-09-747-408-11
/ Sequence 11, Application US/09747408
/ Patent No. 6670399
/ GENERAL INFORMATION:
/ APPLICANT: Green, Allan M.
/ TITLE OF INVENTION: Compounds And Methods For Modulating
/ TITLE OF INVENTION: Cerebral Amyloid Angiopathy
/ FILE REFERENCE: NEI-088
/ CURRENT APPLICATION NUMBER: US/09/747,408
/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/171,877
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-747-408-11

Query Match      89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 19
US-08-127-904-14
/ Sequence 14, Application US/08127904
/ Patent No. 5470951
/ GENERAL INFORMATION:
/ APPLICANT: Eugene Roberts
/ TITLE OF INVENTION: Method For Antagonizing
/ TITLE OF INVENTION: Anesthetic Effects of Amyloid n
/ TITLE OF INVENTION: Protein and Improving the
/ TITLE OF INVENTION: Quality of Life in Individuals
/ TITLE OF INVENTION: With Alzheimer Disease
/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: City of Hope
/ STREET: 1500 East Duarte Road
/ CITY: Duarte
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 91010-0269
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3M Double Density 5 1/4" diskette
/ COMPUTER: Wang PC

/ OPERATING SYSTEM: MS DOS Version 3.20
/ SOFTWARE: Microsoft
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/127,904
/ FILING DATE: 29 September 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA: No. 5470951e
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Irons, Edward S.
/ REGISTRATION NUMBER: 16,541
/ REFERENCE/DOCKET NUMBER: No. 5470951e
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 783-6040
/ TELEFAX: (202) 783-6031
/ TELEX: No. 5470951e
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7
/ TYPE: Amino Acid
/ STRANDEDNESS:
/ TOPOLOGY: Unknown
US-08-127-904-14

Query Match      89.7%; Score 26; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 20
US-08-612-785B-7
/ Sequence 7, Application US/08612785B
/ Patent No. 5854204
/ GENERAL INFORMATION:
/ APPLICANT: Findeis, Mark A. et al.
/ TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
/ TITLE OF INVENTION: Aggregation
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 28 State Street, Suite 510
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/612,785B
/ FILING DATE: Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/404,831
/ FILING DATE: 14-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/475,579
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/548,998
/ FILING DATE: 27-OCT-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeConti, Giulio A.
/ REGISTRATION NUMBER: 31,503
/ REFERENCE/DOCKET NUMBER: PPI-002CP3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 742-4214
```

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-612-785B-7

Query Match 89.7%; Score 26; DB 1; Length 7;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 2 KLVFFA 7

RESULT 21

US-08-703-675C-30

; Sequence 30, Application US/08703675C

; Patent No. 6303567

; GENERAL INFORMATION:

; APPLICANT: Findexis, Mark A. et al.

; TITLE OF INVENTION: Modulators of -Amyloid Peptide

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/703.675C

; FILING DATE: 27-AUG-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USN 08/404,831

; FILING DATE: 14-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USN 08/475,579

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USN 08/548,998

; FILING DATE: 27-OCT-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USN 08/616,081

; FILING DATE: 14-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Kara, Catherine J.

; REGISTRATION NUMBER: 41,106

; REFERENCE/DOCKET NUMBER: PPI-016CP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-703-675C-30

Query Match 89.7%; Score 26; DB 2; Length 7;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 2 KLVFFA 7

Db 2 KLVFFA 7

RESULT 22

US-08-617-267C-7

; Sequence 7, Application US/08617267C

; Patent No. 6319498

; GENERAL INFORMATION:

; APPLICANT: Findexis, Mark A. et al.

; TITLE OF INVENTION: Modulators of Amyloid Aggregation

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/617,267C

; FILING DATE: 14-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USN 08/404,831

; FILING DATE: 14-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USN 08/475,579

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USN 08/548,998

; FILING DATE: 27-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: DeConti, Giulio A.

; REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: PPI-002CP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-617-267C-7

Query Match 89.7%; Score 26; DB 2; Length 7;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 2 KLVFFA 7

RESULT 23

US-09-264-709A-13

; Sequence 13, Application US/09264709A

; Patent No. 6320024

; GENERAL INFORMATION:

; APPLICANT: Roberts, Eugene

; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and

; FILE REFERENCE: 2124-310

; CURRENT APPLICATION NUMBER: US/09/264,709A

; CURRENT FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 08/797,782

; PRIOR FILING DATE: 1997-02-07

Qy 1 KLVFFA 6

Db 2 KLVFFA 7

```
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-13

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 24
US-09-747-408-2
; Sequence 2, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      2 KLVFFA 7

RESULT 25
US-09-747-408-18
; Sequence 18, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      2 KLVFFA 7

RESULT 26
US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 27
PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amnestic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
```

REGISTRATION NUMBER: 16,541  
REFERENCE/DOCKET NUMBER: None  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 626-3564 or 783-6030  
TELEFAX: (202) 783-6031  
TELEX: None  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7  
TYPE: Amino Acid  
STRANDEDNESS:  
TOPOLOGY: Unknown  
PCT-US94-10475-14

Query Match 89.7%; Score 26; DB 4; Length 7;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 28  
US-08-612-785B-5  
; Sequence 5, Application US/08612785B  
; Patent No. 5854204  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
; TITLE OF INVENTION: Aggregation  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: LAHIVE & COCKFIELD  
; STREET: 28 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/612,785B  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PFI-002CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-612-785B-5

Query Match 89.7%; Score 26; DB 1; Length 8;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 3 KLVFFA 8

RESULT 29  
US-08-630-645-1  
; Sequence 1, Application US/08630645  
; Patent No. 5948763  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,645  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-630-645-1

Query Match 89.7%; Score 26; DB 1; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 30  
US-08-703-675C-28  
; Sequence 28, Application US/08703675C  
; Patent No. 6303567  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of -Amyloid Peptide  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; Aggregation Comprising D-

```

; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-703-675C-28

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 3 KLVFFA 8

RESULT 31
US-08-617-267C-5
; Sequence 5, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findex, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C

```

```

; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Deconti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-617-267C-5

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 3 KLVFFA 8

RESULT 32
US-09-095-106A-44
; Sequence 44, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Amyloidosis
; US-09-095-106A-44

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 33
US-08-766-596A-1
; Sequence 1, Application US/08766596A
; Patent No. 6462171

```

```
;
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-766-596A-1

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 34
US-09-668-314C-73
; Sequence 73, Application US/09668314C
; Patent No. 6844148
; GENERAL INFORMATION:
; APPLICANT: Guiney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 28341/6280NCP
; CURRENT APPLICATION NUMBER: US/09/668,314C
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
```

```
;
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; US-09-668-314C-73

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 35
PCT-US96-10220-1
; Sequence 1, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-10220-1

Query Match 89.7%; Score 26; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
```



Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 36  
US-08-766-596A-64  
; Sequence 64, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA: US 08/478,326  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-64

Query Match 89.7%; Score 26; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 2 KLVFFA 7

RESULT 37  
US-09-747-408-20  
; Sequence 20, Application US/09747408  
; Patent No. 6670399  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.

; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-408-20

Query Match 89.7%; Score 26; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 4 KLVFFA 9

RESULT 38  
US-08-970-833-3  
; Sequence 3, Application US/08970833  
; Patent No. 6022859  
; GENERAL INFORMATION:  
; APPLICANT: Kiesel, Laura L.  
; APPLICANT: Murphy, Regina M.  
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 411 East Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53202-4497  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/970,833  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baker, Jean C.  
; REGISTRATION NUMBER: 35,433  
; REFERENCE/DOCKET NUMBER: 960296.94291  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 277-5709  
; TELEFAX: (414) 271-3552  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-970-833-3

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

```
RESULT 39
US-09-724-961-20
; Sequence 20, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |:||||
Db 5 KLVFFA 10

RESULT 40
US-09-724-961-21
; Sequence 21, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |:||||
Db 5 KLVFFA 10

RESULT 41
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |:||||
Db 4 KLVFFA 9

RESULT 42
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

```
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |:||||
Db 4 KLVFFA 9

RESULT 41
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
   |:||||
Db 3 KLVFFA 8

RESULT 42
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

```
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US 09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-23

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      2 KLVFFA 7

RESULT 43
US-09-724-961-24
; Sequence 24, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US 09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-25
```

```
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-24

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      1 KLVFFA 6

RESULT 44
US-09-580-018-20
; Sequence 20, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US 09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-580-018-20

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      5 KLVFFA 10

RESULT 45
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US 09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-580-018-21
```

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 4 KLVFFA 9

RESULT 46  
US-09-580-018-22  
; Sequence 22, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-22

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 3 KLVFFA 8

RESULT 47  
US-09-580-018-23  
; Sequence 23, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-23

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KVVFFA 6  
|:||||  
Db 2 KLVFFA 7

RESULT 48  
US-09-580-018-24  
; Sequence 24, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-24

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 49  
US-09-724-551-20  
; Sequence 20, Application US/09724551  
; Patent No. 6787637  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/724,551  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-551-20

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 KVVFFA 6
      |:|||||
Db      5 KLVFFA 10

RESULT 50
US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      4 KLVFFA 9

RESULT 51
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      2 KLVFFA 7

RESULT 53
US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      3 KLVFFA 8

RESULT 52
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      2 KLVFFA 7

RESULT 53
US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Best Local Similarity 83.3%; Pred. No. 8.4; Mismatches 1; Indels 0; Gaps 0;  
Matches 5; Conservative 1;

Qy 1 KVVFFA 6  
Db 1 KLVFFA 6

## RESULT 54

US-09-724-940-20  
; Sequence 20, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-20

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 5 KLVFFA 10

## RESULT 55

US-09-724-940-21  
; Sequence 21, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-21

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 4 KLVFFA 9

## RESULT 56

US-09-724-940-22  
; Sequence 22, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-22

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 3 KLVFFA 8

```

RESULT 57
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
        |:||||
Db      2 KLVFFA 7

RESULT 58
US-09-724-940-24
; Sequence 24, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
        |:||||
Db      2 KLVFFA 7

```

```

; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
        |:||||
Db      1 KLVFFA 6

RESULT 59
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-630-645-14

Query Match      89.7%; Score 26; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
        |:||||
Db      2 KLVFFA 7

```

RESULT 60  
US-08-766-596A-14  
; Sequence 14, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-14  
  
Query Match 89.7%; Score 26; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 9.3;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KLVFFA 6  
Db 2 KLVFFA 7  
  
RESULT 61  
US-09-988-842-9  
; Sequence 9, Application US/09988842  
; Patent No. 6716589  
; GENERAL INFORMATION:  
; APPLICANT: Johansson, Jan  
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION  
; TITLE OF INVENTION: OF AMYLOID FORMATION  
; FILE REFERENCE: 12125-002001  
; CURRENT APPLICATION NUMBER: US/09/988,842  
; FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: US 60/251,662  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 60/253,695  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Synthetically generated peptide  
US-09-988-842-9  
  
Query Match 89.7%; Score 26; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 9.3;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KLVFFA 6  
Db 2 KLVFFA 7  
  
RESULT 62  
US-09-988-842-25  
; Sequence 25, Application US/09988842  
; Patent No. 6716589  
; GENERAL INFORMATION:  
; APPLICANT: Johansson, Jan  
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION  
; TITLE OF INVENTION: OF AMYLOID FORMATION  
; FILE REFERENCE: 12125-002001  
; CURRENT APPLICATION NUMBER: US/09/988,842  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: US 60/251,662  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 60/253,695  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
US-09-988-842-25  
  
Query Match 89.7%; Score 26; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 9.3;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KLVFFA 6  
Db 2 KLVFFA 7  
  
RESULT 63  
PCT-US96-10220-14  
; Sequence 14, Application PC/TUS9610220  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10220  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US96-10220-14

Query Match 89.7%; Score 26; DB 4; Length 11;  
Best Local Similarity 83.3%; Pred. No. 9.3;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
DB 2 KLVFFA 7

RESULT 64  
US-09-594-366-5  
Sequence 5, Application US/09594366  
Patent No. 6582945  
GENERAL INFORMATION:  
APPLICANT: Raso, Victor  
TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO  
FILE REFERENCE: BBRI-2004  
CURRENT APPLICATION NUMBER: US/09/594,366  
CURRENT FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/139,408  
PRIOR FILING DATE: 1999-06-16  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-594-366-5

Query Match 89.7%; Score 26; DB 2; Length 14;  
Best Local Similarity 83.3%; Pred. No. 12;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
DB 4 KLVFFA 9

RESULT 65  
US-09-992-800-5  
Sequence 5, Application US/09992800  
Patent No. 6872554  
GENERAL INFORMATION:

APPLICANT: Raso, Victor  
TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO  
FILE REFERENCE: BBRI-2006  
CURRENT APPLICATION NUMBER: US/09/992,800  
CURRENT FILING DATE: 2001-11-06  
PRIOR APPLICATION NUMBER: 09/594,366  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/139,408  
PRIOR FILING DATE: 1999-06-16  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-992-800-5

Query Match 89.7%; Score 26; DB 2; Length 14;  
Best Local Similarity 83.3%; Pred. No. 12;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
DB 4 KLVFFA 9

RESULT 66  
US-08-612-785B-14  
Sequence 14, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
TITLE OF INVENTION: Aggregation  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal  
US-08-612-785B-14

Query Match 89.7%; Score 26; DB 1; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

## RESULT 67

US-08-612-785B-37  
; Sequence 37, Application US/08612785B  
; Patent No. 5854204  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: AD Peptides that Modulate b-Amyloid  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/612,785B  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-612-785B-37

Query Match 89.7%; Score 26; DB 1; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 6 KLVFFA 11

## RESULT 68

US-08-617-267C-14

; Sequence 14, Application US/08617267C  
; Patent No. 6319498  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/617,267C  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-617-267C-14

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

## RESULT 69

US-08-766-596A-56  
; Sequence 56, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.

; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-56

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 5 KLVFFA 10

RESULT 70  
US-08-766-596A-57  
; Sequence 57, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-57

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 5 KLVFFA 10

RESULT 71  
US-08-766-596A-58  
; Sequence 58, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-58

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 5 KLVFFA 10

## RESULT 72

US-08-766-596A-60  
; Sequence 60, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/766.596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 60:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-60

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||

Db 5 KLVFFA 10

## RESULT 73

US-08-766-596A-61  
; Sequence 61, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/766.596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-61

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 5 KLVFFA 10

## RESULT 74

US-08-766-596A-62  
; Sequence 62, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

```
;
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-766-596A-62

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 5 KVLFFA 10

RESULT 75
US-08-766-596A-63
; Sequence 63, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-766-596A-63

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 5 KLVFFA 10

Search completed: December 29, 2005, 17:52:39
Job time : 21.1323 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds  
(without alignments)  
32.238 Million cell updates/sec

Title: US-10-009-122-17

Perfect score: 29  
Sequence: 1 KVPFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : A\_Geneseq\_21:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4	AAB48482
2	29	100.0	6	4	AAB48490
3	29	100.0	6	4	AAB82630
4	29	100.0	6	4	AAB82638
5	29	100.0	6	5	AAB96818
6	29	100.0	6	5	AAB96826
7	29	100.0	6	5	AAB11664
8	29	100.0	6	5	AAB11656
9	29	100.0	6	8	AAB35452
10	29	100.0	6	8	AAB37277
11	29	100.0	6	8	AAB37321
12	29	100.0	6	8	AAB37329
13	29	100.0	6	9	ADY37928
14	29	100.0	6	9	ADY37936
15	29	100.0	22	8	ADQ09761
16	29	100.0	23	8	ADQ09761
17	29	100.0	37	3	ABO5510
18	29	100.0	37	8	ADK34080
19	29	100.0	37	8	ADL70727
20	29	100.0	77	3	AGD02840
21	29	100.0	175	4	AAO11219
22	29	100.0	186	7	ADC07962
23	29	100.0	186	7	ADC07948
24	29	100.0	190	4	AAM83792

25	29	100.0	854	8	ADQ66704
26	29	100.0	922	8	ABM83252
27	29	100.0	925	7	ADF76335
28	29	100.0	925	7	ADF70225
29	29	100.0	925	8	ADJ75428
30	29	100.0	925	8	ADJ75495
31	29	100.0	925	8	ADN04860
32	29	100.0	925	8	ADR14233
33	29	100.0	925	8	ADP25011
34	29	100.0	925	8	ADR97294
35	29	100.0	925	9	ADY17516
36	29	100.0	925	9	AEA23525
37	29	100.0	1144	2	AAR77360
38	29	100.0	1144	2	AAW51246
39	29	100.0	1144	4	AAG64500
40	29	100.0	1144	6	ABU79138
41	29	100.0	1144	7	ADF43404
42	29	100.0	1144	7	ADF77432
43	29	100.0	1144	8	ADJ76212
44	29	100.0	1144	8	ADJ76136
45	29	100.0	1144	9	AEA03075
46	28	96.6	6	4	AAB48483
47	28	96.6	6	4	AAB48474
48	28	96.6	6	4	AAB82623
49	28	96.6	6	4	AAB82631
50	28	96.6	6	5	AAU96819
51	28	96.6	6	5	AAU96811
52	28	96.6	6	5	AAU11657
53	28	96.6	6	5	AAU11648
54	28	96.6	6	6	AAE35446
55	28	96.6	6	6	AAE35438
56	28	96.6	6	8	ADQ37322
57	28	96.6	6	8	ADQ37270
58	28	96.6	6	8	ADQ37313
59	28	96.6	6	8	ADQ37262
60	28	96.6	6	9	ADY37921
61	28	96.6	6	9	ADY37929
62	28	96.6	99	4	ABG26598
63	28	96.6	123	9	ABM94314
64	28	96.6	393	8	ADM16726
65	28	96.6	393	8	ADM16684
66	28	96.6	399	8	ADO43456
67	27	93.1	564	4	ABB61977
68	27	93.1	1443	6	ABB68472
69	26	89.7	6	2	AAW02314
70	26	89.7	6	2	AAW89378
71	26	89.7	6	4	AAB48484
72	26	89.7	6	4	AAB48476
73	26	89.7	6	4	AAB82632
74	26	89.7	6	5	ABG71009
75	26	89.7	6	5	ABB05157
76	26	89.7	6	5	AAU96820
77	26	89.7	6	5	ABB83305
78	26	89.7	6	5	AAU11658
79	26	89.7	6	5	AAU11650
80	26	89.7	6	6	AAE35445
81	26	89.7	6	6	AAE35434
82	26	89.7	6	8	ADJ64060
83	26	89.7	6	8	ADQ37271
84	26	89.7	6	8	ADQ37315
85	26	89.7	6	8	ADQ37368
86	26	89.7	6	8	ADQ37269
87	26	89.7	6	8	ADQ37292
88	26	89.7	6	8	ADQ37258
89	26	89.7	6	8	ADQ37353
90	26	89.7	6	8	ADQ37323
91	26	89.7	6	9	ADY37930
92	26	89.7	6	9	ADY37948
93	26	89.7	6	9	ADY37947
94	26	89.7	6	9	AEA23039
95	26	89.7	7	2	AAR88300
96	26	89.7	7	2	AAR87921
97	26	89.7	7	2	AAW02312

98	26	89.7	7	2	AAW89376	Aaw89376 Beta-amyl	171	26	89.7	9	9	AEA51417	AeA51417 C-A 16-23
99	26	89.7	7	4	AAW67281	Aab67281 Residues	172	26	89.7	9	9	AEA62825	AeA62825 Immunocon
100	26	89.7	7	4	AAW48475	Aab48475 Antifibri	173	26	89.7	9	9	AEA62828	AeA62828 Immunocon
101	26	89.7	7	4	AAW48492	Aab48492 Antifibri	174	26	89.7	10	3	AAV79938	Aay79938 Beta-amyl
102	26	89.7	7	4	AAW48491	Aab48491 Antifibri	175	26	89.7	10	4	AAW46226	Aab46226 Human APP
103	26	89.7	7	4	AAW82624	Aab82624 All-D pep	176	26	89.7	10	4	AAW46225	Aab46225 Human APP
104	26	89.7	7	4	AAW82640	Aab82640 All-D pep	177	26	89.7	10	4	AAW46228	Aab46228 Human APP
105	26	89.7	7	4	AAW82639	Aab82639 All-D pep	178	26	89.7	10	4	AAW46224	Aab46224 Human APP
106	26	89.7	7	5	ABG71007	Abg71007 Long form	179	26	89.7	10	4	AAW46227	Aab46227 Human APP
107	26	89.7	7	5	ABW05155	Abw05155 Beta amyl	180	26	89.7	10	4	AAW82641	Aab82641 All-D pep
108	26	89.7	7	5	AAU96827	Aau96827 Amyloid t	181	26	89.7	10	5	AAU96829	Aau96829 Amyloid t
109	26	89.7	7	5	AAU96812	Aau96812 Amyloid t	182	26	89.7	10	6	ABP57511	Abp57511 Different
110	26	89.7	7	5	AAU96828	Aau96828 Amyloid t	183	26	89.7	10	6	AAU96829	Aau96829 Amyloid t
111	26	89.7	7	5	ABW04920	Abw04920 Human amy	184	26	89.7	10	8	AAU96829	Aau96829 Amyloid t
112	26	89.7	7	5	AAU11665	Aau11665 Peptide #	185	26	89.7	10	8	AAU96829	Aau96829 Amyloid t
113	26	89.7	7	5	AAU11649	Aau11649 Peptide #	186	26	89.7	10	8	AAU96829	Aau96829 Amyloid t
114	26	89.7	7	5	AAU11666	Aau11666 Peptide #	187	26	89.7	10	8	AAU96829	Aau96829 Amyloid t
115	26	89.7	7	6	ABW82630	Abw82630 Beta fib	188	26	89.7	11	2	AAW32560	Aaw32560 Anti-amyl
116	26	89.7	7	6	AAW35439	Aae35439 Beta pep	189	26	89.7	11	2	AAW32560	Aaw32560 Anti-amyl
117	26	89.7	7	6	AAW35454	Aae35454 Beta pep	190	26	89.7	11	4	AAW32560	Aaw32560 Anti-amyl
118	26	89.7	7	6	AAW35453	Aae35453 Beta pep	191	26	89.7	11	5	AAU99431	Aau99431 Human amy
119	26	89.7	7	6	ADA90937	Ada90937 Solid-pha	192	26	89.7	11	5	AAU99431	Aau99431 Human amy
120	26	89.7	7	6	ADA90154	Ada90154 Anti-Abet	193	26	89.7	11	6	ABU79013	Abu79013 Amyloidog
121	26	89.7	7	7	ADW20746	Adw20746 Human bet	194	26	89.7	11	7	ABW84683	Abw84683 Aggregat
122	26	89.7	7	7	ADW50855	Adw50855 Human cal	195	26	89.7	11	7	ABW84683	Abw84683 Aggregat
123	26	89.7	7	8	ADW64058	Adw64058 Human bet	196	26	89.7	12	6	ABR91837	AbR91837 P. papata
124	26	89.7	7	8	ADW64922	Adw64922 Beta-amyl	197	26	89.7	12	6	AAE35464	Aae35464 Beta pep
125	26	89.7	7	8	ADQ37278	Adq37278 Vaccine a	198	26	89.7	12	6	AAE35435	Aae35435 Beta pep
126	26	89.7	7	8	ADQ37314	Adq37314 Antifibri	199	26	89.7	12	6	AAE35466	Aae35466 Beta pep
127	26	89.7	7	8	ADQ37263	Adq37263 Vaccine a	200	26	89.7	12	7	ADW20745	Adw20745 Human bet
128	26	89.7	7	8	ADQ37279	Adq37279 Vaccine a	201	26	89.7	12	7	ADW20744	Adw20744 Human bet
129	26	89.7	7	8	ADQ37330	Adq37330 Antifibri	202	26	89.7	12	8	ADU71476	AdU71476 N-termina
130	26	89.7	7	8	ADQ37331	Adq37331 Antifibri	203	26	89.7	12	8	ADQ37407	AdQ37407 Amyloid-b
131	26	89.7	7	8	ADQ37351	Adq37351 Beta-amyl	204	26	89.7	12	8	ADQ37289	AdQ37289 Vaccine a
132	26	89.7	7	9	ADY37922	Ady37922 Amyloid-t	205	26	89.7	12	8	ADQ37259	AdQ37259 Vaccine a
133	26	89.7	7	9	ADY37938	Ady37938 Amyloid-t	206	26	89.7	12	9	ADZ08890	AdZ08890 Human bet
134	26	89.7	7	9	ADY37937	Ady37937 Amyloid-t	207	26	89.7	12	9	ADZ08892	AdZ08892 Human bet
135	26	89.7	7	9	ADZ08903	Adz08903 Human bet	208	26	89.7	13	6	AAE35465	Aae35465 Beta pep
136	26	89.7	8	2	AAW02310	Aaw02310 Beta-amyl	209	26	89.7	13	6	AAE35467	Aae35467 Beta pep
137	26	89.7	8	2	AAW45967	Aaw45967 Peptide d	210	26	89.7	13	6	ADA37467	Ada37467 Human amy
138	26	89.7	8	2	AAW32551	Aaw32551 Amyloidog	211	26	89.7	13	8	ADU71477	AdU71477 N-termina
139	26	89.7	8	2	AAW89374	Aaw89374 Beta-amyl	212	26	89.7	13	8	ADU71464	AdU71464 N-termina
140	26	89.7	8	4	AAE10663	Aae10663 Human amy	213	26	89.7	13	8	ADQ37408	AdQ37408 Amyloid-b
141	26	89.7	8	4	AAE02615	Aae02615 Human amy	214	26	89.7	13	8	ADQ37290	AdQ37290 Vaccine a
142	26	89.7	8	5	ABG71005	Abg71005 Long form	215	26	89.7	14	6	ADA89887	Ada89887 Beta-A4 s
143	26	89.7	8	5	ABW78624	Abw78624 Human alp	216	26	89.7	14	8	ADU71452	AdU71452 N-termina
144	26	89.7	8	5	ABW05153	Abw05153 Beta amyl	217	26	89.7	14	8	ADU71465	AdU71465 N-termina
145	26	89.7	8	6	ABW09765	Abw09765 Amyloidog	218	26	89.7	14	8	ADU71478	AdU71478 N-termina
146	26	89.7	8	6	ABW61959	Abw61959 Human amy	219	26	89.7	14	9	ADZ08889	AdZ08889 Human bet
147	26	89.7	8	7	ABW00134	Abw00134 Beta-amyl	220	26	89.7	15	2	AAW02334	Aaw02334 Beta-amyl
148	26	89.7	8	8	ADJ64056	Adj64056 Human bet	221	26	89.7	15	2	AAW89358	Aaw89358 Beta-amyl
149	26	89.7	8	8	ADQ37385	Adq37385 Antifibri	222	26	89.7	15	5	ABG71014	Abg71014 Long form
150	26	89.7	8	8	ADQ37349	Adq37349 Beta-amyl	223	26	89.7	15	5	ABG71014	Abg71014 Long form
151	26	89.7	8	9	ADZ08900	Adz08900 Human bet	224	26	89.7	15	5	ABW05162	Abw05162 Beta amyl
152	26	89.7	8	9	AEA51423	Aea51423 C-Abeta 1	225	26	89.7	15	6	AAE26271	Aae26271 Human bet
153	26	89.7	8	9	AEA51420	Aea51420 A 16-22-C	226	26	89.7	15	6	ABU79057	Abu79057 Aggregati
154	26	89.7	8	9	AEA62831	Aea62831 Immunocon	227	26	89.7	15	6	ABU79059	Abu79059 Aggregati
155	26	89.7	8	9	AEA62834	Aea62834 Immunocon	228	26	89.7	15	6	ABU79059	Abu79059 Aggregati
156	26	89.7	9	2	AAW45239	Aaw45239 Mutant am	229	26	89.7	15	6	ABU79055	Abu79055 Aggregati
157	26	89.7	9	4	AAW48493	Aaw48493 Antifibri	230	26	89.7	15	6	ABU79056	Abu79056 Aggregati
158	26	89.7	9	5	AAU11667	Aau11667 Peptide #	231	26	89.7	15	6	ABU79062	Abu79062 Aggregati
159	26	89.7	9	6	ABP57517	Abp57517 Different	232	26	89.7	15	6	ABU79061	Abu79061 Aggregati
160	26	89.7	9	6	AAU79063	Aau79063 Aggregati	233	26	89.7	15	7	ABW00190	Abw00190 Peptide #
161	26	89.7	9	6	AAU79063	Aau79063 Aggregati	234	26	89.7	15	7	ABW00190	Abw00190 Peptide #
162	26	89.7	9	7	ABW00197	Abw00197 Peptide #	235	26	89.7	15	7	ABW00198	Abw00198 Peptide #
163	26	89.7	9	8	ADJ36003	Adj36003 Amyloid b	236	26	89.7	15	7	ABW00189	Abw00189 Peptide #
164	26	89.7	9	8	ADJ35849	Adj35849 Amyloid b	237	26	89.7	15	7	ABW00193	Abw00193 Peptide #
165	26	89.7	9	8	ADJ35874	Adj35874 Amyloid b	238	26	89.7	15	7	ABW00191	Abw00191 Peptide #
166	26	89.7	9	8	ADJ35871	Adj35871 Amyloid b	239	26	89.7	15	7	ABW00196	Abw00196 Peptide #
167	26	89.7	9	8	ADJ35903	Adj35903 Amyloid b	240	26	89.7	15	7	ABW00195	Abw00195 Peptide #
168	26	89.7	9	8	ADQ37260	Adq37260 Vaccine a	241	26	89.7	15	7	ABW00194	Abw00194 Peptide #
169	26	89.7	9	8	ADQ37332	Adq37332 Antifibri	242	26	89.7	15	7	ADK82697	AdK82697 Beta-amyl
170	26	89.7	9	9	AEA51414	Aea51414 A 16-23-C	243	26	89.7	15	7	ADK82700	AdK82700 Beta-amyl

244	26	89.7	15	7	ADK82698	Adk82698 Beta-amyl
245	26	89.7	15	7	ADK82699	Adk82699 Beta-amyl
246	26	89.7	15	8	ADJ71466	Adj71466 N-termina
247	26	89.7	15	8	ADJ71453	Adj71453 N-termina
248	26	89.7	15	8	ADJ71479	Adj71479 N-termina
249	26	89.7	15	8	ADJ71440	Adj71440 N-termina
250	26	89.7	15	8	ADJ64065	Adj64065 Human bet
251	26	89.7	15	8	AAE26330	AAE26330 Human bet
252	26	89.7	16	8	ADJ71454	Adj71454 N-termina
253	26	89.7	16	8	ADJ71480	Adj71480 N-termina
254	26	89.7	16	8	ADJ71441	Adj71441 N-termina
255	26	89.7	16	8	ADJ71467	Adj71467 N-termina
256	26	89.7	16	8	ADJ71428	Adj71428 N-termina
257	26	89.7	17	2	AAE54703	AAE54703 Beta-amyl
258	26	89.7	17	2	AAW18880	AAW18880 Beta-amyl
259	26	89.7	17	2	AAW18880	AAW18880 Beta-amyl
260	26	89.7	17	4	AAW18880	AAW18880 Beta-amyl
261	26	89.7	17	4	AAW18880	AAW18880 Beta-amyl
262	26	89.7	17	5	AAW18880	AAW18880 Beta-amyl
263	26	89.7	17	6	AAW18880	AAW18880 Beta-amyl
264	26	89.7	17	6	AAW18880	AAW18880 Beta-amyl
265	26	89.7	17	8	ADJ93165	Adj93165 Novel exp
266	26	89.7	17	8	ADJ65843	Adj65843 Amyloid B
267	26	89.7	17	8	ADN02827	ADN02827 Mammalian
268	26	89.7	17	8	ADQ37291	ADQ37291 Vaccine a
269	26	89.7	17	8	ADL18447	ADL18447 Amyloid-b
270	26	89.7	18	3	AAW10963	AAW10963 Beta-amyl
271	26	89.7	18	3	AAW10963	AAW10963 Beta-amyl
272	26	89.7	19	2	AAW18881	AAW18881 Trip-Beta-
273	26	89.7	19	2	AAW18881	AAW18881 Trip-Beta-
274	26	89.7	19	4	AAW18881	AAW18881 Trip-Beta-
275	26	89.7	19	4	AAW18881	AAW18881 Trip-Beta-
276	26	89.7	19	4	AAW18881	AAW18881 Trip-Beta-
277	26	89.7	19	8	ADU24440	ADU24440 Novel glu
278	26	89.7	19	8	ADU24442	ADU24442 Novel glu
279	26	89.7	19	8	ADU46714	ADU46714 Amyloid b
280	26	89.7	19	9	ADZ71366	ADZ71366 Human bet
281	26	89.7	19	9	ADZ71368	ADZ71368 Human bet
282	26	89.7	19	9	AEA35401	AEA35401 Novel QC
283	26	89.7	19	9	AEA35399	AEA35399 Novel QC
284	26	89.7	19	9	AEA35399	AEA35399 Novel QC
285	26	89.7	19	9	AEA35399	AEA35399 Novel QC
286	26	89.7	20	3	AAW18881	AAW18881 Trip-Beta-
287	26	89.7	20	5	AAW18881	AAW18881 Trip-Beta-
288	26	89.7	20	6	AAW18881	AAW18881 Trip-Beta-
289	26	89.7	21	2	AAW18881	AAW18881 Trip-Beta-
290	26	89.7	21	8	ADU24439	ADU24439 Novel glu
291	26	89.7	21	8	ADU46713	ADU46713 Amyloid b
292	26	89.7	21	8	ADV86872	ADV86872 Beta-amyl
293	26	89.7	21	9	ADZ71365	ADZ71365 Human bet
294	26	89.7	21	9	AEA35398	AEA35398 Novel QC
295	26	89.7	21	9	AEA35398	AEA35398 Novel QC
296	26	89.7	22	8	ADR83670	ADR83670 Amyloidog
297	26	89.7	24	2	AAW18881	AAW18881 Trip-Beta-
298	26	89.7	24	2	AAW18881	AAW18881 Trip-Beta-
299	26	89.7	24	9	AAW18881	AAW18881 Trip-Beta-
300	26	89.7	24	9	AAW18881	AAW18881 Trip-Beta-

ALIGNMENTS

RESULT 1  
ID AAB48482 standard; peptide; 6 AA.  
XX  
AC AAB48482;  
XX

02-MAR-2001 (first entry)  
XX

Antifibrillogenetic peptide #9.  
XX

Nootropic; neuroprotective; antifibrillogenetic; amyloidosis inhibition;  
KW

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
KW Alzheimer's disease.  
XX Homo sapiens.  
OS WO200068263-A2.  
PN 16-NOV-2000.  
PD  
XX  
XX 04-MAY-2000; 2000WO-CA000515.  
PF  
XX 05-MAY-1999; 99US-0132592P.  
PR (NEUR-) NEUROCHEM INC.  
PA  
XX Challifour R, Gervais F, Gupta A;  
PI WPI; 2001-031852/04.  
DR  
XX  
XX  
PT Antifibrillogenetic agent useful for inhibiting amyloidosis and/or for  
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
PT its isomer or peptidomimetic.  
PS Claim 7; Page 25; 46pp; English.  
CC Peptides AAB48474-B48496 are antifibrillogenetic agents that can be used  
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
CC binding region and the prot-prot interaction region of the human amyloid  
CC protein  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 29; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KVVFFA 6  
Db 1 KVVFFA 6  
RESULT 2  
AAB48490  
ID AAB48490 standard; peptide; 6 AA.  
XX  
AC AAB48490;  
XX  
XX 02-MAR-2001 (first entry)  
DT  
XX  
XX Antifibrillogenetic peptide #17.  
XX  
XX Nootropic; neuroprotective; antifibrillogenetic; amyloidosis inhibition;  
KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
KW Alzheimer's disease.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 6 /note= "C-terminal amide"  
FT  
XX  
XX WO200068263-A2.  
PN  
XX  
PD 16-NOV-2000.  
XX  
XX 04-MAY-2000; 2000WO-CA000515.  
PF  
XX  
XX 05-MAY-1999; 99US-0132592P.  
PR  
XX  
XX (NEUR-) NEUROCHEM INC.  
PA



XX Chalifour R, Gervais F, Gupta A;  
 XX WPI; 2001-031852/04.  
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.  
 XX Claim 7; Page 25; 46pp; English.  
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein  
 XX Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;  
 QY 1 KVVFFA 6  
 Db 1 KVVFFA 6  
 RESULT 3  
 AAB82630  
 ID AAB82630 standard; peptide; 6 AA.  
 XX AAB82630;  
 XX 02-OCT-2001 (first entry)  
 XX All-D peptide used in Alzheimer's disease vaccine.  
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..6 /note= "all D-form residues"  
 FT  
 XX WO200139796-A2.  
 XX 07-JUN-2001.  
 XX 29-NOV-2000; 2000WO-CA001413.  
 XX 29-NOV-1999; 99US-0168594P.  
 PR 28-NOV-2000; 2000US-00724842.  
 XX (NEUR-) NEUROCHEM INC.  
 XX Chalifour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT which elicits production of antibodies to prevent fibrillogenesis and  
 PT associated cellular toxicity.  
 XX Disclosure; Page 11; 31pp; English.  
 XX The present sequence is that of an all-D peptide suitable for use for  
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients  
 XX Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;  
 QY 1 KVVFFA 6  
 Db 1 KVVFFA 6  
 RESULT 4  
 AAB82638  
 ID AAB82638 standard; peptide; 6 AA.  
 XX AAB82638;  
 XX 02-OCT-2001 (first entry)  
 XX All-D peptide used in Alzheimer's disease vaccine.  
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..6 /note= "all D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"  
 FT  
 XX WO200139796-A2.  
 XX 07-JUN-2001.  
 XX 29-NOV-2000; 2000WO-CA001413.  
 PR 29-NOV-1999; 99US-0168594P.  
 PR 28-NOV-2000; 2000US-00724842.  
 XX (NEUR-) NEUROCHEM INC.  
 XX Chalifour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and  
 FT associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in  
 XX preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 1 KVVFFA 6

RESULT 5  
 AAU96818  
 ID AAU96818 standard; peptide; 6 AA.

XX AAU96818;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #8.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6 /note= "Preferably D-form residue"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 FT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A-(A<sub>1</sub>n<sub>1</sub>k)<sub>z</sub>-A<sub>1</sub>a<sub>1</sub>b<sub>1</sub> (I) where z = 0-1;  
 CC A<sub>1</sub> is an amyloid targeting moiety; A<sub>1</sub>n<sub>1</sub>k = a linker moiety; and A<sub>1</sub>a<sub>1</sub>b<sub>1</sub>  
 CC = a labelling moiety. Also included are imaging amyloid deposition or  
 CC diagnosing an amyloid-related condition in a patient involving  
 CC administering (I) to the patient, and ultrasound imaging (I) in the  
 CC patient to determine the presence of amyloid or amyloid-related condition  
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising  
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and  
 CC instructions for the preparation and use of the radiopharmaceutical in  
 CC the imaging of amyloid or an amyloid-related condition. The agents are  
 CC used for imaging amyloid deposition and for diagnosing an amyloid related  
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible  
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 1 KVVFFA 6

RESULT 6

AAU96826

ID AAU96826 standard; peptide; 6 AA.

XX AAU96826;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #16.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6

```

FT Modified-site 6 /note= "Preferably D-form residue"
FT FT /note= "Ala is amidated"
XX PN WO200207781-A2.
XX PD 31-JAN-2002.
XX PF 25-JUL-2001; 2001WO-CA001071.
XX PR 25-JUL-2000; 2000US-0220808P.
XX PR 24-JUL-2001; 2001US-00915092.
XX PA (NEUR-) NEUROCHEM INC.
XX PI Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2002-371447/40.
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX Claim 49; Page 21; 57pp; English.
XX CC The invention relates to an amyloid-targeting imaging agent comprising an
XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX agent is of general formula A1-L1-A2 where z = 0 - 1;
XX A1 is an amyloid targeting moiety; L1 is a linker moiety; and A2 is a
XX labelling moiety. Also included are imaging amyloid deposition or
XX diagnosing an amyloid-related condition in a patient involving
XX administering (i) to the patient, and ultrasound imaging (i) in the
XX patient to determine the presence of amyloid or amyloid-related condition
XX ; and a kit for preparing a radiopharmaceutical preparation comprising
XX (i), a reducing agent, a buffering agent, a transchelating agent, and
XX instructions for the preparation and use of the radiopharmaceutical in
XX the imaging of amyloid or an amyloid-related condition. The agents are
XX used for imaging amyloid deposition and for diagnosing an amyloid related
XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX cerebral amyloidosis (transmissible virus dementias), familial CJD,
XX scrapie, transmissible mink encephalopathy, bovine spongiform
XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX amyloid angiopathy. The agents are capable of crossing the blood-brain
XX barrier and are capable of binding specifically to amyloid plaques. The
XX present sequence is a peptide forming the amyloid targeting moiety of the
XX agent of the invention
XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 1 KVVFFA 6

RESULT 7
AAU11664
ID AAU11664 standard; peptide; 6 AA.
AC AAU11664;
XX 09-APR-2002 (first entry)
XX Peptide #17, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 1 KVVFFA 6

RESULT 8
AAU11656
ID AAU11656 standard; peptide; 6 AA.
AC AAU11656;
XX 09-APR-2002 (first entry)
XX Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX Synthetic.
XX WO200185093-A2.
XX 15-NOV-2001.
XX 22-DEC-2000; 2000WO-IB002078.
XX 23-DEC-1999; 99US-0171877P.
XX (NEUR-) NEUROCHEM INC.
XX Green AM, Gervais F;
XX WPI; 2002-075222/10.
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX inhibitor.
XX Disclosure; Page 10; 60pp; English.
XX The present invention relates to a new method of inhibiting cerebral
XX amyloid angiopathy. The new method of the invention involves contacting a
XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX can be used for treating disease states characterised by cerebral amyloid
XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX The present sequence represents one of a group of peptides (AAU11648-
XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX was used in the invention to treat a disease state characterised by
XX cerebral amyloid angiopathy (CAA)
XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 1 KVVFFA 6

RESULT 8
AAU11656
ID AAU11656 standard; peptide; 6 AA.
AC AAU11656;
XX 09-APR-2002 (first entry)
XX Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX Synthetic.
XX WO200185093-A2.
XX 15-NOV-2001.
XX 22-DEC-2000; 2000WO-IB002078.
XX 23-DEC-1999; 99US-0171877P.

```

```

XX FA (NEUR-) NEUROCHEM INC.
XX FI Green AM, Gervais F;
XX FT WPI; 2002-075222/10.
XX DR
XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX FT disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX FT inhibitor.
XX PS Disclosure; Page 10; 68pp; English.
XX CC The present invention relates to a new method of inhibiting cerebral
XX CC amyloid angiopathy. The new method of the invention involves contacting a
XX CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX CC can be used for treating disease states characterised by cerebral amyloid
XX CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX CC The present sequence represents one of a group of peptides (AAU11648-
XX CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX CC was used in the invention to treat a disease state characterised by
XX CC cerebral amyloid angiopathy (CAA)
XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVVFFFA 6
Db 1 KVVFFFA 6
|||||
1 KVVFFFA 6

RESULT 9
AAE35452
ID AAE35452 standard; peptide; 6 AA.
AC AAE35452;
DT 17-JUN-2003 (first entry)
DE Abeta peptide #23.
KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1. .6
XX FT /note= "D-form residues"
XX FT Modified-site 6
XX FT /note= "C-terminal amide"
XX PN WO200296937-A2.
XX PD 05-DEC-2002.
XX PP 29-MAY-2002; 2002WO-CA000763.
XX PR 29-MAY-2001; 2001US-00867847.
XX PA (NEUR-) NEUROCHEM INC.
XX PI Gervais F, Hebert L, Chalifour RJ, Kong X;

```

```

XX DR WPI; 2003-201269/19.
XX CC Prevention and/or treatment of an amyloid-related disease e.g.
XX FT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
XX PS Claim 1; Page 59; 44pp; English.
XX CC The invention relates to a method for prevention and/or treatment of an
XX CC amyloid-related disease which comprises administration of an all-D -
XX CC amyloid-beta peptide. The method is used for preventing and/or treating
XX CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
XX CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
XX CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
XX CC the mammal; and reducing or inhibiting the formation of plaques. It is
XX CC also used for treating AA (reactive) amyloid diseases including
XX CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
XX CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
XX CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
XX CC disease. AA deposits are also produced as a result of chronic microbial
XX CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
XX CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
XX CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
XX CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
XX CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
XX CC present sequence is an Abeta peptide used to illustrate the method of the
XX CC invention
XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVVFFFA 6
Db 1 KVVFFFA 6
|||||
1 KVVFFFA 6

RESULT 10
ADQ37277
ID ADQ37277 standard; peptide; 6 AA.
AC ADQ37277;
XX DT 07-OCT-2004 (first entry)
XX DE Vaccine antigen amyloid-beta related amino acid sequence.
XX KW amyloid-beta; amyloid-beta related disease;
XX KW amyloid-beta fibril formation; immune response; nontropic;
XX KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
XX KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;
XX KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
XX KW cardiant; antidepressant; endocrine; hypnotic;
XX KW amyloid-beta fibril formation modulator; immune system modulator;
XX KW Alzheimer's disease; mild cognitive impairment;
XX KW mild-to-moderate cognitive impairment; vascular dementia;
XX KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
XX KW senile dementia; Down's syndrome; inclusion body myositis;
XX KW age-related macular degeneration; hypothyroidism;
XX KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
XX KW behavioural dysfunction; neurological condition; psychological condition;
XX KW vaccine antigen.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1. .6
XX FT /note= "D-form residues"
XX FT Modified-site 6
XX FT /note= "amidated"
XX

```

PN	WO2004058239-A1.	ID	ADQ37321 standard; peptide; 6 AA.
XX		XX	
PD	15-JUL-2004.	AC	ADQ37321;
XX		XX	
PF	24-DEC-2003; 2003WO-CA002021.	DT	07-OCT-2004 (first entry)
XX		XX	
PR	24-DEC-2002; 2002US-0436379P.	DE	Antifibrillogenic amyloidosis inhibiting peptide.
PR	23-JUN-2003; 2003US-0482214P.	XX	
XX		XX	
PA	(NEUR-) NEUROCHEM INT LTD.	KW	amyloid-beta; amyloid-beta related disease;
XX		KW	amyloid-beta fibril formation; immune response; nootropic;
PI	Gervais F, Bellini F;	KW	neuroprotective; cerebroprotective; haemostatic; ophthalmological;
XX		KW	antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
XX		KW	anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
DR	WPI; 2004-543342/52.	KW	cardiant; antidepressant; endocrine; hypnotic;
XX		KW	amyloid-beta fibril formation modulator; immune system modulator;
XX		KW	Alzheimer's disease; mild cognitive impairment;
PT	Composition for treating e.g. Alzheimer's disease comprises first agent	KW	mild-to-moderate cognitive impairment; vascular dementia;
PT	that prevents or treats amyloid-beta related disease and second agent	KW	cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
PT	that is either a peptide or peptidomimetic or an immune system modulator.	KW	senile dementia; Down's syndrome; inclusion body myositis;
XX		KW	age-related macular degeneration; hypothyroidism;
XX		KW	cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
PS	Disclosure; Page 67; 143pp; English.	KW	behavioural dysfunction; neurological condition; psychological condition;
XX		KW	vaccine antigen.
CC	The present invention describes compositions (C) comprising: (a) a first	OS	Synthetic.
CC	agent (a1) that prevents or treats amyloid-beta related disease; and (b)	XX	
CC	a second agent (a2) that is: (i) a peptide or peptidomimetic that	XX	
CC	modulates amyloid-beta fibril formation or induces a prophylactic or	XX	
CC	therapeutic immune response against amyloid-beta fibril formation; or	XX	
CC	(ii) an immune system modulator that prevents or inhibits amyloid-beta	PN	WO2004058239-A1.
CC	fibril formation. Also described is a kit comprising (C). (C) have	XX	
CC	nootropic, neuroprotective, cerebroprotective, haemostatic,	PD	15-JUL-2004.
CC	ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,	XX	
CC	uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,	XX	
CC	neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,	PF	24-DEC-2003; 2003WO-CA002021.
CC	and can be used as amyloid-beta fibril formation modulators, and as	XX	
CC	immune system modulators. (C) can be used for preventing or treating an	PR	24-DEC-2002; 2002US-0436379P.
CC	amyloid-beta related disease e.g. Alzheimer's disease (including sporadic	PR	23-JUN-2003; 2003US-0482214P.
CC	(non-hereditary) or familial (hereditary)), mild cognitive impairment,	XX	
CC	amyloid-beta related disease e.g. Alzheimer's disease (including sporadic	XX	
CC	mild-to-moderate cognitive impairment, vascular dementia, cerebral	PA	(NEUR-) NEUROCHEM INT LTD.
CC	amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,	XX	
CC	Down's syndrome, inclusion body myositis, age-related macular	PI	Gervais F, Bellini F;
CC	degeneration, or a condition associated with Alzheimer's disease	XX	
CC	(including hypothyroidism, cerebrovascular disease, cardiovascular	DR	WPI; 2004-543342/52.
CC	disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,	XX	
CC	aggression, or incontinence), a neurological condition (e.g. Huntington's	PT	Composition for treating e.g. Alzheimer's disease comprises first agent
CC	disease, amyotrophic lateral sclerosis, acquired immunodeficiency,	PT	that prevents or treats amyloid-beta related disease and second agent
CC	Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia	PT	that is either a peptide or peptidomimetic or an immune system modulator.
CC	with Lewy bodies, altered muscle tone, seizures, sensory loss, visual	XX	
CC	field deficits, incoordination, gait disturbance, transient ischaemic	PS	Disclosure; Page 67; 143pp; English.
CC	attack or stroke, transient alertness, attention deficit, frequent falls,	XX	
CC	syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural	XX	
CC	haematoma, brain tumour, posttraumatic brain injury, or posthypoxic	XX	
CC	damage), or a psychological condition (e.g. depression, delusions,	XX	
CC	illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep	XX	
CC	disturbance, insomnia, behavioural disinhibition, poor insight, suicidal	XX	
CC	ideation, depressed mood, irritability, anhedonia, social withdrawal, or	XX	
CC	excessive guilt) in a subject e.g. human having a genomic mutation in an	XX	
CC	amyloid precursor protein gene, an ApoE gene, or a presenilin gene;	XX	
CC	having amyloid-beta deposits. The present sequence represents a peptide	XX	
CC	that can be used as a vaccine antigen in the exemplification of the	XX	
XX	present invention.	XX	
SQ	Sequence 6 AA;	XX	
	Query Match 100.0%; Score 29; DB 8; Length 6;		
	Best Local Similarity 100.0%; Pred. No. 2e+06;		
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 KVVFFA 6		
Db	1 KVVFFA 6		
RESULT 11			
ADQ37321			

CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 1 KVVFFA 6

RESULT 12

ADQ37329  
 ID ADQ37329 standard; peptide; 6 AA.

AC ADQ37329;

DT 07-OCT-2004 (first entry)

DE Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antihypertensive; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiac; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.

XX Synthetic.

Key Location/Qualifiers  
 FT Modified-site 6 /note= "amidated"

XX WO2004058239-A1.

PD 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

PR 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 FT that prevents or treats amyloid-beta related disease and second agent

PT that is either a peptide or peptidomimetic or an immune system modulator.  
 XX  
 PS Disclosure; Page 70; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 1 KVVFFA 6

RESULT 13

ADY37928

ID ADY37928 standard; peptide; 6 AA.

XX AC ADY37928;

XX 19-MAY-2005 (first entry)

DE Amyloid-targeting peptide, SEQ ID NO:8, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;

XX transmissible spongiform encephalopathy; scrapie; BSE;

XX Alzheimers disease; neurological disease; amyloidosis;

XX non-insulin dependent diabetes; metabolic disorder.

XX Synthetic.

XX US2005048000-A1.

PD 03-MAR-2005.  
 XX  
 PF 03-DEC-2003; 2003US-00728028.  
 XX  
 PR 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.  
 PR 29-JAN-2003; 2003US-0443291P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX  
 XX Gervais F, Kong X, Chalifour R, Migneault D;  
 XX WPI; 2005-212201/22.  
 XX  
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform  
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.  
 XX  
 PS Disclosure; SEQ ID NO 8; 34pp; English.  
 XX  
 CC The invention relates to an amyloid-targeting imaging agent. The imaging  
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 CC a labeling moiety via a linking moiety, and is preferably able to cross  
 CC the blood-brain barrier. The invention also relates to a kit for  
 CC preparing a radiopharmaceutical preparation from the imaging agent of the  
 CC invention, a method for imaging amyloid deposition in a patient and a  
 CC method for diagnosing an amyloid-related condition in a patient. The  
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,  
 CC transmissible cerebral amyloidoses (also known as transmissible virus  
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 CC mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1 KVVFFA 6  
 RESULT 14  
 ID ADY37936  
 XX  
 AC ADY37936;  
 XX  
 DT 19-MAY-2005 (first entry)  
 XX  
 DE Amyloid-targeting peptide, SEQ ID NO:16, for use in imaging agent.  
 XX  
 KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 KW transmissible spongiform encephalopathy; scrapie; BSE;  
 KW Alzheimers disease; neurological disease; amyloidosis;  
 KW non-insulin dependent diabetes; metabolic disorder.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 PH Modified-site 6  
 FT

FT  
 XX  
 PN US2005048000-A1.  
 XX  
 PD 03-MAR-2005.  
 XX  
 PF 03-DEC-2003; 2003US-00728028.  
 XX  
 PR 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.  
 PR 29-JAN-2003; 2003US-0443291P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX  
 XX Gervais F, Kong X, Chalifour R, Migneault D;  
 XX WPI; 2005-212201/22.  
 XX  
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform  
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.  
 XX  
 PS Disclosure; SEQ ID NO 16; 34pp; English.  
 XX  
 CC The invention relates to an amyloid-targeting imaging agent. The imaging  
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 CC a labeling moiety via a linking moiety, and is preferably able to cross  
 CC the blood-brain barrier. The invention also relates to a kit for  
 CC preparing a radiopharmaceutical preparation from the imaging agent of the  
 CC invention, a method for imaging amyloid deposition in a patient and a  
 CC method for diagnosing an amyloid-related condition in a patient. The  
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,  
 CC transmissible cerebral amyloidoses (also known as transmissible virus  
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 CC mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1 KVVFFA 6  
 RESULT 15  
 ID ADQ09761  
 XX  
 AC ADQ09761;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Rice 26kDa globulin signal sequence SEQ ID NO:117.  
 XX  
 KW prolamine; rice; plant; seed; transgenic plant; signal.  
 XX  
 OS Oryza sativa.  
 XX  
 FN WO2004056993-A1.

/note= "C-terminal amide"



XX PD 08-JUL-2004.  
XX PF 09-DEC-2003; 2003WO-JP015753.  
XX PR 20-DEC-2002; 2002JP-00369700.  
XX PA (NAG-) NAT AGRIC & BIO-ORIENTED RES ORG.  
XX PI Kuroda M;  
XX DR WPI; 2004-525439/50.  
XX DR N-ESDB; ADQ09760.  
XX  
PT Novel nucleic acid molecule antisense to nucleic acid sequence encoding  
PT prolamine, useful for reducing expression dose of protein in seed, and  
PT for producing transgenic plant, preferably rice plant having reduced  
PT storage protein.  
XX  
PS Example 13; SEQ ID NO 117; 272pp; Japanese.  
XX  
CC The present invention describes a nucleic acid molecule (I) comprising a  
CC consecutive nucleic acid sequence (S1) of at least 15 bp in length and  
CC complementary with a nucleic acid sequence encoding a prolamine  
CC polypeptide or a nucleic acid sequence having a homology of at least  
CC about 70% to (S1). Also described: (1) a nucleic acid molecule (N1)  
CC comprising a nucleic acid sequence (A) having about 70% homology to a  
CC nucleic acid sequence encoding a prolamine polypeptide and a nucleic acid  
CC sequence (B) having about 70% homology to the complement of the nucleic  
CC acid sequence encoding a prolamine polypeptide; (2) a factor (II) capable  
CC of causing RNA interference of the gene sequence encoding a prolamine  
CC polypeptide; (3) a nucleic acid cassette (III) containing (1); (4)  
CC producing (III); (5) a vector (IV) comprising (1); (6) a plant cell (V)  
CC comprising (1); (7) a plant tissue (VI) comprising (V); (8) a plant (VII)  
CC containing (1) or (V); (9) a seed (VIII) produced by (VII); (10) starch  
CC preparation produced from (VII) or (VIII); and (11) a composition  
CC containing gene product of foreign gene produced from (VII) or (VIII).  
CC (I) is useful for decreasing the expression level of a protein in the  
CC seed of a plant, for expressing a foreign gene in the seed of a plant and  
CC for decreasing the expression of a natural protein in the seed of a  
CC plant. The method of decreasing the amount of expression level of a  
CC protein in the seed of a plant involves providing (I), introducing (I)  
CC into the cell of the plant, redifferentiating the cell, producing a  
CC transgenic plant, and obtaining the seed from the transgenic plant. The  
CC method after the step of introduction, further involves selecting the  
CC cell introduced with (I), by determining resistance with respect to  
CC antibiotics. The method of expressing a foreign gene in the seed of a  
CC plant, involves providing (I) and the nucleic acid molecule encoding a  
CC foreign gene product, introducing (I) and the nucleic acid molecule  
CC encoding a foreign gene product into cell of the plant, re-  
CC differentiating the cell, producing a transgenic plant, and obtaining the  
CC seed from the transgenic plant. The method further involves isolating the  
CC gene product of the foreign gene from the seed. (I) is useful for  
CC producing transgenic plants having reduced expression of storage proteins  
CC and for reducing the expression dose of a protein in a seed of a plant.  
CC The present sequence represents a rice 26kDa globulin signal sequence,  
XX which is used in the exemplification of the present invention.  
XX  
SQ Sequence 22 AA;  
Query Match 100.0%; Score 29; DB 8; Length 22;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KVVFFA 6  
Db |||||  
4 KVVFFA 9  
RESULT 16  
ADT93984  
ID ADT93984 standard; peptide; 23 AA.  
XX

AC ADT93984;  
XX 27-JAN-2005 (first entry)  
XX Rice 26 kDa peptide.  
XX  
XX Storage protein; allergen specific T cell epitope;  
XX vesicle anchoring signal; transgenic plant; rice albumen;  
XX T cell epitope-attached peptide; 7crp; seed; glutenin; edible vaccine;  
XX Japanese cedar pollen antigen; Cry11; Cry12; allergic disease; hay fever;  
XX antiallergic; plant; 26 kDa.  
XX  
XX Oryza sativa.  
XX  
XX WO2004094637-A1.  
XX  
XX 04-NOV-2004.  
XX  
XX 23-APR-2004; 2004WO-JP005938.  
XX  
XX 24-APR-2003; 2003JP-00120639.  
XX  
XX (NORQ) NAT INST AGROBIOLOGICAL SCI.  
XX  
XX Takaiwa F, Takagi H;  
XX  
XX WPI; 2004-784905/77.  
XX  
XX Novel DNA having sequence encoding allergen specific T-cell epitope  
XX peptide, useful for accumulating T-cell epitope peptide in plants and for  
XX treating allergic diseases such as pollinosis.  
XX  
XX Disclosure; SEQ ID NO 5; 79pp; Japanese.  
XX  
XX This invention relates to a DNA (I) having a sequence under the control  
XX of a storage protein promoter, chosen from a sequence encoding storage  
XX protein signal sequence at the 5' end of a sequence encoding allergen  
XX specific T cell epitope peptide and/or a sequence encoding vesicle  
XX anchoring signal sequence at the 3' end, and a DNA sequence encoding a  
XX polypeptide having allergen specific T-cell epitope peptide inserted in  
XX the variable region of a storage protein. Also disclosed is a vector (II)  
XX for T-cell epitope accumulated plant preparation, and a method of  
XX accumulating allergen specific T-cell epitope in a plant. The method  
XX involves introducing (I) or (II) to a plant, obtaining DNA encoding  
XX allergen specific T-cell epitope peptide, adding a DNA encoding a storage  
XX protein signal sequence to the 5' end and/or a vesicle anchoring signal  
XX sequence to the 3' end of the obtained DNA, and expressing the DNA in a  
XX plant under the control of a storage protein promoter, or obtaining DNA  
XX encoding allergen specific T-cell epitope peptide, inserting a DNA into  
XX the variable region of storage protein of the plant and expressing the  
XX peptide in the transgenic plant. The invention describes the accumulation  
XX of human T cell epitope in rice albumen, a method of accumulating T cell  
XX epitope-attached peptide (7crp) in seeds, a method of inserting the 7crp  
XX into the variable region of glutenin (the major storage protein of rice),  
XX and expressing and accumulating 7crp as part of the glutenin. The rice  
XX capable of producing the 7crp is useful as an edible vaccine against  
XX Japanese (Cryptomeria japonica) cedar pollen antigen. The pollen allergen  
XX is Cry11 or Cry12. The T-cell epitope is integrated on an edible region  
XX such as the seed of a plant. The method of the invention is useful for  
XX producing a plant accumulated with allergen specific T-cell epitope, and  
XX manufacturing a transgenic plant, preferably rice, integrated with T-cell  
XX epitope. The method is useful for preventing or treating allergic disease  
XX such as hay fever. The method enables the production of allergen specific  
XX T-cell epitope at a low cost and also reduces the amount for  
XX administration. The allergen specific T-cell epitope accumulated in a  
XX seed is stable for storage. This sequence represents rice 26 kDa peptide.  
XX  
SQ Sequence 23 AA;  
Query Match 100.0%; Score 29; DB 8; Length 23;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

QY      1 KVVFFA 6
DB      4 KVVFFA 9

RESULT 17
AAB05910
ID      AAB05910 standard; peptide; 37 AA.
XX
XX      AC
XX      AAB05910;
XX
DT      16-OCT-2000 (first entry)
XX
DE      Mouse inducible nitric oxide synthase calmodulin-binding region.
XX
XX      Mouse; inducible nitric oxide synthase; iNOS;
KW      endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;
KW      AMP-activated protein kinase; AMPK; calmodulin; CaM;
KW      eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;
KW      obstructive airways disease.
XX
OS      Mus sp.
XX
PN      WO200028076-A1.
XX
PD      18-MAY-2000.
XX
PF      05-NOV-1999; 99WO-AU000968.
XX
PR      06-NOV-1998; 98AU-00006976.
XX
PA      (SVIN-) ST VINCENTS INST MEDICAL RES.
XX
PI      Stapleton DJ, Chen Z, Michell BJ, Kemp BE, Mitchellhill KI;
XX      WPI; 2000-376583/32.
XX
XX      Identifying modulators of AMP-activated protein kinase-mediated
PT      activation of a nitric oxide synthase (NOS), for use in ischemic heart
PT      disease, comprises testing for the increase or decrease in
PT      phosphorylation of NOS.
XX
XX      Example 4; Fig 5; 4lpp; English.
XX
XX      The present sequence is the calmodulin (CaM)-binding region of mouse
CC      inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
CC      the enzyme NOS, which synthesises nitric oxide from the amino acid L-
CC      arginine. The sequence is provided for comparison with endothelial nitric
CC      oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
CC      phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
CC      Ca2+-CaM. Phosphorylation results in inhibition of eNOS. In the presence
CC      of Ca2+-CaM, phosphorylation by AMPK occurs predominantly at Ser-1177 and
CC      eNOS is activated. Modulators which activate AMPK may be used in the
CC      treatment of ischaemic heart disease by promoting glucose and fatty acid
CC      metabolism, and improving nutrient and oxygen supply to the myocytes.
CC      They may also be used for the treatment of pulmonary hypertension and
CC      obstructive airways disease
XX
XX      Sequence 37 AA;
XX
XX      Query Match      100.0%; Score 29; DB 3; Length 37;
XX      Best Local Similarity 100.0%; Pred. No. 22;
XX      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
DB      18 KVVFFA 23

RESULT 18
ADK34080
ID      ADK34080 standard; peptide; 37 AA.
XX

```

```

AC      ADK34080;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human nNOS calmodulin binding domain peptide seqid 7.
XX
KW      vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;
KW      eNOS; endothelial nitric oxide synthase; angiogenesis;
KW      microvascular dysfunction; human; calmodulin binding domain;
KW      neuronal nitric oxide; nNOS.
XX
OS      Homo sapiens.
XX
PN      WO2004016761-A2.
XX
PD      26-FEB-2004.
XX
PP      15-AUG-2003; 2003WO-US025626.
XX
PR      16-AUG-2002; 2002US-0403637P.
XX
PA      (SCHD ) SCHERING AG.
XX
PI      Dole WP, Kauser K, Qian HS, Rubanyi G;
XX      WPI; 2004-203789/19.
XX
XX      Treating critical limb ischemia (CLI), or angiogenesis comprises
PT      administering to a patient a polynucleotide encoding a mammalian
PT      endothelial nitric oxide synthase (eNOS) polypeptide.
XX
XX      Example 1; SEQ ID NO 7; 82pp; English.
XX
XX      The invention describes a method of creating critical limb ischaemia
CC      (CLI) comprising administering to a patient a polynucleotide encoding a
CC      mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
CC      described are: a method for treating angiogenesis by administering to a
CC      patient a polynucleotide encoding eNOS; and ameliorating microvascular
CC      dysfunction by administering to the patient the polynucleotide encoding
CC      the eNOS polypeptide. The method is useful for treating critical limb
CC      ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
CC      This is the amino acid sequence of a human neuronal nitric synthase
CC      (nNOS) calmodulin binding domain peptide.
XX
XX      Sequence 37 AA;
XX
XX      Query Match      100.0%; Score 29; DB 8; Length 37;
XX      Best Local Similarity 100.0%; Pred. No. 22;
XX      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
DB      18 KVVFFA 23

RESULT 19
ADL70727
ID      ADL70727 standard; peptide; 37 AA.
XX
XX      ADL70727;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Mouse iNOS calmodulin-binding site amino acid sequence SEQ ID NO:7.
XX
KW      mouse; endothelial nitric oxide synthase; eNOS; enzyme; mutant;
KW      calmodulin-binding domain; vasotropic; antiarteriosclerotic; hypotensive;
KW      antidiabetic; vulnerary; antilipaeamic; anorectic;
KW      reduced calcium dependence; ischaemia; atherosclerosis; hypertension;
KW      diabetes; Raynaud's phenomenon; poor wound healing; hyperlipidaemia;
XX      obesity; iNOS.
XX
XX      Mus musculus.
XX

```

```

XX PN WO2004016764-A2.
XX PD 26-FEB-2004.
XX PP 15-AUG-2003; 2003WO-US025745.
XX PR 16-AUG-2002; 2002US-0403638P.
XX PA (SCHD ) SCHERING AG.
XX PI Blasko E, Kauser K, Parkinson J;
XX PR WPI; 2004-203792/19.
XX PT New isolated endothelial nitric oxide synthase polypeptide mutant, useful
XX PT for diagnosing or treating ischemia, atherosclerosis, hypertension,
XX PT diabetes, Raynaud's phenomenon, poor wound healing, hyperlipidemia or
XX PT obesity.
XX PS Example 1; SEQ ID NO 7; 57pp; English.
XX CC The present sequence represents the calmodulin-binding site of mouse iNOS
XX CC amino acid sequence. The present invention describes endothelial nitric
XX CC oxide synthase (eNOS) mutants having one or more mutations in an amino
XX CC acid sequence corresponding to a functional domain of a mammalian eNOS.
XX CC At least one of the mutations is at a position corresponding to an amino
XX CC acid residue in a calmodulin-binding domain that is phosphorylated in
XX CC mammalian cells, and not an amino acid substitution to Ala or Asp. Also
XX CC described: (1) an isolated eNOS polypeptide mutant that is substantially
XX CC homologous, or has a 95-99% sequence identity to the amino acid sequence
XX CC of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide
XX CC encoding the polypeptide mutant; (3) a recombinant vector comprising the
XX CC polynucleotide operably linked to at least one regulatory sequence; (4) a
XX CC pharmaceutical composition comprising the polypeptide mutant or the
XX CC polynucleotide; (5) a binding partner of the polypeptide mutant; (6)
XX CC modulating eNOS activity in a cell by administering to the cell the
XX CC polypeptide mutant; (7) modulating eNOS activity in a cell by
XX CC administering the polypeptide mutant or the polynucleotide to the cell,
XX CC such that the polypeptide mutant is expressed in the cell; (8) diagnosing
XX CC a condition associated with aberrant eNOS activity by contacting a cell
XX CC of a patient with the polynucleotide, and detecting a level of eNOS
XX CC activity indicative of the medical condition; and (9) prophylactic and
XX CC therapeutic methods of treating a condition associated with aberrant eNOS
XX CC activity by administering the polypeptide mutant or polynucleotide to the
XX CC patient. The eNOS mutant has vasotropic, antiarteriosclerotic,
XX CC hypotensive, antidiabetic, vulnary, antilipemic and anorectic
XX CC activities, and has reduced calcium dependence and increased activity.
XX CC The polypeptide mutant, polynucleotide and methods are useful for
XX CC diagnosing or treating a condition associated with aberrant eNOS
XX CC activity, e.g. ischemia, atherosclerosis, hypertension, diabetes,
XX CC Raynaud's phenomenon, poor wound healing, hyperlipidemia or obesity.
XX SQ Sequence 37 AA;
Query Match 100.0%; Score 29; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 18 KVVFFA 23

RESULT 20
AAG02840
XX AC AAG02840 standard; protein; 77 AA.
XX AC AAG02840;
XX XX
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein, SEQ ID NO: 6921.

```

```

XX XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping.
XX XX Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX XX 21-FEB-2000; 2000EP-00200610.
XX PF 26-FEB-1999; 99US-0122487P.
XX PR (BEST ) GENSET.
XX PA Dumas Milne Edwards J, Duclert A, Giordano J;
XX PI WPI; 2000-500381/45.
XX DR N-PSDB; AAC02846.
XX XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 13; SEQ ID NO 6921; 71pp + Sequence Listing; English.
XX CC The present sequence is a polypeptide encoded by one of a large number of
XX CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX CC tissues. EST sequences usually correspond mainly to the 3' untranslated
XX CC region (UTR) of the mRNA because they are often obtained from oligo-dT
XX CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX CC sequences derived from the 5' ends of mRNAs and even in those cases where
XX CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX CC are also used in diagnostic, forensic, gene therapy and chromosome
XX CC mapping procedures. They are used to obtain upstream regulatory sequences
XX CC and to design expression and secretion vectors
XX SQ Sequence 77 AA;
Query Match 100.0%; Score 29; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 38 KVVFFA 43

RESULT 21
AAO11219
ID AAO11219 standard; protein; 175 AA.
XX AC AAO11219;
XX XX
XX DT 06-NOV-2001 (first entry)
XX XX Human polypeptide SEQ ID NO 25111.
XX DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorders; arthritis; inflammation.
XX XX Homo sapiens.
XX OS WO200164835-A2.
XX PN 07-SEP-2001.
XX PD
XX XX

```

```

PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
XX
XX WPI; 2003-229341/22.
XX N-PSDB; ADC07961.
XX
XX New plant genes encoding polypeptides having an activity involved in or
XX associated with the synthesis, metabolism or degradation of carbohydrates
XX in the plant grain useful in generating plants having improved
XX nutritional properties.
XX
XX Claim 15; SEQ ID NO 228; 130pp; English.
XX
XX This invention, in the area of plant biotechnology, relates to novel
XX polynucleotides comprising a nucleotide sequence encoding a protein which
XX is involved in or associated with the synthesis, metabolism or
XX degradation of carbohydrates in the plant grain and the expression of
XX which is up-regulated during grain filling. The plant is selected from
XX corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
XX sugarbeet, wheat, and rice. The invention may be useful for the
XX improvement of protein, oil, starch, fibre and moisture content of the
XX cereal grains. In addition, carbohydrate levels may be modified to a more
XX desirable level using the present invention. The present sequence is the
XX amino acid sequence of a rice protein of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/publishedpct_sequences.
XX
XX Sequence 186 AA;
XX
XX Query Match 100.0%; Score 29; DB 7; Length 186;
XX Best Local Similarity 100.0%; Pred. NO. 1.1e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX QY 1 KVVFFA 6
XX DB 4 KVVFFA 9
XX |||||
XX
XX RESULT 23
XX ADC07948
XX ID ADC07948 standard; protein; 186 AA.
XX AC ADC07948;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Rice protein sequence Seq ID214 related to grain filling.
XX
XX KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
XX tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
XX wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
XX gene; ds; plant.
XX
XX OS Oryza sativa.
XX
XX PN WO200300905-A2.
XX
XX PD 03-JAN-2003.
XX
XX PF 21-JUN-2002; 2002WO-IB002450.
XX
XX PR 22-JUN-2001; 2001US-0300112P.
XX
XX PR 26-SEP-2001; 2001US-0325277P.
XX
XX PR 20-DEC-2001; 2001US-0342327P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
XX Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
XX
XX WPI; 2003-229341/22.
XX N-PSDB; ADC07947.
XX

```

4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
8

PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249246P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Barash SC, Ruben SM;  
 DR N-PSDB; AAK56573.  
 DR WPI; 2001-483426/52.  
 XX N-PSDB; AAK56573.  
 XX  
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
 useful for preventing, diagnosing and/or treating cancers and metastasis.  
 XX  
 PS Claim 11; SEQ ID NO 11385; 3071bp + Sequence Listing; English.  
 XX  
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
 CC amino acid sequences given in AAK82170 to AAK51921. (I) have cytostatic  
 CC activity, and can be used in gene therapy and vaccine production. (I)  
 CC proteins and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC example, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patient's own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting the  
 CC nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) proteins and polynucleotides may be used to prevent,  
 CC diagnose and treat immune/hematopoietic-related diseases, especially  
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
 CC to AAK87694 represent human immune/hematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
 CC represent sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 190 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 14 KVVFFA 19  
 |||||  
 |||||  
 RESULT 25  
 ADQ66704  
 ID ADQ66704 standard; protein; 854 AA.  
 XX  
 AC ADQ66704;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Novel human protein sequence #1677.  
 XX  
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;  
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;  
 XX cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1440981-A2.  
 XX  
 PD 28-JUL-2004.  
 XX  
 PF 21-JAN-2004; 2004EP-00001196.  
 XX  
 PR 21-JAN-2003; 2003JP-00102206.  
 PR 09-MAY-2003; 2003JP-00131392.  
 XX  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Nagai K, Irie R;  
 XX WPI; 2004-535376/52.  
 DR N-PSDB; ADQ64516.  
 XX  
 PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,  
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
 XX  
 PS Claim 1; SEQ ID NO 3865; 2449pp; English.  
 XX  
 CC The invention relates to 2495 novel polynucleotides (I) and their encoded  
 CC polypeptides, sequences hybridizing to these nucleotides, sequences  
 CC encoding partial polypeptides and sequences having 70% or 90% identity to  
 CC the nucleotide and protein sequences. The nucleotides and polypeptides  
 CC are useful as diagnostic markers or therapeutic target for the diseases  
 CC or morbid states. They are also useful for treating osteoporosis,  
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,  
 CC dementia and various cancers. This sequence corresponds to a protein  
 CC sequence of the invention.  
 XX  
 SQ Sequence 854 AA;  
 Query Match 100.0%; Score 29; DB 8; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 221 KVVFFA 226  
 |||||  
 |||||

RESULT 26  
 ID ABM83252 standard; protein; 922 AA.  
 XX  
 AC ABM83252;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3501.  
 XX  
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004023973-A2.  
 XX  
 XX 25-MAR-2004.  
 XX  
 XX 12-SEP-2003; 2003WO-US028227.  
 XX  
 XX 12-SEP-2002; 2002US-0410259P.  
 XX  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX  
 XX (INCY-) INCYTE CORP.  
 XX  
 XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
 PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, AU AP, Gerstin EH;  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
 PI Legace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patury S, Shi X, Suarez CJ;  
 XX  
 DR WPI; 2004-329368/30.  
 DR N-PSDB; ACN41904.  
 XX  
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 PS Claim 27; Page; 190pp; English.  
 XX  
 CC The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dithp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dithp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
 XX  
 SQ Sequence 922 AA;

Query Match 100.0%; Score 29; DB 8; Length 922;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 291 KVVFFA 296

RESULT 27  
 ADF76335  
 ID ADF76335 standard; protein; 925 AA.  
 XX  
 AC ADF76335;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein SeqID 8.  
 XX  
 KW human; PRO; membrane bound protein; membrane bound receptor;  
 KW cell proliferation; cell migration; cell differentiation;  
 KW mitogenic factor; survival factor; cytotoxic factor;  
 KW differentiation factor; neuropeptide; hormone; cell receptor;  
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003072035-A2.  
 XX  
 XX 04-SEP-2003.  
 XX  
 XX 21-FEB-2003; 2003WO-US005241.  
 XX  
 XX 22-FEB-2002; 2002US-0359461P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;  
 PI Williams PM, Wood WI, Wu TD;  
 XX  
 XX WPI; 2003-721702/68.  
 DR N-PSDB; ADF76334.  
 XX  
 XX New PRO polypeptides, useful for diagnosing and treating an immune  
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or  
 PT diabetes mellitus.  
 XX  
 PS Claim 10; SEQ ID NO 8; 918pp; English.  
 XX  
 CC This invention relates to novel nucleic acids encoding human PRO secreted  
 CC and transmembrane proteins. Extracellular proteins play important roles  
 CC in the formation, differentiation and maintenance of multicellular  
 CC organisms. The fate of many individual cells (for example proliferation,  
 CC migration or differentiation) is typically governed by information  
 CC received from other cells and the immediate environment. The information  
 CC is often transmitted by secreted polypeptides (for example mitogenic  
 CC factors, survival factors, cytotoxic factors, differentiation factors,  
 CC neuropeptides and hormones) which are received and interpreted by diverse  
 CC cell receptors or membrane bound proteins. These membrane bound proteins  
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such  
 CC as in the blocking of receptor-ligand interactions. The current invention  
 CC provides the amino acid sequences of novel human membrane bound receptors  
 CC and proteins, along with the cDNA sequences encoding them. The novel  
 CC proteins of the invention may have cytostatic activities through the  
 CC stimulation of chondrocytes. The nucleic acids of the invention may be  
 CC useful for the manufacture of a medicament for diagnosing or treating a  
 CC tumour in a mammal. In addition, they may be useful for measuring or  
 CC detecting the expression of a tumour associated gene. The present  
 CC sequence is the amino acid sequence of a human PRO protein of the  
 CC invention.  
 XX  
 SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 7; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 292 KVVFFA 297

RESULT 28  
ADJ70225  
ID ADJ70225 standard; protein; 925 AA.  
XX  
XX  
AC ADJ70225;  
XX  
XX  
DT 06-MAY-2004 (first entry)  
XX  
XX  
DE Human heat mitochondrial protein as a therapeutic target SeqID2031.  
XX  
XX  
KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX  
OS Homo sapiens.  
XX  
XX  
EN WO2003087768-A2.  
XX  
XX  
PD 23-OCT-2003.  
XX  
XX  
PF 04-APR-2003; 2003WO-US010870.  
XX  
XX  
PR 12-APR-2002; 2002US-0372843P.  
PR 17-JUN-2002; 2002US-0389987P.  
PR 20-SEP-2002; 2002US-0412418P.  
XX  
XX  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX  
XX  
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
XX  
XX  
WPI; 2003-845369/78.  
XX  
XX  
XX  
PT Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX  
XX  
PS Claim 1; SEQ ID NO 2031; 180pp; English.  
XX  
XX  
CC This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, neurotropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytostatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX  
SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 7; Length 925;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVEFA 6  
|||||  
Db 292 KVVEFA 297

RESULT 29  
ADJ75428  
ID ADJ75428 standard; protein; 925 AA.  
XX  
XX  
AC ADJ75428;  
XX  
XX  
DT 20-MAY-2004 (first entry)  
XX  
XX  
DE Marker gene related amino acid sequence SEQ ID NO:680.  
XX  
XX  
KW bronchial asthma; chronic obstructive pulmonary disease;  
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
KW gene therapy; marker.  
XX  
OS Homo sapiens.  
XX  
XX  
EN EP1394274-A2.  
XX  
XX  
PD 03-MAR-2004.  
XX  
XX  
PF 04-AUG-2003; 2003EP-00254857.  
XX  
XX  
PR 06-AUG-2002; 2002JP-00229312.  
PR 20-MAR-2003; 2003JP-00077212.  
XX  
XX  
PA (GENO-) GENOX RES INC.  
XX  
XX  
PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;  
XX  
XX  
DR WPI; 2004-193155/19.  
XX  
XX  
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by  
PT comparing the expression level of a marker gene in a biological sample  
PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.  
XX  
XX  
PS Example 11; SEQ ID NO 680; 241pp; English.  
XX  
XX  
CC The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic  
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
CC genes (S1) whose expression levels increase when respiratory epithelial  
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
CC whose expression levels decrease when respiratory epithelial cells are  
CC stimulated with interleukin-13. Also described: (1) a reagent (1) for  
CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
CC (2) a kit for screening for a candidate compound for a therapeutic agent  
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
CC an animal model for bronchial asthma or chronic obstructive pulmonary  
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
CC method for producing an animal model for bronchial asthma or chronic  
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
CC a marker gene or an antisense nucleic acid corresponding to a portion of  
CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
CC expression of the gene through an RNAi effect or an antibody recognising  
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
CC probe has been immobilised to assay a marker gene. (1) has respiratory  
CC and antiasthmatic activities, and can be used in gene therapy. The method  
CC is useful for testing for or screening for a therapeutic agent for  
CC bronchial asthma or chronic obstructive pulmonary disease. The present  
CC sequence is used in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 KVVFFA 6  
 Db 292 KVVFFA 297

RESULT 30  
 ID ADJ75495 standard; protein; 925 AA.  
 AC ADJ75495;  
 XX  
 DT 20-MAY-2004 (first entry)  
 DE Marker gene related amino acid sequence SEQ ID NO:747.  
 KW bronchial asthma; chronic obstructive pulmonary disease;  
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
 KW gene therapy; marker.  
 XX  
 OS Homo sapiens.  
 XX  
 FN EPI394274-A2.  
 XX  
 PD 03-MAR-2004.  
 XX  
 PP 04-AUG-2003; 2003EP-00254857.  
 XX  
 PR 06-AUG-2002; 2002JP-00229312.  
 PR 20-MAR-2003; 2003JP-00077212.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Ontani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;  
 DR WPI; 2004-193155/19.  
 XX  
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by  
 PT comparing the expression level of a marker gene in a biological sample  
 PT from a subject with the expression level of the gene in a sample from a  
 PT healthy subject.  
 XX  
 PS Example 11; SEQ ID NO 747; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (I) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (I) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 925 AA;  
 Query Match 100.0%; Score 29; DB 8; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 Db 292 KVVFFA 297

RESULT 31  
 ADN04860  
 ID ADN04860 standard; protein; 925 AA.  
 XX  
 AC ADN04860;  
 XX  
 DT 01-JUL-2004 (first entry)  
 DE Antipsoriatic protein sequence #610.  
 KW antipsoriatic; gene therapy; psoriasis; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004028479-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PP 25-SEP-2003; 2003WO-US030907.  
 PR 25-SEP-2002; 2002US-0414006P.  
 XX  
 PA (CBTH ) GENENTECH INC.  
 XX  
 PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
 PI Wu TD;  
 XX  
 DR WPI; 2004-305105/28.  
 DR N-PSDB; ADN04859.  
 XX  
 PT New PRO nucleic acid or polypeptide, useful for preparing a  
 PT pharmaceutical composition for diagnosing or treating psoriasis in a  
 PT mammal.  
 XX  
 PS Claim 9; SEQ ID NO 1254; 3069pp; English.  
 XX  
 CC The invention relates to novel polynucleotide and polypeptides for  
 CC treating psoriasis or a sequence having at least 80% identity to the  
 CC above sequences. The nucleic acid is useful for preparing a composition  
 CC for diagnosing or treating psoriasis in a mammal. This sequence  
 CC corresponds to one of the polypeptides of the invention.

XX SQ Sequence 925 AA;  
 Query Match 100.0%; Score 29; DB 8; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 Db 292 KVVFFA 297

RESULT 32  
 ADR14233  
 ID ADR14233 standard; protein; 925 AA.  
 XX  
 AC ADR14233;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX



DE Human NF-kappaB pathway-associated protein SeqID234.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;

KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;

KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;

KW immunosuppressive; vulnery; gene therapy; immune disorder;

KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;

KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;

KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;

KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;

KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;

KW viral replication; host cell survival; evasion of immune response;

KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;

KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;

KW autoimmune disorder; hyper immune activity;

KW aberrant acute phase response; hypercongenital condition; birth defect;

KW necrotic lesion; wound; organ transplant rejection;

KW aberrant signal transduction; proliferating disorder; cancer;

KW HIV propagation; human.

XX Homo sapiens.

OS

XX

XX WO2004065577-A2.

XX

XX 05-AUG-2004.

XX

XX 13-JAN-2004; 2004WO-US000798.

XX

XX 14-JAN-2003; 2003US-0440068P.

PR

PR 12-MAY-2003; 2003US-0469757P.

XX

PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX

XX Nadler SG, Neubauer MG, Feder JN, Carman J;

PI

PI WPI; 2004-562168/54.

DR

DR N-PSDB; ADRI4232.

XX

XX New isolated polynucleotides and polypeptides associated with NF-kappaB

PT pathway, useful for diagnosing, treating, or preventing disorders or

PT diseases associated with NF-kappaB pathway.

XX

XX Claim 6; SEQ ID NO 234; 237pp; English.

PS

XX This invention relates to the novel association of protein sequences (and

CC the genes which encode them) to the NF-kappaB pathway. The invention may

CC be useful for the production of compounds with an antiinflammatory,

CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,

CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,

CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or

CC vulnery activity or for gene therapy. The proteins and nucleotides are

CC useful for diagnosing, preventing, treating, or ameliorating conditions

CC or diseases associated with the NF-kappaB pathway. The condition is an

CC immune disorder, an inflammatory disorder, an inflammatory disorder

CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,

CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM

CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic

CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,

CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell

CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory

CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick

CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper

CC immune activity, disorders related to aberrant acute phase responses,

CC hypercongenital conditions, birth defects, necrotic lesions, wounds,

CC organ transplant rejection, conditions related to organ transplant

CC rejection, disorders related to aberrant signal transduction,

CC proliferating disorders, cancers and HIV propagation in cells infected

CC with other viruses. The present sequence is that of a human protein which

CC is subject to the novel association with the NF-kappaB pathway of the

CC invention. Note: This sequence does not appear in the specification but

CC was obtained by the indexer from Genbank.

XX

XX Sequence 925 AA;

XX

Query Match 100.0%; Score 29; DB 8; Length 925;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

DB 292 KVVFFA 297

RESULT 33

ADP25011

ID ADP25011 standard; protein; 925 AA.

XX

AC ADP25011;

XX

DT 18-NOV-2004 (first entry)

XX

DE PRO polypeptide SEQ ID NO:2189.

XX

KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;

KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX

OS Unidentified.

XX

XX WO2004041170-A2.

XX

XX 21-MAY-2004.

XX

XX 30-OCT-2003; 2003WO-US034312.

PF

XX

XX 01-NOV-2002; 2002US-0423394P.

PR

XX

XX (GETH ) GENENTECH INC.

PA

XX

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

PI

PI Wu TD;

XX

XX WPI; 2004-419628/39.

DR

DR N-PSDB; ADP25010.

XX

XX New PRO polypeptides and polynucleotides, useful for treating e.g.

PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated

PT renal disease, or demyelinating diseases of the central or peripheral

PT nervous system.

XX

XX Claim 7; SEQ ID NO 2189; 2940pp; English.

PS

XX The invention relates to a novel isolated nucleic acid and the PRO

CC polypeptide encoded by it. A protein of the invention has

CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,

CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide

CC of the invention may have a use in gene therapy. The PRO polypeptide, its

CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous

CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,

CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary

CC disease, infectious or autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,

CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's

CC disease, an autoimmune or immune-mediated skin disease, a bullous skin

CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic

CC disease, asthma, allergic rhinitis, atopic dermatitis, food

CC hypersensitivity, urticaria, an immunologic disease of the lung,

CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity

CC pneumonia, a transplantation associated disease, graft rejection or  
 CC graft-versus-host disease. The present sequence represents a PRO protein  
 CC of the invention.

SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 292 KVVFFA 297

RESULT 34

ID ADR97294 standard; protein; 925 AA.

XX ADR97294;

DT 02-DEC-2004 (first entry)

DE Human RIG-I-DEAD/H box protein, an apoptosis related target Seq 2.

XX human; enzyme; apoptosis; cancer; inflammation; autoimmune;  
 KW neurodegenerative disorder; cytostatic; antiinflammatory;  
 KW immunosuppressive; neuroprotective; gene therapy; RIG-I-DEAD/H box.

XX Homo sapiens.

XX WO2004078783-A2.

XX 16-SEP-2004.

XX 05-MAR-2004; 2004WO-GB000957.

XX 07-MAR-2003; 2003GB-00005267.

XX (EIRX-) EIRX THERAPEUTICS LTD.

XX Murphy FJ, Sheehan DE, Keating KE, Hayes I, Seera L;

XX WPI; 2004-662402/64.

XX N-PSDB; ADR97293.

PT Identifying an agent that modulates the function of an apoptosis-  
 PT associated polypeptide, useful for diagnosing or treating e.g. cancer,  
 PT comprises comparing the binding of the polypeptide to the candidate agent  
 PT and to a control agent.

PS Claim 1; SEQ ID NO 2; 304pp; English.

XX This invention relates to novel agents that modulates the function of  
 CC human apoptosis-associated proteins specified within the specification.  
 CC Specifically, it refers to a method for the identification of target  
 CC genes whose expression is correlated with an early stage in the  
 CC regulation of apoptosis. The present invention describes a method of  
 CC contacting either candidate agents or control agents to the target genes  
 CC and assessing the difference of binding and inhibitory activity, where  
 CC the candidate agent is selected from a low molecular weight organic  
 CC molecule, an antibody or fragment thereof, an antisense oligonucleotide,  
 CC a small inhibitory dsRNA, or a ribozyme. As such, the compositions and  
 CC methods are useful for diagnosing and treating diseases or conditions  
 CC associated with abnormal apoptosis in mammalian tissue, such as cancer,  
 CC inflammation, autoimmune or neurodegenerative disorders. Accordingly,  
 CC they exhibit cytostatic, antiinflammatory, immunosuppressive and  
 CC neuroprotective activities. These may also be used for drug screening  
 CC purposes and in gene therapy. This polypeptide sequence is a human target  
 CC protein, an enzyme associated with the regulation of apoptosis whose  
 CC expression is modulated by novel agents of the invention.

XX Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 292 KVVFFA 297

RESULT 35

ADY17516

ID ADY17516 standard; protein; 925 AA.

XX ADY17516;

DT 05-MAY-2005 (first entry)

DE PRO polypeptide SEQ ID NO 3322.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
 KW Antiallergic; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH ) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

PS Claim 8; SEQ ID NO 3322; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO  
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,  
 CC composition, and method are useful for diagnosing and treating an immune  
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
 CC arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 925 AA;

Query Match 100.0%; Score 29; DB 9; Length 925;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 292 KVVFFA 297

RESULT 36

AEA23525

ID AEA23525 standard; protein; 925 AA.

XX AEA23525;

DT 11-AUG-2005 (first entry)

XX

XX PD

CC The invention relates to two DNA molecules encoding inducible nitric  
 CC oxide synthase (iNOS) proteins, where the DNA molecules comprise defined  
 CC sequences of 4041 and 4165 base pairs given in the specification and the  
 CC proteins have 1144 amino acids. Also claimed are expression vectors  
 CC containing the DNA molecules, and recombinant host cells containing the  
 CC vectors. The DNA molecules are useful for producing the recombinant  
 CC proteins. The present sequence represents inducible nitric oxide, long  
 CC isoform. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 2; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 514 KVVFFA 519

RESULT 39  
 AAG64500  
 ID AAG64500 standard; protein; 1144 AA.

XX AAG64500;

DT 02-OCT-2001 (first entry)  
 DE Mouse inducible nitric oxide synthase 2.

KW Antisense oligonucleotide; inducible nitric oxide synthase;  
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;  
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;  
 KW 2'-O-methoxyethyl; phosphorothioate; mouse.

XX Mus sp.

XX WO200152902-A1.

XX 26-JUL-2001.

XX 15-JAN-2001; 2001WO-US001381.

XX 24-JAN-2000; 2000US-00490208.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dean NM, Cowbert LM;

XX WPI; 2001-465340/50.

XX N-PSDB; AAH47974.

PT New antisense oligonucleotides for modulating the expression of inducible  
 PT nitric oxide synthase in cells or tissues, particularly useful for  
 PT treating e.g. immunological, cardiovascular or neurological disorders, or  
 PT ischemia.

PS Example 17; Page 110-114; 144pp; English.

CC The invention relates to antisense compounds, especially  
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible  
 CC nitric oxide synthase and which specifically hybridise to and modulate  
 CC expression of inducible nitric oxide synthase. The antisense compounds  
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,  
 CC neuroprotective, disorder and vasotropic activity. The antisense  
 CC oligonucleotides are useful for inhibiting the expression of inducible  
 CC nitric oxide synthase in cells or tissues. In particular, the antisense  
 CC oligonucleotides are useful for treating diseases or disorders associated  
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological  
 CC disorder, cardiovascular disorder, neurological disorder or  
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also  
 CC useful for research and diagnostics. The present sequence is that of  
 CC mouse inducible nitric oxide synthase

XX SQ Sequence 1144 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 514 KVVFFA 519

RESULT 40  
 ABU79138  
 ID ABU79138 standard; protein; 1144 AA.

XX ABU79138;

XX 18-JUN-2003 (first entry)

XX Inducible nitric oxide synthase protein.

KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;  
 KW gene therapy; mammalian cell receptor; cytostatic;  
 KW tumour associated lipid; energy; T cell; antigen presenting cell; APC;  
 KW tumouricidal immunocyte; antitumour.

XX Unidentified.

XX US2002177551-A1.

XX 28-NOV-2002.

XX 30-MAY-2001; 2001US-00870759.

XX 31-MAY-2000; 2000US-0208128P.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2003-361759/34.

XX N-PSDB; ACA64740.

PT A mammalian cell receptor, useful in the treatment of cancer by binding  
 PT to tumor associated lipids where the binding induces energy or apoptosis  
 PT in T cells and antigen presenting cells.

PS Example 2; Page; 167pp; English.

CC The invention relates to a mammalian cell receptor, useful in the  
 CC treatment of cancer, which binds to tumour associated lipids and induces  
 CC energy or apoptosis in the T cells and antigen presenting cells (APCs).  
 CC Also included are a mammalian cell useful in the treatment of cancer  
 CC where the receptor which binds tumour associated lipids and induces  
 CC cellular inactivation or death is deleted or functionally deactivated,  
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal  
 CC (by allowing tumour associated lipids to contact immunocytes in which  
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,  
 CC sphingolipids, glycosphingolipids, phosphoglycolipids, gangliosides,  
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or  
 CC deleted), a construct useful in the treatment of cancer comprising a  
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell  
 CC useful in the treatment of cancer (where an adaptor protein which  
 CC inhibits T cell activation by tumour associated antigens is deleted or  
 CC functionally deactivated), a composition useful in the treatment of  
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing  
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by  
 CC allowing tumour associated lipids to contact immunocytes, in which  
 CC receptors for the lipids are inactivated or deleted to produce a  
 CC tumouricidal immunocyte population, and administering the tumouricidal  
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC  
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to

CC contact APCs, in which receptors for the tumour associated lipids are  
 CC inactivated or deleted to produce a tumouricidally activated population,  
 CC and administering APCs to the host), producing a tumouricidal T cell  
 CC population ex vivo in a mammal) by allowing a tumour associated lipids to  
 CC contact T cells, in which adaptor proteins, which inhibit T cell  
 CC activation by tumour associated antigens, are deleted or functionally  
 CC deactivated to produce a tumouricidal population of T cells, and  
 CC administering the tumouricidally activated T cells to the host, or  
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and  
 CC administering the tumouricidally activated T cells to the host), treating  
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which  
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)  
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a  
 CC tumour associated antigen to contact immunocytes in which adaptor  
 CC proteins which inhibit T cell activation by tumour associated antigens  
 CC are deleted or functionally deactivated) and producing (M7) a  
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a  
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The  
 CC receptors, methods and compositions are useful for treating cancers and  
 CC tumours. Bacterial superantigens are co-administered or administered as  
 CC fusion constructs with anti-tumour proteins or motifs. The present  
 CC sequence represents an anti-tumour protein which is co-administered with  
 CC or incorporated into a fusion construct with a superantigen. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format from the US patent  
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"  
 XX  
 XX Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 6; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 76+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 514 KVVFFA 519

RESULT 41  
 ADF43404  
 ID ADF43404 standard; protein; 1144 AA.

AC ADF43404;

XX 12-FEB-2004 (first entry)

XX INOS polypeptide seqid 124.

XX receptor; lipid-based tumour associated antigen; cytostatic;  
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;  
 KW infectious disease; iNOS.

XX Unidentified.

XX US2003157113-A1.

XX 21-AUG-2003.

XX 28-DEC-2000; 2000US-00751708.

XX 28-DEC-1999; 99US-0173371P.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2003-787326/74.

XX N-PSDB; ADF43403.

XX New receptor in a mammalian cell that inhibits regular activation by  
 PT receptors specific for lipid-based tumor associated antigens, useful for  
 PT treating a neoplastic disease or tumor, and infectious diseases.

PS Example 3; SEQ ID NO 124; 151pp; English.  
 XX The invention describes a receptor in a mammalian cell that inhibits  
 CC regular activation by receptors specific for lipid-based tumour  
 CC associated antigen. The receptor has cytostatic and antimicrobial  
 CC properties and is suitable for use in gene therapy. The receptors,  
 CC methods and compositions are useful for treating a neoplastic disease or  
 CC tumour (cancer), and infectious diseases. This sequence represents iNOS  
 CC polypeptide, a cell surface moiety, the DNA of which can be transfected  
 CC into a cell with superantigen DNA to generate antitumour immunity.

XX Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 7; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 76+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 514 KVVFFA 519

RESULT 42

ADP77432  
 ID ADF77432 standard; protein; 1144 AA.

XX ADF77432;

XX 26-FEB-2004 (first entry)

XX Mouse inducible nitric oxide synthase, iNOS.

KW Mouse; inducible nitric oxide synthase; iNOS; cardiant; vasodilator;  
 KW cytostatic; gynaecological; restenotic response; angioplasty;  
 KW vasodilation; angina; cancer; cell death; premature labour; tumour;  
 KW nervous system; brain; erectile dysfunction; uterus; lung; vascular tone;  
 KW regional blood flow.

XX Mus musculus.

XX US6620616-B1.

XX 16-SEP-2003.

XX 13-SEP-2000; 2000US-00661258.

XX 13-SEP-2000; 2000US-00661258.

XX (CLEV-) CLEVELAND CLINIC FOUND.

XX Stuehr DJ, Adak S;

XX WPI; 2003-895427/82.

XX New isolated polynucleotide encoding a variant of a corresponding wild-  
 PT type nitric oxide synthase, useful for reducing the restenotic response  
 PT after angioplasty, or for inhibiting the development or onset of  
 PT premature labor.

XX Disclosure; SEQ ID NO 5; 35pp; English.

XX The invention relates to an isolated polynucleotide encoding a variant of  
 CC a corresponding wild-type nitric oxide synthase (NOS). The variant has  
 CC the tryptophan in the alpha 3 helix substituted by tyrosine or  
 CC phenylalanine. Also included are a nucleic acid construct comprising the  
 CC nucleotide sequence that encodes a variant of a corresponding wild-type  
 CC nitric oxide synthase and a promoter operably linked to the encoding  
 CC sequence of the variant and a transformed cell comprising the construct,  
 CC where the cell expresses the nitric oxide synthase variant. The variant  
 CC has an in vitro enzymatic activity that is greater than the in vitro  
 CC enzymatic activity of the corresponding wild-type nitric oxide synthase.  
 CC The variant can preferably be of a corresponding wild-type endothelial  
 CC nitric oxide synthase (eNOS), neuronal nitric oxide synthase (nNOS), or

inducible nitric oxide synthase (iNOS). The polynucleotides are useful for reducing the restenotic response after angioplasty, or related interventional procedures, or to enhance the vasodilation response in treating angina, for anticancer therapy to promote cell death, and for inhibiting the development or onset of premature labour. The polynucleotides are useful to achieve or augment expression of NOS variant proteins or polypeptides in vivo to increase NOS production in target tissue, tumour tissue, tissue of the nervous system, including brain, penis (e.g. in erectile dysfunction) and uterine tissue, and lung tissue. NOS is useful for maintaining vascular tone and regulating regional blood flow. The present sequence is wild-type mouse iNOS.

XX Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 7; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519  
|||||

#### RESULT 43

ADJ76212  
ID ADJ76212 standard; protein; 1144 AA.

XX AC

XX ADJ76212;

XX DT 20-MAY-2004 (first entry)

XX DE Marker gene related amino acid sequence SEQ ID NO:1464.

XX KW bronchial asthma; chronic obstructive pulmonary disease;

XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
XX KW gene therapy; marker.

XX OS Mus musculus.

XX PN EPI394274-A2.

XX PD 03-MAR-2004.

XX PF 04-AUG-2003; 2003EP-00254857.

XX PR 06-AUG-2002; 2002JP-00229312.

XX PR 20-MAR-2003; 2003JP-00077212.

XX PA (GENO-) GENOX RES INC.

XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuohara K;

XX DR WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by  
PT comparing the expression level of a marker gene in a biological sample  
PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.

XX PS Claim 16; SEQ ID NO 1464; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic  
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
CC genes (S1) whose expression levels increase when respiratory epithelial  
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
CC whose expression levels decrease when respiratory epithelial cells are  
CC stimulated with interleukin-13. Also described: (1) a reagent (1) for  
CC testing for bronchial asthma or chronic obstructive pulmonary disease;

CC (2) a kit for screening for a candidate compound for a therapeutic agent  
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
CC an animal model for bronchial asthma or chronic obstructive pulmonary  
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
CC method for producing an animal model for bronchial asthma or chronic  
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
CC a marker gene or an antisense nucleic acid corresponding to a portion of  
CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
CC expression of the gene through an RNAi effect or an antibody recognising  
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
CC probe has been immobilised to assay a marker gene. (1) has respiratory  
CC and antiasthmatic activities, and can be used in gene therapy. The method  
CC is useful for testing for or screening for a therapeutic agent for  
CC bronchial asthma or chronic obstructive pulmonary disease. The present  
CC sequence is used in the exemplification of the present invention.

XX Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 8; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519  
|||||

#### RESULT 44

ADJ76136  
ID ADJ76136 standard; protein; 1144 AA.

XX AC ADJ76136;

XX DT 20-MAY-2004 (first entry)

XX DE Marker gene related amino acid sequence SEQ ID NO:1388.

XX KW bronchial asthma; chronic obstructive pulmonary disease;  
XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
XX KW gene therapy; marker.

XX OS Mus musculus.

XX PN EPI394274-A2.

XX PD 03-MAR-2004.

XX PF 04-AUG-2003; 2003EP-00254857.

XX PR 06-AUG-2002; 2002JP-00229312.

XX PR 20-MAR-2003; 2003JP-00077212.

XX PA (GENO-) GENOX RES INC.

XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuohara K;

XX DR WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by  
PT comparing the expression level of a marker gene in a biological sample  
PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.

XX PS Claim 16; SEQ ID NO 1388; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic

CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
 CC genes (S1) whose expression levels increase when respiratory epithelial  
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
 CC whose expression levels decrease when respiratory epithelial cells are  
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for  
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
 CC (2) a kit for screening for a candidate compound for a therapeutic agent  
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
 CC an animal model for bronchial asthma or chronic obstructive pulmonary  
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
 CC method for producing an animal model for bronchial asthma or chronic  
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
 CC a marker gene or an antisense nucleic acid corresponding to a portion of  
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
 CC expression of the gene through an RNAi effect or an antibody recognising  
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
 CC probe has been immobilised to assay a marker gene. (I) has respiratory  
 CC and antiasthmatic activities, and can be used in gene therapy. The method  
 CC is useful for testing for or screening for a therapeutic agent for  
 CC bronchial asthma or chronic obstructive pulmonary disease. The present  
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 8; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 DB 514 KVVFFA 519

RESULT 45

AEA03075  
 ID AEA03075 standard; protein; 1144 AA.

XX AC AEA03075;

XX DT 28-JUL-2005 (first entry)

XX DE VEGF amino acid sequence SEQ ID NO:101.

XX KW tumor; neoplasm; gene therapy; immunotherapy; cytostatic;  
 XX KM vascular endothelial cell growth factor.

XX OS Unidentified.

XX PN US2005112141-A1.

XX PD 26-MAY-2005.

XX PF 08-SEP-2004; 2004US-00937758.

XX PR 30-AUG-2000; 2000US-00650884.

XX PA (TERM/) TERMAN D S.

XX PI Terman DS;

XX DR N-PSDB; AEA03074.

XX DR N-PSDB; AEA03074.

XX PT New composition for treating a tumor or neoplastic disease in a subject  
 XX PT comprises conjugates comprising superantigen polypeptides or nucleic  
 XX PT acids with other molecules that produce a tumoricidal response.

XX PS Example 3; SEQ ID NO 101; 125pp; English.

XX CC The invention relates to a composition for treating a tumor or neoplastic  
 XX CC disease in a subject. Also described: (1) a mammalian cell comprising an

CC exogenous nucleic acid encoding a superantigen expressed in the cell,  
 CC which cell also produces or expresses all alpha-anomers of  
 CC monoglycosylceramide or diglycosylceramide, where expression of the  
 CC superantigen and the mono- or diglycosylceramide is capable of eliciting  
 CC an antitumor immune response in a mammal into which the cell is  
 CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)  
 CC preparing a population of immunotherapeutic T or natural killer T (NKT)  
 CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an  
 CC apoptotic cell preparation or lysate useful for treating a tumor or  
 CC neoplastic disease in a subject, comprising a cell population that has  
 CC been transfected with naked DNA encoding a superantigen, and treated to  
 CC undergo apoptosis or lysis; and (5) a cell that has ingested or been  
 CC transfected with the above apoptotic preparation or lysate, thus,  
 CC rendering the cell effective in presenting material expressed from  
 CC transfecting nucleic acid or material ingested to the immune system of a  
 CC mammal to elicit an anti-tumor immune response. The composition and  
 CC methods are useful for treating tumors or neoplastic diseases. The  
 CC present sequence represents a VEGF protein sequence, which is used in an  
 CC example from the present invention. Note - The sequence data for this  
 CC patent is not represented in the printed specification, but was obtained  
 CC in electronic format directly from the USPTO web site.

XX SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 9; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 DB 514 KVVFFA 519

RESULT 46

AAB48483  
 ID AAB48483 standard; peptide; 6 AA.

XX AC AAB48483;

XX DT 02-MAR-2001 (first entry)

XX DE Antifibrillogenic peptide #10.

XX KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 XX KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 XX KW Alzheimer's disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX FT Modified-site 6 /note= "C-terminal amide"

XX PN WO200068263-A2.

XX PD 16-NOV-2000.

XX PF 04-MAY-2000; 2000WO-CA0000515.

XX PR 05-MAY-1999; 99US-0132592P.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Chalifour R, Gervais F, Gupta A;

XX XX WPI; 2001-031852/04.

XX DR Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 XX PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 XX PT its isomer or peptidomimetic.

XX PS Claim 7; Page 25; 46pp; English.



CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0;

Qy 1 KVVFFA 6  
 |:||||  
 Db 1 KIVFFA 6

RESULT 47  
 AAB48474  
 ID AAB48474 standard; peptide; 6 AA.

AC AAB48474;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Antifibrillogenic peptide #1.

XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.

XX Homo sapiens.  
 XX WO200068263-A2.  
 XX 16-NOV-2000.

XX 04-MAY-2000; 2000WO-CA000515.  
 XX 05-MAY-1999; 99US-0132592P.

XX (NEUR-) NEUROCHEM INC.  
 XX Chalfour R, Gervais F, Gupta A;  
 XX WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:||||  
 Db 1 KIVFFA 6

RESULT 48  
 AAB82623

ID AAB82623 standard; peptide; 6 AA.

XX AAB82623;

XX 02-OCT-2001 (first entry)

XX All-D peptide used in Alzheimer's disease vaccine.

XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6 /note= "all D-form residues"

XX WO200139796-A2.

XX 07-JUN-2001.

XX 29-NOV-2000; 2000WO-CA001413.

XX 29-NOV-1999; 99US-0168594P.

XX 28-NOV-2000; 2000US-00724842.

XX (NEUR-) NEUROCHEM INC.

XX Chalfour R, Hebert L, Kong X, Gervais F;

XX WPI; 2001-441458/47.

XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT which elicits production of antibodies to prevent fibrillogenesis and  
 PT associated cellular toxicity.

XX Disclosure; Page 10; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for  
 CC preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



QY 1 KVVFFA 6  
XX |:|||||  
SQ 1 KIVFFA 6

RESULT 49  
ID AAB82631 standard; peptide; 6 AA.  
XX AAB82631;  
XX AAB82631;  
XX 02-OCT-2001 (first entry)  
XX All-D peptide used in Alzheimer's disease vaccine.  
XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
XX therapy; antigen.  
XX Synthetic.  
XX Key Location/Qualifiers  
FT Misc-difference 1. 6 /note= "all D-form residues"  
FT Modified-site 6 /note= "C-terminal amide"  
FT WO200139796-A2.  
XX 07-JUN-2001.  
XX 29-NOV-2000; 2000WO-CA001413.  
XX 29-NOV-1999; 99US-0168594P.  
XX 28-NOV-2000; 2000US-00724842.  
XX (NEUR-) NEUROCHEM INC.  
XX Chalifour R, Hebert L, Kong X, Gervais F;  
XX WPI; 2001-441458/47.  
XX Preventing/treating amyloid-related disease, especially Alzheimer's  
XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
XX which elicits production of antibodies to prevent fibrillogenesis and  
XX associated cellular toxicity.  
XX Disclosure; Page 11; 31pp; English.

The present sequence is that of an all-D peptide suitable for use for  
preparing vaccines for preventing or treating Alzheimer's disease and  
other amyloid related disorders in humans. It is based on a portion of  
an amyloid-beta peptide (see AAB82622), and may be modified by removing or  
inserting 1 or more amino acid residues, or by substituting 1 or more  
amino acid residues with other amino acid residues or non-amino acid  
fragments. Vaccines of the invention are produced using 'non-self'  
peptides synthesised from the unnatural D-configuration amino acids to  
avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
aggregated to be operative or immunogenic. They preferably interact with  
at least 1 region of an amyloid protein, eg. the beta-sheet region or  
CAG-binding site region, the amyloid-beta peptide, or their immunogenic  
fragments, protein conjugates, immunogenic derivative peptides and  
immunogenic peptidomimetics. Examples include all-D peptides  
corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
preventing fibrillogenesis and associated cellular toxicity. The amyloid  
related diseases may be localised amyloidosis, eg. diabetes type II,  
neurodegenerative diseases, eg. bovine spongiform encephalitis,  
Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
prion protein related disorders, or systemic amyloidosis associated with  
chronic infection (eg. tuberculosis) or chronic inflammation (eg.  
rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic

CC amyloidosis found in long-term haemodialysis patients  
XX Sequence 6 AA;  
SQ

Query Match 96.6%; Score 28; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
XX |:|||||  
DB 1 KIVFFA 6

RESULT 50  
AAU96819  
ID AAU96819 standard; peptide; 6 AA.  
XX AAU96819;  
XX 30-JUL-2002 (first entry)  
XX Amyloid targeting peptide #9.  
XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
XX transmissible cerebral amyloidosis; transmissible virus dementia;  
KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
KW bovine spongiform encephalopathy; inflammation associated amyloid;  
KW primary amyloidosis; feline spongiform encephalopathy;  
KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
KW dialysis-related amyloidosis; light chain-related amyloidosis;  
KW cerebral amyloid angiopathy.  
XX Synthetic.  
XX Key Location/Qualifiers  
FT Misc-difference 1. 6 /note= "Preferably D-form residue"  
FT Modified-site 6 /note= "Ala is amidated"  
FT WO200207781-A2.  
XX 31-JAN-2002.  
XX 25-JUL-2001; 2001WO-CA001071.  
XX 25-JUL-2000; 2000US-0220808P.  
XX 24-JUL-2001; 2001US-00915092.  
XX (NEUR-) NEUROCHEM INC.  
XX Gervais F, Kong X, Chalifour R, Migneault D;  
XX WPI; 2002-371447/40.  
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
XX plaques and/or for the treatment of amyloidosis disorders.  
XX Claim 49; Page 21; 57pp; English.

The invention relates to an amyloid-targeting imaging agent comprising an  
amyloid targeting moiety, a linker moiety and a labelling moiety. The  
agent is of general formula A-t-(A<sub>1</sub>n<sub>k</sub>) z-A<sub>1</sub>a<sub>b</sub> (I) where z = 0 - 1;  
A-t = an amyloid targeting moiety; A<sub>1</sub>n<sub>k</sub> = a linker moiety; and A<sub>1</sub>a<sub>b</sub>  
= a labelling moiety. Also included are imaging amyloid deposition or  
diagnosing an amyloid-related condition in a patient involving  
administering (i) to the patient, and ultrasound imaging (i) in the  
patient to determine the presence of amyloid or amyloid-related condition  
; and a kit for preparing a radiopharmaceutical preparation comprising  
(I), a reducing agent, a buffering agent, a transchelating agent, and  
instructions for the preparation and use of the radiopharmaceutical in  
the imaging of amyloid or an amyloid-related condition. The agents are  
used for imaging amyloid deposition and for diagnosing an amyloid related

CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible  
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:||||  
 Db 1 KVVFFA 6

RESULT 51  
 AAU96811 ID AAU96811 standard; peptide; 6 AA.

XX AC AAU96811;  
 XX DT 30-JUL-2002 (first entry)

XX DE Amyloid targeting peptide #1.

XX KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Misc-difference 1, 6 /note= "Preferably D-form residue"

XX PN WO200207781-A2.

XX PD 31-JAN-2002.

XX PF 25-JUL-2001; 2001WO-CA001071.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Gervais F, Kong X, Chalifour R, Migneault D;

XX DR WPI; 2002-371447/40.

XX PT New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 PT plaques and/or for the treatment of amyloidosis disorders.

XX PS Claim 49; Page 21; 57pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A<sub>1</sub>-A<sub>2</sub>-A<sub>3</sub>-A<sub>4</sub>-A<sub>5</sub>-A<sub>6</sub>-A<sub>7</sub>-A<sub>8</sub>-A<sub>9</sub>-A<sub>10</sub>-A<sub>11</sub>-A<sub>12</sub>-A<sub>13</sub>-A<sub>14</sub>-A<sub>15</sub>-A<sub>16</sub>-A<sub>17</sub>-A<sub>18</sub>-A<sub>19</sub>-A<sub>20</sub>-A<sub>21</sub>-A<sub>22</sub>-A<sub>23</sub>-A<sub>24</sub>-A<sub>25</sub>-A<sub>26</sub>-A<sub>27</sub>-A<sub>28</sub>-A<sub>29</sub>-A<sub>30</sub>-A<sub>31</sub>-A<sub>32</sub>-A<sub>33</sub>-A<sub>34</sub>-A<sub>35</sub>-A<sub>36</sub>-A<sub>37</sub>-A<sub>38</sub>-A<sub>39</sub>-A<sub>40</sub>-A<sub>41</sub>-A<sub>42</sub>-A<sub>43</sub>-A<sub>44</sub>-A<sub>45</sub>-A<sub>46</sub>-A<sub>47</sub>-A<sub>48</sub>-A<sub>49</sub>-A<sub>50</sub>-A<sub>51</sub>-A<sub>52</sub>-A<sub>53</sub>-A<sub>54</sub>-A<sub>55</sub>-A<sub>56</sub>-A<sub>57</sub>-A<sub>58</sub>-A<sub>59</sub>-A<sub>60</sub>-A<sub>61</sub>-A<sub>62</sub>-A<sub>63</sub>-A<sub>64</sub>-A<sub>65</sub>-A<sub>66</sub>-A<sub>67</sub>-A<sub>68</sub>-A<sub>69</sub>-A<sub>70</sub>-A<sub>71</sub>-A<sub>72</sub>-A<sub>73</sub>-A<sub>74</sub>-A<sub>75</sub>-A<sub>76</sub>-A<sub>77</sub>-A<sub>78</sub>-A<sub>79</sub>-A<sub>80</sub>-A<sub>81</sub>-A<sub>82</sub>-A<sub>83</sub>-A<sub>84</sub>-A<sub>85</sub>-A<sub>86</sub>-A<sub>87</sub>-A<sub>88</sub>-A<sub>89</sub>-A<sub>90</sub>-A<sub>91</sub>-A<sub>92</sub>-A<sub>93</sub>-A<sub>94</sub>-A<sub>95</sub>-A<sub>96</sub>-A<sub>97</sub>-A<sub>98</sub>-A<sub>99</sub>-A<sub>100</sub>-A<sub>101</sub>-A<sub>102</sub>-A<sub>103</sub>-A<sub>104</sub>-A<sub>105</sub>-A<sub>106</sub>-A<sub>107</sub>-A<sub>108</sub>-A<sub>109</sub>-A<sub>110</sub>-A<sub>111</sub>-A<sub>112</sub>-A<sub>113</sub>-A<sub>114</sub>-A<sub>115</sub>-A<sub>116</sub>-A<sub>117</sub>-A<sub>118</sub>-A<sub>119</sub>-A<sub>120</sub>-A<sub>121</sub>-A<sub>122</sub>-A<sub>123</sub>-A<sub>124</sub>-A<sub>125</sub>-A<sub>126</sub>-A<sub>127</sub>-A<sub>128</sub>-A<sub>129</sub>-A<sub>130</sub>-A<sub>131</sub>-A<sub>132</sub>-A<sub>133</sub>-A<sub>134</sub>-A<sub>135</sub>-A<sub>136</sub>-A<sub>137</sub>-A<sub>138</sub>-A<sub>139</sub>-A<sub>140</sub>-A<sub>141</sub>-A<sub>142</sub>-A<sub>143</sub>-A<sub>144</sub>-A<sub>145</sub>-A<sub>146</sub>-A<sub>147</sub>-A<sub>148</sub>-A<sub>149</sub>-A<sub>150</sub>-A<sub>151</sub>-A<sub>152</sub>-A<sub>153</sub>-A<sub>154</sub>-A<sub>155</sub>-A<sub>156</sub>-A<sub>157</sub>-A<sub>158</sub>-A<sub>159</sub>-A<sub>160</sub>-A<sub>161</sub>-A<sub>162</sub>-A<sub>163</sub>-A<sub>164</sub>-A<sub>165</sub>-A<sub>166</sub>-A<sub>167</sub>-A<sub>168</sub>-A<sub>169</sub>-A<sub>170</sub>-A<sub>171</sub>-A<sub>172</sub>-A<sub>173</sub>-A<sub>174</sub>-A<sub>175</sub>-A<sub>176</sub>-A<sub>177</sub>-A<sub>178</sub>-A<sub>179</sub>-A<sub>180</sub>-A<sub>181</sub>-A<sub>182</sub>-A<sub>183</sub>-A<sub>184</sub>-A<sub>185</sub>-A<sub>186</sub>-A<sub>187</sub>-A<sub>188</sub>-A<sub>189</sub>-A<sub>190</sub>-A<sub>191</sub>-A<sub>192</sub>-A<sub>193</sub>-A<sub>194</sub>-A<sub>195</sub>-A<sub>196</sub>-A<sub>197</sub>-A<sub>198</sub>-A<sub>199</sub>-A<sub>200</sub>-A<sub>201</sub>-A<sub>202</sub>-A<sub>203</sub>-A<sub>204</sub>-A<sub>205</sub>-A<sub>206</sub>-A<sub>207</sub>-A<sub>208</sub>-A<sub>209</sub>-A<sub>210</sub>-A<sub>211</sub>-A<sub>212</sub>-A<sub>213</sub>-A<sub>214</sub>-A<sub>215</sub>-A<sub>216</sub>-A<sub>217</sub>-A<sub>218</sub>-A<sub>219</sub>-A<sub>220</sub>-A<sub>221</sub>-A<sub>222</sub>-A<sub>223</sub>-A<sub>224</sub>-A<sub>225</sub>-A<sub>226</sub>-A<sub>227</sub>-A<sub>228</sub>-A<sub>229</sub>-A<sub>230</sub>-A<sub>231</sub>-A<sub>232</sub>-A<sub>233</sub>-A<sub>234</sub>-A<sub>235</sub>-A<sub>236</sub>-A<sub>237</sub>-A<sub>238</sub>-A<sub>239</sub>-A<sub>240</sub>-A<sub>241</sub>-A<sub>242</sub>-A<sub>243</sub>-A<sub>244</sub>-A<sub>245</sub>-A<sub>246</sub>-A<sub>247</sub>-A<sub>248</sub>-A<sub>249</sub>-A<sub>250</sub>-A<sub>251</sub>-A<sub>252</sub>-A<sub>253</sub>-A<sub>254</sub>-A<sub>255</sub>-A<sub>256</sub>-A<sub>257</sub>-A<sub>258</sub>-A<sub>259</sub>-A<sub>260</sub>-A<sub>261</sub>-A<sub>262</sub>-A<sub>263</sub>-A<sub>264</sub>-A<sub>265</sub>-A<sub>266</sub>-A<sub>267</sub>-A<sub>268</sub>-A<sub>269</sub>-A<sub>270</sub>-A<sub>271</sub>-A<sub>272</sub>-A<sub>273</sub>-A<sub>274</sub>-A<sub>275</sub>-A<sub>276</sub>-A<sub>277</sub>-A<sub>278</sub>-A<sub>279</sub>-A<sub>280</sub>-A<sub>281</sub>-A<sub>282</sub>-A<sub>283</sub>-A<sub>284</sub>-A<sub>285</sub>-A<sub>286</sub>-A<sub>287</sub>-A<sub>288</sub>-A<sub>289</sub>-A<sub>290</sub>-A<sub>291</sub>-A<sub>292</sub>-A<sub>293</sub>-A<sub>294</sub>-A<sub>295</sub>-A<sub>296</sub>-A<sub>297</sub>-A<sub>298</sub>-A<sub>299</sub>-A<sub>300</sub>-A<sub>301</sub>-A<sub>302</sub>-A<sub>303</sub>-A<sub>304</sub>-A<sub>305</sub>-A<sub>306</sub>-A<sub>307</sub>-A<sub>308</sub>-A<sub>309</sub>-A<sub>310</sub>-A<sub>311</sub>-A<sub>312</sub>-A<sub>313</sub>-A<sub>314</sub>-A<sub>315</sub>-A<sub>316</sub>-A<sub>317</sub>-A<sub>318</sub>-A<sub>319</sub>-A<sub>320</sub>-A<sub>321</sub>-A<sub>322</sub>-A<sub>323</sub>-A<sub>324</sub>-A<sub>325</sub>-A<sub>326</sub>-A<sub>327</sub>-A<sub>328</sub>-A<sub>329</sub>-A<sub>330</sub>-A<sub>331</sub>-A<sub>332</sub>-A<sub>333</sub>-A<sub>334</sub>-A<sub>335</sub>-A<sub>336</sub>-A<sub>337</sub>-A<sub>338</sub>-A<sub>339</sub>-A<sub>340</sub>-A<sub>341</sub>-A<sub>342</sub>-A<sub>343</sub>-A<sub>344</sub>-A<sub>345</sub>-A<sub>346</sub>-A<sub>347</sub>-A<sub>348</sub>-A<sub>349</sub>-A<sub>350</sub>-A<sub>351</sub>-A<sub>352</sub>-A<sub>353</sub>-A<sub>354</sub>-A<sub>355</sub>-A<sub>356</sub>-A<sub>357</sub>-A<sub>358</sub>-A<sub>359</sub>-A<sub>360</sub>-A<sub>361</sub>-A<sub>362</sub>-A<sub>363</sub>-A<sub>364</sub>-A<sub>365</sub>-A<sub>366</sub>-A<sub>367</sub>-A<sub>368</sub>-A<sub>369</sub>-A<sub>370</sub>-A<sub>371</sub>-A<sub>372</sub>-A<sub>373</sub>-A<sub>374</sub>-A<sub>375</sub>-A<sub>376</sub>-A<sub>377</sub>-A<sub>378</sub>-A<sub>379</sub>-A<sub>380</sub>-A<sub>381</sub>-A<sub>382</sub>-A<sub>383</sub>-A<sub>384</sub>-A<sub>385</sub>-A<sub>386</sub>-A<sub>387</sub>-A<sub>388</sub>-A<sub>389</sub>-A<sub>390</sub>-A<sub>391</sub>-A<sub>392</sub>-A<sub>393</sub>-A<sub>394</sub>-A<sub>395</sub>-A<sub>396</sub>-A<sub>397</sub>-A<sub>398</sub>-A<sub>399</sub>-A<sub>400</sub>-A<sub>401</sub>-A<sub>402</sub>-A<sub>403</sub>-A<sub>404</sub>-A<sub>405</sub>-A<sub>406</sub>-A<sub>407</sub>-A<sub>408</sub>-A<sub>409</sub>-A<sub>410</sub>-A<sub>411</sub>-A<sub>412</sub>-A<sub>413</sub>-A<sub>414</sub>-A<sub>415</sub>-A<sub>416</sub>-A<sub>417</sub>-A<sub>418</sub>-A<sub>419</sub>-A<sub>420</sub>-A<sub>421</sub>-A<sub>422</sub>-A<sub>423</sub>-A<sub>424</sub>-A<sub>425</sub>-A<sub>426</sub>-A<sub>427</sub>-A<sub>428</sub>-A<sub>429</sub>-A<sub>430</sub>-A<sub>431</sub>-A<sub>432</sub>-A<sub>433</sub>-A<sub>434</sub>-A<sub>435</sub>-A<sub>436</sub>-A<sub>437</sub>-A<sub>438</sub>-A<sub>439</sub>-A<sub>440</sub>-A<sub>441</sub>-A<sub>442</sub>-A<sub>443</sub>-A<sub>444</sub>-A<sub>445</sub>-A<sub>446</sub>-A<sub>447</sub>-A<sub>448</sub>-A<sub>449</sub>-A<sub>450</sub>-A<sub>451</sub>-A<sub>452</sub>-A<sub>453</sub>-A<sub>454</sub>-A<sub>455</sub>-A<sub>456</sub>-A<sub>457</sub>-A<sub>458</sub>-A<sub>459</sub>-A<sub>460</sub>-A<sub>461</sub>-A<sub>462</sub>-A<sub>463</sub>-A<sub>464</sub>-A<sub>465</sub>-A<sub>466</sub>-A<sub>467</sub>-A<sub>468</sub>-A<sub>469</sub>-A<sub>470</sub>-A<sub>471</sub>-A<sub>472</sub>-A<sub>473</sub>-A<sub>474</sub>-A<sub>475</sub>-A<sub>476</sub>-A<sub>477</sub>-A<sub>478</sub>-A<sub>479</sub>-A<sub>480</sub>-A<sub>481</sub>-A<sub>482</sub>-A<sub>483</sub>-A<sub>484</sub>-A<sub>485</sub>-A<sub>486</sub>-A<sub>487</sub>-A<sub>488</sub>-A<sub>489</sub>-A<sub>490</sub>-A<sub>491</sub>-A<sub>492</sub>-A<sub>493</sub>-A<sub>494</sub>-A<sub>495</sub>-A<sub>496</sub>-A<sub>497</sub>-A<sub>498</sub>-A<sub>499</sub>-A<sub>500</sub>-A<sub>501</sub>-A<sub>502</sub>-A<sub>503</sub>-A<sub>504</sub>-A<sub>505</sub>-A<sub>506</sub>-A<sub>507</sub>-A<sub>508</sub>-A<sub>509</sub>-A<sub>510</sub>-A<sub>511</sub>-A<sub>512</sub>-A<sub>513</sub>-A<sub>514</sub>-A<sub>515</sub>-A<sub>516</sub>-A<sub>517</sub>-A<sub>518</sub>-A<sub>519</sub>-A<sub>520</sub>-A<sub>521</sub>-A<sub>522</sub>-A<sub>523</sub>-A<sub>524</sub>-A<sub>525</sub>-A<sub>526</sub>-A<sub>527</sub>-A<sub>528</sub>-A<sub>529</sub>-A<sub>530</sub>-A<sub>531</sub>-A<sub>532</sub>-A<sub>533</sub>-A<sub>534</sub>-A<sub>535</sub>-A<sub>536</sub>-A<sub>537</sub>-A<sub>538</sub>-A<sub>539</sub>-A<sub>540</sub>-A<sub>541</sub>-A<sub>542</sub>-A<sub>543</sub>-A<sub>544</sub>-A<sub>545</sub>-A<sub>546</sub>-A<sub>547</sub>-A<sub>548</sub>-A<sub>549</sub>-A<sub>550</sub>-A<sub>551</sub>-A<sub>552</sub>-A<sub>553</sub>-A<sub>554</sub>-A<sub>555</sub>-A<sub>556</sub>-A<sub>557</sub>-A<sub>558</sub>-A<sub>559</sub>-A<sub>560</sub>-A<sub>561</sub>-A<sub>562</sub>-A<sub>563</sub>-A<sub>564</sub>-A<sub>565</sub>-A<sub>566</sub>-A<sub>567</sub>-A<sub>568</sub>-A<sub>569</sub>-A<sub>570</sub>-A<sub>571</sub>-A<sub>572</sub>-A<sub>573</sub>-A<sub>574</sub>-A<sub>575</sub>-A<sub>576</sub>-A<sub>577</sub>-A<sub>578</sub>-A<sub>579</sub>-A<sub>580</sub>-A<sub>581</sub>-A<sub>582</sub>-A<sub>583</sub>-A<sub>584</sub>-A<sub>585</sub>-A<sub>586</sub>-A<sub>587</sub>-A<sub>588</sub>-A<sub>589</sub>-A<sub>590</sub>-A<sub>591</sub>-A<sub>592</sub>-A<sub>593</sub>-A<sub>594</sub>-A<sub>595</sub>-A<sub>596</sub>-A<sub>597</sub>-A<sub>598</sub>-A<sub>599</sub>-A<sub>600</sub>-A<sub>601</sub>-A<sub>602</sub>-A<sub>603</sub>-A<sub>604</sub>-A<sub>605</sub>-A<sub>606</sub>-A<sub>607</sub>-A<sub>608</sub>-A<sub>609</sub>-A<sub>610</sub>-A<sub>611</sub>-A<sub>612</sub>-A<sub>613</sub>-A<sub>614</sub>-A<sub>615</sub>-A<sub>616</sub>-A<sub>617</sub>-A<sub>618</sub>-A<sub>619</sub>-A<sub>620</sub>-A<sub>621</sub>-A<sub>622</sub>-A<sub>623</sub>-A<sub>624</sub>-A<sub>625</sub>-A<sub>626</sub>-A<sub>627</sub>-A<sub>628</sub>-A<sub>629</sub>-A<sub>630</sub>-A<sub>631</sub>-A<sub>632</sub>-A<sub>633</sub>-A<sub>634</sub>-A<sub>635</sub>-A<sub>636</sub>-A<sub>637</sub>-A<sub>638</sub>-A<sub>639</sub>-A<sub>640</sub>-A<sub>641</sub>-A<sub>642</sub>-A<sub>643</sub>-A<sub>644</sub>-A<sub>645</sub>-A<sub>646</sub>-A<sub>647</sub>-A<sub>648</sub>-A<sub>649</sub>-A<sub>650</sub>-A<sub>651</sub>-A<sub>652</sub>-A<sub>653</sub>-A<sub>654</sub>-A<sub>655</sub>-A<sub>656</sub>-A<sub>657</sub>-A<sub>658</sub>-A<sub>659</sub>-A<sub>660</sub>-A<sub>661</sub>-A<sub>662</sub>-A<sub>663</sub>-A<sub>664</sub>-A<sub>665</sub>-A<sub>666</sub>-A<sub>667</sub>-A<sub>668</sub>-A<sub>669</sub>-A<sub>670</sub>-A<sub>671</sub>-A<sub>672</sub>-A<sub>673</sub>-A<sub>674</sub>-A<sub>675</sub>-A<sub>676</sub>-A<sub>677</sub>-A<sub>678</sub>-A<sub>679</sub>-A<sub>680</sub>-A<sub>681</sub>-A<sub>682</sub>-A<sub>683</sub>-A<sub>684</sub>-A<sub>685</sub>-A<sub>686</sub>-A<sub>687</sub>-A<sub>688</sub>-A<sub>689</sub>-A<sub>690</sub>-A<sub>691</sub>-A<sub>692</sub>-A<sub>693</sub>-A<sub>694</sub>-A<sub>695</sub>-A<sub>696</sub>-A<sub>697</sub>-A<sub>698</sub>-A<sub>699</sub>-A<sub>700</sub>-A<sub>701</sub>-A<sub>702</sub>-A<sub>703</sub>-A<sub>704</sub>-A<sub>705</sub>-A<sub>706</sub>-A<sub>707</sub>-A<sub>708</sub>-A<sub>709</sub>-A<sub>710</sub>-A<sub>711</sub>-A<sub>712</sub>-A<sub>713</sub>-A<sub>714</sub>-A<sub>715</sub>-A<sub>716</sub>-A<sub>717</sub>-A<sub>718</sub>-A<sub>719</sub>-A<sub>720</sub>-A<sub>721</sub>-A<sub>722</sub>-A<sub>723</sub>-A<sub>724</sub>-A<sub>725</sub>-A<sub>726</sub>-A<sub>727</sub>-A<sub>728</sub>-A<sub>729</sub>-A<sub>730</sub>-A<sub>731</sub>-A<sub>732</sub>-A<sub>733</sub>-A<sub>734</sub>-A<sub>735</sub>-A<sub>736</sub>-A<sub>737</sub>-A<sub>738</sub>-A<sub>739</sub>-A<sub>740</sub>-A<sub>741</sub>-A<sub>742</sub>-A<sub>743</sub>-A<sub>744</sub>-A<sub>745</sub>-A<sub>746</sub>-A<sub>747</sub>-A<sub>748</sub>-A<sub>749</sub>-A<sub>750</sub>-A<sub>751</sub>-A<sub>752</sub>-A<sub>753</sub>-A<sub>754</sub>-A<sub>755</sub>-A<sub>756</sub>-A<sub>757</sub>-A<sub>758</sub>-A<sub>759</sub>-A<sub>760</sub>-A<sub>761</sub>-A<sub>762</sub>-A<sub>763</sub>-A<sub>764</sub>-A<sub>765</sub>-A<sub>766</sub>-A<sub>767</sub>-A<sub>768</sub>-A<sub>769</sub>-A<sub>770</sub>-A<sub>771</sub>-A<sub>772</sub>-A<sub>773</sub>-A<sub>774</sub>-A<sub>775</sub>-A<sub>776</sub>-A<sub>777</sub>-A<sub>778</sub>-A<sub>779</sub>-A<sub>780</sub>-A<sub>781</sub>-A<sub>782</sub>-A<sub>783</sub>-A<sub>784</sub>-A<sub>785</sub>-A<sub>786</sub>-A<sub>787</sub>-A<sub>788</sub>-A<sub>789</sub>-A<sub>790</sub>-A<sub>791</sub>-A<sub>792</sub>-A<sub>793</sub>-A<sub>794</sub>-A<sub>795</sub>-A<sub>796</sub>-A<sub>797</sub>-A<sub>798</sub>-A<sub>799</sub>-A<sub>800</sub>-A<sub>801</sub>-A<sub>802</sub>-A<sub>803</sub>-A<sub>804</sub>-A<sub>805</sub>-A<sub>806</sub>-A<sub>807</sub>-A<sub>808</sub>-A<sub>809</sub>-A<sub>810</sub>-A<sub>811</sub>-A<sub>812</sub>-A<sub>813</sub>-A<sub>814</sub>-A<sub>815</sub>-A<sub>816</sub>-A<sub>817</sub>-A<sub>818</sub>-A<sub>819</sub>-A<sub>820</sub>-A<sub>821</sub>-A<sub>822</sub>-A<sub>823</sub>-A<sub>824</sub>-A<sub>825</sub>-A<sub>826</sub>-A<sub>827</sub>-A<sub>828</sub>-A<sub>829</sub>-A<sub>830</sub>-A<sub>831</sub>-A<sub>832</sub>-A<sub>833</sub>-A<sub>834</sub>-A<sub>835</sub>-A<sub>836</sub>-A<sub>837</sub>-A<sub>838</sub>-A<sub>839</sub>-A<sub>840</sub>-A<sub>841</sub>-A<sub>842</sub>-A<sub>843</sub>-A<sub>844</sub>-A<sub>845</sub>-A<sub>846</sub>-A<sub>847</sub>-A<sub>848</sub>-A<sub>849</sub>-A<sub>850</sub>-A<sub>851</sub>-A<sub>852</sub>-A<sub>853</sub>-A<sub>854</sub>-A<sub>855</sub>-A<sub>856</sub>-A<sub>857</sub>-A<sub>858</sub>-A<sub>859</sub>-A<sub>860</sub>-A<sub>861</sub>-A<sub>862</sub>-A<sub>863</sub>-A<sub>864</sub>-A<sub>865</sub>-A<sub>866</sub>-A<sub>867</sub>-A<sub>868</sub>-A<sub>869</sub>-A<sub>870</sub>-A<sub>871</sub>-A<sub>872</sub>-A<sub>873</sub>-A<sub>874</sub>-A<sub>875</sub>-A<sub>876</sub>-A<sub>877</sub>-A<sub>878</sub>-A<sub>879</sub>-A<sub>880</sub>-A<sub>881</sub>-A<sub>882</sub>-A<sub>883</sub>-A<sub>884</sub>-A<sub>885</sub>-A<sub>886</sub>-A<sub>887</sub>-A<sub>888</sub>-A<sub>889</sub>-A<sub>890</sub>-A<sub>891</sub>-A<sub>892</sub>-A<sub>893</sub>-A<sub>894</sub>-A<sub>895</sub>-A<sub>896</sub>-A<sub>897</sub>-A<sub>898</sub>-A<sub>899</sub>-A<sub>900</sub>-A<sub>901</sub>-A<sub>902</sub>-A<sub>903</sub>-A<sub>904</sub>-A<sub>905</sub>-A<sub>906</sub>-A<sub>907</sub>-A<sub>908</sub>-A<sub>909</sub>-A<sub>910</sub>-A<sub>911</sub>-A<sub>912</sub>-A<sub>913</sub>-A<sub>914</sub>-A<sub>915</sub>-A<sub>916</sub>-A<sub>917</sub>-A<sub>918</sub>-A<sub>919</sub>-A<sub>920</sub>-A<sub>921</sub>-A<sub>922</sub>-A<sub>923</sub>-A<sub>924</sub>-A<sub>925</sub>-A<sub>926</sub>-A<sub>927</sub>-A<sub>928</sub>-A<sub>929</sub>-A<sub>930</sub>-A<sub>931</sub>-A<sub>932</sub>-A<sub>933</sub>-A<sub>934</sub>-A<sub>935</sub>-A<sub>936</sub>-A<sub>937</sub>-A<sub>938</sub>-A<sub>939</sub>-A<sub>940</sub>-A<sub>941</sub>-A<sub>942</sub>-A<sub>943</sub>-A<sub>944</sub>-A<sub>945</sub>-A<sub>946</sub>-A<sub>947</sub>-A<sub>948</sub>-A<sub>949</sub>-A<sub>950</sub>-A<sub>951</sub>-A<sub>952</sub>-A<sub>953</sub>-A<sub>954</sub>-A<sub>955</sub>-A<sub>956</sub>-A<sub>957</sub>-A<sub>958</sub>-A<sub>959</sub>-A<sub>960</sub>-A<sub>961</sub>-A<sub>962</sub>-A<sub>963</sub>-A<sub>964</sub>-A<sub>965</sub>-A<sub>966</sub>-A<sub>967</sub>-A<sub>968</sub>-A<sub>969</sub>-A<sub>970</sub>-A<sub>971</sub>-A<sub>972</sub>-A<sub>973</sub>-A<sub>974</sub>-A<sub>975</sub>-A<sub>976</sub>-A<sub>977</sub>-A<sub>978</sub>-A<sub>979</sub>-A<sub>980</sub>-A<sub>981</sub>-A<sub>982</sub>-A<sub>983</sub>-A<sub>984</sub>-A<sub>985</sub>-A<sub>986</sub>-A<sub>987</sub>-A<sub>988</sub>-A<sub>989</sub>-A<sub>990</sub>-A<sub>991</sub>-A<sub>992</sub>-A<sub>993</sub>-A<sub>994</sub>-A<sub>995</sub>-A<sub>996</sub>-A<sub>997</sub>-A<sub>998</sub>-A<sub>999</sub>-A<sub>1000</sub>-A<sub>1001</sub>-A<sub>1002</sub>-A<sub>1003</sub>-A<sub>1004</sub>-A<sub>1005</sub>-A<sub>1006</sub>-A<sub>1007</sub>-A<sub>1008</sub>-A<sub>1009</sub>-A<sub>1010</sub>-A<sub>1011</sub>-A<sub>1012</sub>-A<sub>1013</sub>-A<sub>1014</sub>-A<sub>1015</sub>-A<sub>1016</sub>-A<sub>1017</sub>-A<sub>1018</sub>-A<sub>1019</sub>-A<sub>1020</sub>-A<sub>1021</sub>-A<sub>1022</sub>-A<sub>1023</sub>-A<sub>1024</sub>-A<sub>1025</sub>-A<sub>1026</sub>-A<sub>1027</sub>-A<sub>1028</sub>-A<sub>1029</sub>-A<sub>1030</sub>-A<sub>1031</sub>-A<sub>1032</sub>-A<sub>1033</sub>-A<sub>1034</sub>-A<sub>1035</sub>-A<sub>1036</sub>-A<sub>1037</sub>-A<sub>1038</sub>-A<sub>1039</sub>-A<sub>1040</sub>-A<sub>1041</sub>-A<sub>1042</sub>-A<sub>1043</sub>-A<sub>1044</sub>-A<sub>1045</sub>-A<sub>1046</sub>-A<sub>1047</sub>-A<sub>1048</sub>-A<sub>1049</sub>-A<sub>1050</sub>-A<sub>1051</sub>-A<sub>1052</sub>-A<sub>1053</sub>-A<sub>1054</sub>-A<sub>1055</sub>-A<sub>1056</sub>-A<sub>1057</sub>-A<sub>1058</sub>-A<sub>1059</sub>-A<sub>1060</sub>-A<sub>1061</sub>-A<sub>1062</sub>-A<sub>1063</sub>-A<sub>1064</sub>-A<sub>1065</sub>-A<sub>1066</sub>-A<sub>1067</sub>-A<sub>1068</sub>-A<sub>1069</sub>-A

CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
 CC The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)  
 XX  
 SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 Db |:||||  
 1 KIVFFA 6

RESULT 53  
 AAU11648  
 ID AAU11648 standard; peptide; 6 AA.  
 XX

AC AAU11648;  
 XX  
 XX 09-APR-2002 (first entry)  
 DT  
 XX

DE Peptide #1, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 XX  
 XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.  
 XX  
 OS Synthetic.

XX  
 XX WO200185093-A2.  
 PN  
 XX 15-NOV-2001.  
 PD

XX 22-DEC-2000; 2000WO-IB002078.  
 PF  
 XX 23-DEC-1999; 99US-0171877P.  
 PR

XX (NEUR-) NEUROCHEM INC.  
 PA  
 XX Green AM, Gervais F;  
 PI

XX WPI; 2002-075222/10.  
 DR  
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40  
 PT inhibitor.

XX Disclosure; Page 10; 68pp; English.  
 PS  
 XX The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting a  
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.

XX The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)  
 XX

SQ Sequence 6 AA;  
 Query Match 96.6%; Score 28; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db |:||||  
 1 KIVFFA 6

RESULT 54  
 AAE35446  
 ID AAE35446 standard; peptide; 6 AA.  
 XX  
 AC AAE35446;  
 XX

XX 17-JUN-2003 (first entry)  
 DT  
 XX Abeta peptide #17.  
 DE

XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..6 /note= "D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"

FT WO200296937-A2.  
 XX  
 XX 05-DEC-2002.  
 PD

XX 29-MAY-2002; 2002WO-CA000763.  
 PF  
 XX 29-MAY-2001; 2001US-00867847.  
 PR

XX (NEUR-) NEUROCHEM INC.  
 PA  
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;  
 PI WPI; 2003-201269/19.

XX Prevention and/or treatment of an amyloid-related disease e.g.  
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 FT  
 XX Claim 1; Page 59; 44pp; English.

XX The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).

XX Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention  
 XX

SQ Sequence 6 AA;  
 Query Match 96.6%; Score 28; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;

Query Match 96.6%; Score 28; DB 6; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 1 KIVFFA 6

## RESULT 55

AAE35438  
ID AAE35438 standard; peptide; 6 AA.

AC AAE35438;

DT 17-JUN-2003 (first entry)

DE Abeta peptide #9.

KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotic;  
KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotrophic;  
KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

OS Unidentified.

FH Key Location/Qualifiers

FT Misc-difference 1..6

FT /note= "D-form residues"

PN WO200296937-A2.

XX 05-DEC-2002.

PF 29-MAY-2002; 2002WO-CA000763.

PR 29-MAY-2001; 2001US-00867847.

PA (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;

DR WPI; 2003-201269/19.

XX Prevention and/or treatment of an amyloid-related disease e.g.

PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.

PS Claim 1; Page 58; 44pp; English.

CC The invention relates to a method for prevention and/or treatment of an  
CC amyloid-related disease which comprises administration of an all-D -  
CC amyloid-beta peptide. The method is used for preventing and/or treating  
CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
CC the mammal; and reducing or inhibiting the formation of plaques. It is  
CC also used for treating AA (reactive) amyloid diseases including  
CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
CC disease. AA deposits are also produced as a result of chronic microbial  
CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
CC present sequence is an Abeta peptide used to illustrate the method of the  
CC invention

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 6; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 1 KIVFFA 6

## RESULT 56

ADQ37322  
ID ADQ37322 standard; peptide; 6 AA.

XX AC ADQ37322;

XX 07-OCT-2004 (first entry)

XX Antifibrillogenic amyloidosis inhibiting peptide.

KW amyloid-beta; amyloid-beta related disease;  
KW amyloid-beta fibril formation; immune response; neurotropic;  
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;  
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
KW cardiant; antidepressant; endocrine; hypnotic;  
KW amyloid-beta fibril formation modulator; immune system modulator;  
KW Alzheimer's disease; mild cognitive impairment;  
KW mild-to-moderate cognitive impairment; vascular dementia;  
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
KW senile dementia; Down's syndrome; inclusion body myositis;  
KW age-related macular degeneration; hypothyroidism;  
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
KW behavioural dysfunction; neurological condition; psychological condition;  
KW vaccine antigen.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-eite 6 /note= "amidated"

XX WO2004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent  
XX that prevents or treats amyloid-beta related disease and second agent  
XX that is either a peptide or peptidomimetic or an immune system modulator.  
XX Disclosure; Page 69; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
XX agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
XX a second agent (a2) that is: (i) a peptide or peptidomimetic that  
XX modulates amyloid-beta fibril formation or induces a prophylactic or  
XX therapeutic immune response against amyloid-beta fibril formation; or  
XX (ii) an immune system modulator that prevents or inhibits amyloid-beta  
XX fibril formation. Also described is a kit comprising (C). (C) have  
XX neurotropic, neuroprotective, cerebroprotective, haemostatic, tranquiliser,  
XX ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,

CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.

XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;

Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 1 KIVFFA 6

RESULT 57

ADQ37270

ID ADQ37270 standard; peptide; 6 AA.

XX AC ADQ37270;

XX XT 07-OCT-2004 (first entry)

XX DE Vaccine antigen amyloid-beta related amino acid sequence.

XX KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; utropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 XX KW vaccine antigen.

OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1..6

FT /notes= "D-form residues"

FT Modified-site 6

/note= "amidated"

XX WO2004058239-A1.

XX PD 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 FT that prevents or treats amyloid-beta related disease and second agent  
 FT that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,  
 CC utropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as a vaccine antigen in the exemplification of the  
 CC present invention.

XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;

Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 1 KIVFFA 6

RESULT 58  
ADQ37313  
ID ADQ37313 standard; peptide; 6 AA.  
XX  
AC ADQ37313;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Antifibrillogenic amyloidosis inhibiting peptide.  
XX  
KW amyloid-beta; amyloid-beta related disease;  
KW amyloid-beta fibril formation; immune response; neurotropic;  
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
KW antithyroid; vasotrophic; cardiovascular; tranquilliser; uropathic;  
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
KW cardiant; antidepressant; endocrine; hypnotic;  
KW amyloid-beta fibril formation modulator; immune system modulator;  
KW Alzheimer's disease; mild cognitive impairment;  
KW mild-to-moderate cognitive impairment; vascular dementia;  
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
KW senile dementia; Down's syndrome; inclusion body myositis;  
KW age-related macular degeneration; hypothyroidism;  
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
KW behavioural dysfunction; neurological condition; psychological condition;  
KW vaccine antigen.  
XX  
OS Synthetic.  
XX  
FN WO2004058239-A1.  
XX  
PD 15-JUL-2004.  
XX  
PP 24-DEC-2003; 2003WO-CA002021.  
XX  
PR 24-DEC-2002; 2002US-0436379P.  
PR 23-JUN-2003; 2003US-0482214P.  
XX  
XX (NEUR-) NEUROCHEM INT LTD.  
PI Gervais F, Bellini F;  
XX WPI; 2004-543342/52.  
XX  
DR Composition for treating e.g. Alzheimer's disease comprises first agent  
PT that prevents or treats amyloid-beta related disease and second agent  
PT that is either a peptide or peptidomimetic or an immune system modulator.  
PS Disclosure; Page 69; 143pp; English.  
XX  
CC The present invention describes compositions (C) comprising: (a) a first  
CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
CC modulates amyloid-beta fibril formation or induces a prophylactic or  
CC therapeutic immune response against amyloid-beta fibril formation; or  
CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
CC fibril formation. Also described is a kit comprising (C). (C) have  
CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
CC ophthalmological, antithyroid, vasotrophic, cardiovascular, tranquilliser,  
CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
CC and can be used as amyloid-beta fibril formation modulators, and as  
CC immune system modulators. (C) can be used for preventing or treating an  
CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
CC Down's syndrome, inclusion body myositis, age-related macular  
CC degeneration, or a condition associated with Alzheimer's disease  
CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia

CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
CC field deficits, incoordination, gait disturbance, transient ischaemic  
CC attack or stroke, transient alertness, attention deficit, frequent falls,  
CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
CC damage), or a psychological condition (e.g. depression, delusions,  
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
CC having amyloid-beta deposits. The present sequence represents a peptide  
CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 6 AA;  
Query Match 96.6%; Score 28; DB 8; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KWFFFA 6  
Db 1 KIVFFA 6  
RESULT 59  
ADQ37262  
ID ADQ37262 standard; peptide; 6 AA.  
XX  
AC ADQ37262;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Vaccine antigen amyloid-beta related amino acid sequence.  
XX  
KW amyloid-beta; amyloid-beta related disease;  
KW amyloid-beta fibril formation; immune response; neurotropic;  
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
KW antithyroid; vasotrophic; cardiovascular; tranquilliser; uropathic;  
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
KW cardiant; antidepressant; endocrine; hypnotic;  
KW amyloid-beta fibril formation modulator; immune system modulator;  
KW Alzheimer's disease; mild cognitive impairment;  
KW mild-to-moderate cognitive impairment; vascular dementia;  
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
KW senile dementia; Down's syndrome; inclusion body myositis;  
KW age-related macular degeneration; hypothyroidism;  
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
KW behavioural dysfunction; neurological condition; psychological condition;  
KW vaccine antigen.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..6  
FT /note= "D-form residues"  
XX  
FN WO2004058239-A1.  
XX  
PD 15-JUL-2004.  
XX  
PP 24-DEC-2003; 2003WO-CA002021.  
XX  
PR 24-DEC-2002; 2002US-0436379P.  
PR 23-JUN-2003; 2003US-0482214P.  
XX  
XX (NEUR-) NEUROCHEM INT LTD.  
PI Gervais F, Bellini F;  
XX WPI; 2004-543342/52.  
XX

PT Composition for treating e.g. Alzheimer's disease comprises first agent  
 PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.  
 XX  
 XX  
 PS Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, tranquiliser,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as a vaccine antigen in the exemplification of the  
 CC present invention.  
 XX  
 XX

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |:||||  
 Db 1 KIVFFA 6

RESULT 60

ADV37921  
 ID ADY37921 standard; peptide; 6 AA.

XX  
 AC ADY37921;

XX 19-MAY-2005 (first entry)

XX Amyloid-targeting peptide, SEQ ID NO:1, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 XX transmissible spongiform encephalopathy; scrapie; BSE;  
 XX Alzheimer's disease; neurological disease; amyloidosis;  
 XX non-insulin dependent diabetes; metabolic disorder.

OS Synthetic.

XX

PN US2005048000-A1.  
 XX  
 PD 03-MAR-2005.

XX 03-DEC-2003; 2003US-00728028.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

PR 29-JAN-2003; 2003US-0443291P.

XX (NEUR-) NEUROCHEM INT LTD.

PI Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2005-212201/22.

XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform  
 encephalopathy, primary amyloidosis or Alzheimer's disease.

PS Disclosure; SEQ ID NO 1; 34pp; English.

XX The invention relates to an amyloid-targeting imaging agent. The imaging  
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 CC a labeling moiety via a linking moiety, and is preferably able to cross  
 CC the blood-brain barrier. The invention also relates to a kit for  
 CC preparing a radiopharmaceutical preparation from the imaging agent of the  
 CC invention, a method for imaging amyloid deposition in a patient and a  
 CC method for diagnosing an amyloid-related condition in a patient. The  
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,  
 CC transmissible cerebral amyloidosis (also known as transmissible virus  
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 CC mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 9; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |:||||  
 Db 1 KIVFFA 6

RESULT 61

ADV37929

ID ADY37929 standard; peptide; 6 AA.

XX  
 AC ADY37929;

XX 19-MAY-2005 (first entry)

XX Amyloid-targeting peptide, SEQ ID NO:9, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 XX transmissible spongiform encephalopathy; scrapie; BSE;  
 XX Alzheimer's disease; neurological disease; amyloidosis;  
 XX non-insulin dependent diabetes; metabolic disorder.

OS Synthetic.

XX



FH Key Location/Qualifiers  
 FT Modified-site 6  
 XX /note= "C-terminal amide"  
 XX  
 XX US2005048000-A1.  
 XX  
 XX 03-MAR-2005.  
 XX  
 XX 03-DEC-2003; 2003US-00728028.  
 XX  
 XX 25-JUL-2000; 2000US-0220808P.  
 XX  
 XX 24-JUL-2001; 2001US-00915092.  
 XX  
 XX 29-JAN-2003; 2003US-0443291P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX  
 XX Gervais F, Kong X, Chalifour R, Migneault D;  
 XX  
 XX WPI; 2005-212201/22.  
 XX  
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 XX related condition, e.g. Creutzfeldt-Jakob disease, bovine spongiform  
 XX encephalopathy, primary amyloidosis or Alzheimer's disease.  
 XX  
 XX Disclosure; SEQ ID NO 9; 34pp; English.  
 XX  
 XX The invention relates to an amyloid-targeting imaging agent. The imaging  
 XX agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 XX a labeling moiety via a linking moiety, and is preferably able to cross  
 XX the blood-brain barrier. The invention also relates to a kit for  
 XX preparing a radiopharmaceutical preparation from the imaging agent of the  
 XX invention, a method for imaging amyloid deposition in a patient and a  
 XX method for diagnosing an amyloid-related condition in a patient. The  
 XX amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 XX related conditions such as Creutzfeldt-Jakob disease (CJD), Kuru,  
 XX transmissible cerebral amyloidosis (also known as transmissible virus  
 XX dementia), familial CJD, scrapie, transmissible mink encephalopathy,  
 XX bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 XX type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 XX non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 XX mediated diseases, dialysis-related amyloidosis, light chain-related  
 XX amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 XX patient. The agent does not exhibit excessive toxicity or irritation,  
 XX does not induce an allergic response, and permits an earlier diagnosis of  
 XX amyloid-related conditions, thereby allowing earlier treatment and hence  
 XX prevention of the undesirable effects of such disorders. Sequences  
 XX ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 XX the amyloid-targeting moiety in an imaging agent of the invention.  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 96.6%; Score 28; DB 9; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1 KIVFFA 6  
 RESULT 62  
 ABG26598  
 ID ABG26598 standard; protein; 99 AA.  
 XX  
 XX ABG26598;  
 XX  
 XX 18-FEB-2002 (first entry)  
 XX  
 XX Novel human diagnostic protein #26589.  
 XX  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX food supplement; medical imaging; diagnostic; genetic disorder.  
 XX

OS Homo sapiens.  
 XX WO200175067-A2.  
 XX  
 XX 11-OCT-2001.  
 XX  
 XX 30-MAR-2001; 2001WO-US008631.  
 XX  
 XX 31-MAR-2000; 2000US-00540217.  
 XX  
 XX 23-AUG-2000; 2000US-00649167.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 XX  
 XX Dmanac RT, Liu C, Tang YT;  
 XX  
 XX WPI; 2001-639362/73.  
 XX  
 XX N-PSDB; AAS90785.  
 XX  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 XX diagnostics, forensics, gene mapping, identification of mutations  
 XX responsible for genetic disorders or other traits and to assess  
 XX biodiversity.  
 XX  
 XX Claim 20; SEQ ID NO 56957; 103pp; English.  
 XX  
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 XX sequences. (I) is useful as hybridisation probes, polymerase chain  
 XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 XX and in recombinant production of (II). The polynucleotides are also used  
 XX in diagnostics as expressed sequence tags for identifying expressed  
 XX genes. (I) is useful in gene therapy techniques to restore normal  
 XX activity of (II) or to treat disease states involving (II). (II) is  
 XX useful for generating antibodies against it, detecting or quantitating a  
 XX polypeptide in tissue, as molecular weight markers and as a food  
 XX supplement. (II) and its binding partners are useful in medical imaging  
 XX of sites expressing (II). (I) and (II) are useful for treating disorders  
 XX involving aberrant protein expression or biological activity. The  
 XX polypeptide and polynucleotide sequences have applications in  
 XX diagnostics, forensics, gene mapping, identification of mutations  
 XX responsible for genetic disorders or other traits to assess biodiversity  
 XX and to produce other types of data and products dependent on DNA and  
 XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 XX amino acid sequences of the invention. Note: The sequence data for this  
 XX patent did not appear in the printed specification, but was obtained in  
 XX electronic format directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 99 AA;  
 SQ  
 Query Match 96.6%; Score 28; DB 4; Length 99;  
 Best Local Similarity 83.3%; Pred. No. 1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 63 KIVFFA 68  
 RESULT 63  
 ABM94314  
 ID ABM94314 standard; protein; 123 AA.  
 XX  
 XX ABM94314;  
 XX  
 XX 02-JUN-2005 (first entry)  
 XX  
 XX M. xanthus protein sequence, seq id 13513.  
 XX  
 XX Transgenic plant; DNA replication; gene regulation; gene expression.  
 XX  
 XX Myxococcus xanthus.  
 XX  
 XX US6833447-B1.  
 XX



XX PD 21-DEC-2004.  
 XX XX  
 XX PF 10-JUL-2001; 2001US-00902540.  
 XX XX  
 XX PR 10-JUL-2000; 2000US-0217883P.  
 XX XX  
 XX PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX XX  
 XX PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;  
 XX XX  
 XX DR WPI; 2005-028716/03.  
 XX XX  
 XX PT New substantially purified Myxococcus xanthus nucleic acid molecule  
 XX PT encoding a nitrite reductase, useful for determining gene expression,  
 XX PT identifying mutations in a gene of interest, and for constructing  
 XX PT mutations in a gene of interest.  
 XX XX  
 XX PS Example 2; SEQ ID NO 13513; 25pp; English.  
 XX XX  
 XX CC The invention relates to a substantially purified nucleic acid molecule  
 XX CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a  
 XX CC recombinant DNA construct for expression of a nitrite reductase gene in a  
 XX CC plant cell, and a plant cell comprising the recombinant DNA construct.  
 XX CC The nucleic acid is useful for determining gene expression, identifying  
 XX CC mutations in a gene of interest, and for constructing mutations in a gene  
 XX CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent  
 XX CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The  
 XX CC sequence data for this patent did not form part of the printed  
 XX CC specification, but was obtained in electronic format directly from USPTO  
 XX XX  
 XX SQ Sequence 123 AA;  
 Query Match 96.6%; Score 28; DB 9; Length 123;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 ||:||||  
 Db 52 KVIFFA 57  
 RESULT 64  
 ADM16726  
 ID ADM16726 standard; protein; 393 AA.  
 XX AC  
 XX AD M16726;  
 XX XX  
 XX DT 17-JUN-2004 (first entry)  
 XX DE PERL-P7-G8 protein.  
 XX DE Phlebotomus ariasi; Phlebotomus perniciosus; Vaccine;  
 XX KW Leishmania infection.  
 XX XX  
 XX OS Phlebotomus perniciosus.  
 XX XX  
 XX PN WO2004027041-A2.  
 XX XX  
 XX PD 01-APR-2004.  
 XX XX  
 XX PF 18-SEP-2003; 2003WO-US029833.  
 XX XX  
 XX PR 19-SEP-2002; 2002US-0412327P.  
 XX PR 12-NOV-2002; 2002US-0425852P.  
 XX XX  
 XX PA (MERI-) Merial LTD.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX XX  
 XX PI Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;  
 XX PI Audonnet J, Milward F;  
 XX XX  
 XX DR WPI; 2004-295410/27.  
 XX XX

DR N-PSDB; ADM16727.  
 XX XX  
 XX PT New substantially purified salivary Phlebotomus ariasi or Phlebotomus  
 XX PT perniciosus polypeptide, useful for inhibiting, treating or preventing  
 XX PT Leishmania infection in a subject.  
 XX XX  
 XX PS Claim 40; SEQ ID NO 49; 200pp; English.  
 XX XX  
 XX CC The present invention relates to a substantially purified salivary  
 XX CC Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The  
 XX CC composition comprising the polypeptide or the nucleic acid encoding the  
 XX CC polypeptide is useful for manufacture of a medicament. The polypeptides  
 XX CC and nucleic acids are useful for inducing an immune response to a P.  
 XX CC ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a  
 XX CC symptom of a Leishmania infection or preventing a Leishmania infection in  
 XX CC a subject. The present sequence represents a purified Phlebotomus ariasi  
 XX CC protein.  
 XX XX  
 XX SQ Sequence 393 AA;  
 Query Match 96.6%; Score 28; DB 8; Length 393;  
 Best Local Similarity 83.3%; Pred. No. 4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 ||:||||  
 Db 299 KVIFFA 304  
 RESULT 65  
 ADM16684  
 ID ADM16684 standard; protein; 393 AA.  
 XX AC  
 XX AD M16684;  
 XX XX  
 XX DT 17-JUN-2004 (first entry)  
 XX DE PRL-P4-D6 protein.  
 XX XX  
 XX KW Phlebotomus ariasi; Phlebotomus perniciosus; Vaccine;  
 XX KW Leishmania infection.  
 XX XX  
 XX OS Phlebotomus ariasi.  
 XX XX  
 XX PN WO2004027041-A2.  
 XX XX  
 XX PD 01-APR-2004.  
 XX XX  
 XX PF 18-SEP-2003; 2003WO-US029833.  
 XX XX  
 XX PR 19-SEP-2002; 2002US-0412327P.  
 XX PR 12-NOV-2002; 2002US-0425852P.  
 XX XX  
 XX PA (MERI-) Merial LTD.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX XX  
 XX PI Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;  
 XX PI Audonnet J, Milward F;  
 XX XX  
 XX DR WPI; 2004-295410/27.  
 XX DR N-PSDB; ADM16685.  
 XX XX  
 XX PT New substantially purified salivary Phlebotomus ariasi or Phlebotomus  
 XX PT perniciosus polypeptide, useful for inhibiting, treating or preventing  
 XX PT Leishmania infection in a subject.  
 XX XX  
 XX PS Claim 1; SEQ ID NO 7; 200pp; English.  
 XX XX  
 XX CC The present invention relates to a substantially purified salivary  
 XX CC Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The  
 XX CC composition comprising the polypeptide or the nucleic acid encoding the  
 XX CC polypeptide is useful for manufacture of a medicament. The polypeptides  
 XX CC and nucleic acids are useful for inducing an immune response to a P.

CC ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a  
CC symptom of a Leishmania infection or preventing a Leishmania infection in  
CC a subject. The present sequence represents a purified Phlebotomus ariasi  
CC protein.

XX SQ Sequence 393 AA;

Query Match 96.6%; Score 28; DB 8; Length 393;  
Best Local Similarity 83.3%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
||:||||  
Db 298 KVIFFA 303

RESULT 66

ADO43456  
ID ADO43456 standard; protein; 399 AA.

XX AC ADO43456;

XX DT 29-JUL-2004 (first entry)

XX DE Lutzomyia longipalpis (sand fly) salivary protein LJM11.

XX KW LJM11; sand fly; leishmaniasis; diagnosis; vaccine; genetic immunisation.  
XX OS Lutzomyia longipalpis.

XX FH Key Location/Qualifiers  
XX FT Peptide 1..24  
XX FT /label= Signal\_peptide  
XX FT Protein 25..399  
XX FT /label= Mature\_protein

XX PN WO2004039958-A2.

XX PD 13-MAY-2004.

XX PF 29-OCT-2003; 2003WO-US034453.

XX PR 29-OCT-2002; 2002US-0422303P.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PA (PESQ-) CENT PESQUISAS GONCALO MONIZ.

XX PI Valenzuela JG, Ribeiro JMC, Barral A, Netto M, Brodskyn C;  
XX PI Gomes R;

XX DR WPI; 2004-376184/35.  
XX DR N-PSDB; ADO43457.

XX PT Novel salivary Lutzomyia longipalpis polypeptide, useful for inhibiting  
XX PT symptom of Leishmania infection or preventing Leishmania infection in  
XX PT subjects.

XX PS Claim 2; SEQ ID NO 63; 145pp; English.

XX CC The present sequence is the protein sequence of LJM11, a Lutzomyia  
XX CC longipalpis (New World sand fly) salivary polypeptide. The invention  
XX CC provides substantially purified L. longipalpis polypeptides and the  
XX CC polynucleotides encoding them, as well as vectors, host cells, antibodies  
XX CC and pharmaceutical compositions comprising the polypeptides or  
XX CC polynucleotides. A claimed method for inducing an immune response to L  
XX CC longipalpis in a subject involves administering a L. longipalpis salivary  
XX CC polypeptide (or its variant or immunogenic fragment) or a polynucleotide  
XX CC encoding it. The immune response is a T-cell or B-cell response, and the  
XX CC subject is preferably a dog or a human. A claimed method for inhibiting a  
XX CC symptom of a Leishmania infection or preventing a Leishmania infection in  
XX CC a subject comprises administering a L. longipalpis salivary protein or  
XX CC polynucleotide. A claimed method of diagnosing Leishmania infection  
XX CC comprises contacting a solid substrate comprising at least 3, 6 or 10 L.

CC longipalpis salivary polypeptides with a sample from the subject and  
CC detecting binding of a component of the sample to at least one of the  
CC polypeptides.

XX SQ Sequence 399 AA;

Query Match 96.6%; Score 28; DB 8; Length 399;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
||:||||  
Db 305 KVIFFA 310

RESULT 67

ABB61977  
ID ABB61977 standard; protein; 564 AA.

XX AC ABB61977;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 12723.

XX KW Drosophila; developmental biology; cell signalling; insecticide;  
XX KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE ) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.  
XX DR N-PSDB; ABL06080.

XX FT New isolated nucleic acid detection reagent for detecting 1000 or more  
XX FT genes from Drosophila and for elucidating cell signalling and cell-cell  
XX FT interactions.

XX PS Disclosure; SEQ ID NO 12723; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent  
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is  
XX CC useful in developmental biology and in elucidating cell signalling and  
XX CC cell-cell interactions in higher eukaryotes for the development of  
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention  
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (AB857737-  
XX CC AB872072). The sequence data for this patent did not form part of the  
XX CC printed specification, but was obtained in electronic format directly  
XX CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 564 AA;

Query Match 93.1%; Score 27; DB 4; Length 564;  
Best Local Similarity 66.7%; Pred. No. 9.9e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
||:||||  
Db 53 KIIFFA 58

RESULT 68  
 ABB68472  
 ID ABB68472 standard; protein; 1443 AA.  
 XX  
 AC ABB68472;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 32208.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 XX  
 DR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 XX  
 DR N-PSDB; ABL12575.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.  
 XX  
 PS Disclosure; SEQ ID NO 32208; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at filp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1443 AA;  
 Query Match 93.1%; Score 27; DB 4; Length 1443;  
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1204 KIIFFA 1209  
 XX  
 RESULT 69  
 AAW02314  
 ID AAW02314 standard; peptide; 6 AA.  
 XX  
 AC AAW02314;  
 XX  
 DT 02-MAY-1997 (first entry)  
 XX  
 DE Beta-amyloid modulator peptide #5.  
 XX  
 KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;  
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;  
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;  
 KW

KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;  
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;  
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;  
 XX scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.  
 OS Synthetic.  
 XX  
 PN WO9628471-A1.  
 XX  
 PD 19-SEP-1996.  
 XX  
 PF 14-MAR-1996; 96WO-US003492.  
 XX  
 PR 14-MAR-1995; 95US-00404831.  
 PR 07-JUN-1995; 95US-00475579.  
 PR 27-OCT-1995; 95US-00548998.  
 XX  
 PA (PHAR-) PHARM PEPTIDES INC.  
 XX  
 PI Findeis MA, Benjamin H, Garnick MB, Gafter ML, Hundal A;  
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S;  
 PI Kubasek W, Chin J, Lee J, Kelley M;  
 XX  
 DR WPI; 1996-433762/43.  
 XX  
 PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic  
 PT protein coupled (in)directly to at least 1 modifying gp., useful in  
 PT treatment of Alzheimer's disease.  
 XX  
 PS Claim 16; Page 91; 106pp; English.  
 XX  
 CC AAW02310-WO2332 represent the peptide portions of the beta-amyloid  
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4  
 CC kilodalton peptide that is the major protein component of amyloid  
 CC plaques. Amyloid plaques are present both in the brain lesions, and in  
 CC the walls of cerebral blood vessels in Alzheimer's disease patients. The  
 CC amyloid modulators of the invention comprise an amyloidogenic protein or  
 CC peptide (such as this sequence) coupled directly or indirectly to at  
 CC least one modifying group. The modifying group is preferably a cyclic,  
 CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a  
 CC biotin containing group, or a fluorescein containing group. These  
 CC compounds then modulate the aggregation of these sequences to natural  
 CC amyloid proteins or peptides when contacted with the natural  
 CC amyloidogenic proteins or peptides. The modulator compounds can be used  
 CC in the treatment of disorders associated with amyloidosis, such as  
 CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,  
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,  
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset  
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid  
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage  
 CC and other types of amyloidosis. The modulators are also useful for the  
 CC treatment of disorders associated with beta-amyloidosis, especially  
 CC Alzheimer's disease  
 XX  
 SQ Sequence 6 AA;  
 Query Match 89.7%; Score 26; DB 2; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1 KLVFFA 6  
 XX  
 RESULT 70  
 AAW89378  
 ID AAW89378 standard; peptide; 6 AA.  
 XX  
 AC AAW89378;  
 XX  
 DT 02-MAR-1999 (first entry)  
 XX  
 XX

DE Beta-amyloid peptide derivative A-beta-16-21.  
 XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;  
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;  
 KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;  
 KW Creutzfeldt-Jakob disease; BAP.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US5854204-A.  
 XX  
 PD 29-DEC-1998.  
 XX  
 XX 14-MAR-1996; 96US-00612785.  
 XX  
 PR 14-MAR-1995; 95US-00404831.  
 PR 07-JUN-1995; 95US-00475579.  
 PR 27-OCT-1995; 95US-00548998.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 XX  
 XX Hundal A, Geffer ML, Kasman L, Musso G, Molineaux S, Benjamin H;  
 PI Finkel MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;  
 PI Garnick MB, Kubasek W, Signer ER;  
 XX  
 DR WPI; 1999-094964/08.  
 XX  
 XX New peptide(s) derived from beta-amyloid peptide that inhibit amyloid  
 PT aggregation, and neurotoxicity, specifically for treatment and  
 PT prevention of Alzheimer's disease.  
 XX  
 PS Example 12; Col 64; 52pp; English.  
 XX  
 CC The present invention describes beta-amyloid peptide (BAP) derivatives.  
 CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and  
 CC peptides, specifically BAP, and their neurotoxicity, so are useful for  
 CC treating and preventing any disease involving amyloidosis, specifically  
 CC Alzheimer's disease but also Down's syndrome, familial amyloid  
 CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and  
 CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose  
 CC these diseases, in vitro or in vivo, by detecting binding of BAP to  
 CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation  
 CC even when BAP is present in molar excess. The present sequence represents  
 CC a BAP derivative  
 XX  
 SQ Sequence 6 AA;  
 Query Match 89.7%; Score 26; DB 2; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 DB 1 KLVFFA 6  
 RESULT 71  
 AAB48484  
 ID AAB48484 standard; peptide; 6 AA.  
 XX  
 AC AAB48484;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Antifibrillogenic peptide #11.  
 XX  
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX

PH Key Location/Qualifiers  
 FT Modified-site 6 /note= "C-terminal amide"  
 XX WO2000068263-A2.  
 PN 16-NOV-2000.  
 PD  
 XX 04-MAY-2000; 2000WO-CA000515.  
 XX  
 PR 05-MAY-1999; 99US-0132592P.  
 XX  
 PA (NEUR-) NEUROCHEM INC.  
 XX  
 XX Chalifour R, Gervais F, Gupta A;  
 PI WPI; 2001-031852/04.  
 DR  
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.  
 XX  
 PS Claim 7; Page 25; 46pp; English.  
 XX  
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein  
 XX  
 SQ Sequence 6 AA;  
 Query Match 89.7%; Score 26; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 DB 1 KLVFFA 6  
 RESULT 72  
 AAB48476  
 ID AAB48476 standard; peptide; 6 AA.  
 XX  
 AC AAB48476;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Antifibrillogenic peptide #3.  
 XX  
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000068263-A2.  
 XX  
 PD 16-NOV-2000.  
 XX  
 PR 04-MAY-2000; 2000WO-CA000515.  
 XX  
 PR 05-MAY-1999; 99US-0132592P.  
 XX  
 PA (NEUR-) NEUROCHEM INC.  
 XX  
 XX Chalifour R, Gervais F, Gupta A;  
 PI WPI; 2001-031852/04.  
 DR  
 XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
PT its isomer or peptidomimetic.  
XX  
XX  
PS Claim 7; Page 25; 46pp; English.  
XX  
CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
CC binding region and the prot-prot interaction region of the human amyloid  
CC protein  
XX  
XX Sequence 6 AA;  
SQ  
Query Match 89.7%; Score 26; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
Db 1 KLVFFA 6  
|:|||||  
|:|||||  
RESULT 73  
AAB82632  
ID AAB82632 standard; peptide; 6 AA.  
XX  
AC AAB82632;  
XX  
DT 02-OCT-2001 (first entry)  
XX  
DE All-D peptide used in Alzheimer's disease vaccine.  
XX  
KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
KW therapy; antigen.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..6 /note= "all D-form residues"  
FT Modified-site 6 /note= "C-terminal amide"  
FT  
XX WO200139796-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 29-NOV-2000; 2000WO-CA001413.  
XX  
XX 29-NOV-1999; 99US-0168594P.  
XX  
XX 28-NOV-2000; 2000US-00724842.  
XX  
XX (NEUR-) NEUROCHEM INC.  
XX  
XX Chalifour R, Hebert L, Kong X, Gervais F;  
XX  
XX WPI; 2001-441458/47.  
XX  
XX Preventing/treating amyloid-related disease, especially Alzheimer's  
PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
PT which elicits production of antibodies to prevent fibrillogenesis and  
PT associated cellular toxicity.  
XX  
XX Disclosure; Page 11; 31pp; English.  
XX  
XX The present sequence is that of an all-D peptide suitable for use for  
XX preparing vaccines for preventing or treating Alzheimer's disease and  
XX other amyloid related disorders in humans. It is based on a portion of  
CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
CC inserting 1 or more amino acid residues, or by substituting 1 or more

CC amino acid residues with other amino acid residues or non-amino acid  
CC fragments. Vaccines of the invention are produced using 'non-self'  
CC peptides synthesised from the unnatural D-configuration amino acids to  
CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
CC aggregated to be operative or immunogenic. They preferably interact with  
CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
CC fragments, protein conjugates, immunogenic derivative peptides and  
CC immunogenic peptidomimetics. Examples include all-D peptides  
CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
CC prion protein related disorders, or systemic amyloidosis associated with  
CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
CC amyloidosis found in long-term haemodialysis patients. The present all-D  
CC peptide was demonstrated to elicit antibody production in rabbits, and  
CC provided greater anti-fibrillogenic activity than its all-L equivalent  
XX  
XX Sequence 6 AA;  
SQ  
Query Match 89.7%; Score 26; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
Db 1 KLVFFA 6  
|:|||||  
|:|||||  
RESULT 74  
ABG71009  
ID ABG71009 standard; peptide; 6 AA.  
XX  
AC ABG71009;  
XX  
DT 05-DEC-2002 (first entry)  
XX  
DE Long form beta-amyloid protein fragment #6.  
XX  
KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;  
KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;  
KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;  
KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;  
KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;  
KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;  
KW macroglobulinaemia-associated amyloidosis; reactive amyloidosis;  
KW primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;  
KW hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;  
KW hereditary non-neuropathic systemic amyloidosis;  
KW familial Mediterranean Fever.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX US2002098173-A1.  
XX  
XX 25-JUL-2002.  
XX  
XX 04-OCT-2001; 2001US-00972475.  
XX  
XX 14-MAR-1995; 95US-00404831.  
XX 07-JUN-1995; 95US-00475579.  
XX 27-OCT-1995; 95US-00548998.  
XX 14-MAR-1996; 96US-00617267.  
XX  
XX (PRAE-) PRAECIS PHARM INC.  
XX  
XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;  
PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;

XX DR WPI; 2002-697709/75.  
 XX PT Amyloid modulator useful for treating a disorder associated with  
 PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment  
 PT coupled to a modifying group.  
 XX PS Example 12; Page 35; 41pp; English.  
 XX CC The invention describes an amyloid modulator comprising an amyloidogenic  
 CC protein and/or peptide fragment coupled to a modifying group so that the  
 CC compound modulates the aggregation of natural amyloid proteins or  
 CC peptides. The modulator is used for treating a disorder associated with  
 CC amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese  
 CC and Swedish types), familial amyloid cardiomyopathy (Danish type),  
 CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine  
 CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset  
 CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated  
 CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or  
 CC macroglobulinaemia-associated amyloidosis, primary localised cutaneous  
 CC nodular amyloidosis associated with Sjogren's syndrome, reactive  
 CC (secondary) amyloidosis, familial Mediterranean Fever and familial  
 CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),  
 CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,  
 CC amyloidosis associated with long term haemodialysis, hereditary non-  
 CC neuropathic systemic amyloidosis (familial amyloid polyneuropathy III),  
 CC familial amyloidosis of Finnish type, amyloidosis associated with  
 CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary  
 CC renal amyloidosis and lysosome-associated hereditary systemic  
 CC amyloidosis. The compound is capable of altering and inhibiting beta-  
 CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins  
 CC or peptides when contacted with a molar excess amount of natural beta-APs  
 CC relative to the modulator. This sequence represents a fragment of the  
 CC long form of beta-amyloid used in the creation of an amyloid modulator  
 XX SQ Sequence 6 AA;  
 Query Match 89.7%; Score 26; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. NO. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVVFFA 6  
 |:||||  
 Db 1 KLVFFA 6  
 RESULT 75  
 ID ABB05157 standard, peptide; 6 AA.  
 AC ABB05157;  
 XX 02-APR-2002 (first entry)  
 DT Beta amyloid peptide (16-21) SEQ ID NO:9.  
 DE Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;  
 KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;  
 KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;  
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;  
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;  
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;  
 KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX US6319498-B1.  
 PN 20-NOV-2001.  
 PD 14-MAR-1996; 96US-00617267.

PR 14-MAR-1995; 95US-00404831.  
 PR 07-JUN-1995; 95US-00475579.  
 PR 27-OCT-1995; 95US-00548998.  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;  
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;  
 XX WPI; 2002-146668/19.  
 XX Amyloid modulator compound useful for treatment of an amyloidogenic  
 PT disease such as Alzheimer's disease comprises an aggregation core domain  
 PT and a modifying group attached to it.  
 XX Disclosure; Col 18; 54pp; English.  
 XX The present invention describes an amyloid modulator compound (I)  
 CC comprising an aggregation core domain and a modifying group attached to  
 CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,  
 CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic  
 CC and auditory activities, and can be used as a natural amyloid aggregation  
 CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide  
 CC (beta-AP). (I) are used in the manufacture of a medicament for the  
 CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's  
 CC disease and other clinical occurrences of beta amyloid deposition such as  
 CC Down's syndrome individuals and in patients with hereditary cerebral  
 CC haemorrhage with amyloidosis, and for treating a disorder associated with  
 CC amyloidosis such as familial amyloid polyneuropathy. (I) reduces the  
 CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)  
 CC not only reduces the formation of neurotoxic aggregates but also have the  
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The  
 CC present sequence represents a beta-AP peptide, which is used in the  
 CC exemplification of the present invention  
 XX SQ Sequence 6 AA;  
 Query Match 89.7%; Score 26; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. NO. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVVFFA 6  
 |:||||  
 Db 1 KLVFFA 6  
 Search completed: December 29, 2005, 17:33:41  
 Job time : 82.7742 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 seconds  
(without alignments)  
54.137 Million cell updates/sec

Title: US-10-009-122-15

Perfect score: 29

Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	143	2	Q91Y69 MESAU
2	29	100.0	162	2	Q9N284_BOVIN
3	29	100.0	248	2	Q9BGL4_SHEEP
4	29	100.0	261	1	Y1086 HAEIN
5	29	100.0	261	2	Q4QLK2 HAEI8
6	29	100.0	277	2	Q73KX6 TREDE
7	29	100.0	314	2	Q9WY76 ARATH
8	29	100.0	381	2	Q5L1A8 GEOKA
9	29	100.0	389	2	Q8KHB6_CLODI
10	29	100.0	469	2	Q8S8Q7 ARATH
11	29	100.0	632	2	Q9N1P6 CANFA
12	29	100.0	654	2	Q6U7G9 MEIGA
13	29	100.0	660	1	MMP2_HUMAN
14	29	100.0	660	2	Q51Y21_TURGB
15	29	100.0	661	2	Q9SJA4_PIG
16	29	100.0	661	2	Q9GLE5_BOVIN
17	29	100.0	662	1	MMP2_MOUSE
18	29	100.0	662	1	MMP2_RABIT
19	29	100.0	662	1	MMP2_RAT
20	29	100.0	662	2	Q6GM9R RAT
21	29	100.0	663	1	MMP2_CHICK
22	29	100.0	767	2	Q8KTW1_CLODI
23	29	100.0	770	2	Q7XX63_ORYSA
24	29	100.0	840	2	Q6QOH3_ORYSA
25	29	100.0	842	2	Q6QHB5_ORYSA
26	29	100.0	842	2	Q6QDS7_ORYSA
27	29	100.0	945	2	Q9N175_SHEEP
28	29	100.0	1147	1	NOS2 RAT
29	29	100.0	1147	2	Q6XS76 RAT
30	29	100.0	1147	2	Q9QW28_9MURI
31	29	100.0	1147	2	Q9R0W4 RAT

32	28	96.6	118	2	Q8Y1S2	RALSO
33	28	96.6	169	2	Q8UI59	AGRTS
34	28	96.6	283	2	Q19334	CABEL
35	28	96.6	305	2	Q8EM92	OCEIH
36	28	96.6	355	2	Q6LJY6	PHOPR
37	28	96.6	1044	2	Q8XIN5	CLOPE
38	26	89.7	85	2	Q19641	CABEL
39	26	89.7	99	2	Q731J0	WOLPM
40	26	89.7	109	2	Q8XQ19	RALSO
41	26	89.7	126	2	Q6G347	BARHE
42	26	89.7	131	2	Q6C1M8	YARLI
43	26	89.7	131	2	Q6G346	BARHE
44	26	89.7	137	2	Q5SKK3	THT8
45	26	89.7	142	2	Q4JC95	SULAC
46	26	89.7	149	2	Q5WU01	LEGPL
47	26	89.7	149	2	Q5X274	LEGPA
48	26	89.7	149	2	Q5ZSR4	LEGPH
49	26	89.7	150	2	Q51314	9NOSO
50	26	89.7	156	1	GUAD	BACSU
51	26	89.7	156	2	Q5WBB0	BACSK
52	26	89.7	166	2	Q59317	PYRHO
53	26	89.7	185	2	Q67590	AQUAE
54	26	89.7	191	1	CSRPI	CHICK
55	26	89.7	191	1	CSRPI	COTJA
56	26	89.7	229	2	Q9RR88	DEIRA
57	26	89.7	232	2	Q67QU1	SWATH
58	26	89.7	233	2	Q527P8	MAGGR
59	26	89.7	233	2	Q30760	RHOSH
60	26	89.7	235	2	Q9N2Y5	CABEL
61	26	89.7	266	2	Q5UEW2	9PROT
62	26	89.7	268	2	Q5GU79	XANOR
63	26	89.7	276	2	Q7QS35	GIALA
64	26	89.7	285	2	Q48777	ARATH
65	26	89.7	290	2	Q5A5P9	CANAL
66	26	89.7	296	2	Q751V7	ORYSA
67	26	89.7	299	1	VG12	ICHV1
68	26	89.7	318	2	Q8GX50	ARATH
69	26	89.7	321	2	Q8ASCI	DESPPS
70	26	89.7	340	2	Q9EZ99	ZYMNO
71	26	89.7	348	1	CYSA	METCA
72	26	89.7	352	2	Q3MJ3	SHIFL
73	26	89.7	352	2	Q72FT5	DRSVH
74	26	89.7	383	2	Q6MI90	BDEBA
75	26	89.7	390	2	Q4HML6	CANLA
76	26	89.7	403	2	Q4WJL6	ASFPU
77	26	89.7	421	1	YIHN	ECOI1
78	26	89.7	421	2	Q8FBG3	ECOL6
79	26	89.7	421	2	Q8X8F3	ECOS7
80	26	89.7	425	2	Q895U4	CLOTE
81	26	89.7	426	2	Q84QAB	ORYSA
82	26	89.7	428	2	Q4KEQ1	PSEPF5
83	26	89.7	432	2	Q6L6X3	9VIRU
84	26	89.7	432	2	Q6L6X4	9VIRU
85	26	89.7	432	2	Q6L6X5	9VIRU
86	26	89.7	432	2	Q75PQ4	9VIRU
87	26	89.7	453	2	Q5YF80	9VIRU
88	26	89.7	453	2	Q68YS6	9VIRU
89	26	89.7	453	2	Q6GVF2	9VIRU
90	26	89.7	453	2	Q6GVF3	9VIRU
91	26	89.7	453	2	Q6GVF4	9VIRU
92	26	89.7	453	2	Q6GVF6	9VIRU
93	26	89.7	453	2	Q6GVF7	9VIRU
94	26	89.7	453	2	Q6GVF8	9VIRU
95	26	89.7	453	2	Q6GVF9	9VIRU
96	26	89.7	453	2	Q6GVG0	9VIRU
97	26	89.7	453	2	Q6GVG1	9VIRU
98	26	89.7	453	2	Q6GVG2	9VIRU
99	26	89.7	453	2	Q6GVG3	9VIRU
100	26	89.7	453	2	Q6PNE1	9VIRU
101	26	89.7	453	2	Q6QN91	9VIRU
102	26	89.7	453	2	Q6QNG4	9VIRU
103	26	89.7	453	2	Q6QNG5	9VIRU
104	26	89.7	453	2	Q6QNG6	9VIRU

Q8Y1S2	ralatonia s
Q8UI59	agrobacteri
Q19334	caenorhabdi
Q8EM92	oceanobacil
Q6LJY6	photobacter
Q8XIN5	clostridium
Q19641	caenorhabdi
Q731J0	wolbachia p
Q8XQ19	ralatonia s
Q6G347	bartonella
Q6C1M8	yarrowia li
Q6G346	thermus the
Q5SKK3	thermus the
Q4JC95	sulfolobus
Q5WU01	legionella
Q5X274	legionella
Q5ZSR4	legionella
Q51314	nostoc sp.
Q54598	bacillus au
Q5WBB0	bacillus cl
Q59317	pyrococcus
Q67590	aquifex aeo
P67966	gallus gall
P67967	coturnix co
Q9RR88	deinococcus
Q67QU1	symbiobacte
Q527P8	magnaporthe
Q30760	rhodobacter
Q9N2Y5	caenorhabdi
Q5UEW2	uncultured
Q5GU79	xanthomonas
Q7QS35	giardia lam
Q48777	arabidopsis
Q5A5P9	candida alb
Q751V7	oryza sativ
Q00165	ictalurid h
Q8GX50	arabidopsis
Q8AEC1	desulfotale
Q9EZ99	zymomonas m
Q609Q1	methylococc
Q3MJ3	shigella fl
Q72FT5	desulfovibr
Q6MI90	bdellovibr
Q4HML6	campylobact
Q4WJL6	aspergillus
P32135	escherichia
Q8FBG3	escherichia
Q8X8F3	escherichia
Q895U4	clostridium
Q84QAB	oryza sativ
Q4KEQ1	pseudomonas
Q6L6X3	red sea bre
Q6L6X4	rock bream
Q6L6X5	sea bass ir
Q75PQ4	turbot irid
Q5YF80	rock bream
Q68YS6	olive floun
Q6GVF2	korean flou
Q6GVF3	korean flou
Q6GVF4	korean flou
Q6GVF6	korean flou
Q6GVF7	korean flou
Q6GVF8	korean flou
Q6GVF9	korean flou
Q6GVG0	korean flou
Q6GVG1	korean flou
Q6GVG2	korean flou
Q6PNE1	turbot redd
Q6QN91	rock bream
Q6QNG4	rock bream
Q6QNG5	rock bream
Q6QNG6	rock bream



105	26	89.7	453	2	Q6QNG7_9VIRU	Q6qng7 rock bream	178	25	86.2	46	2	Q81W20_BACAN	Q81w20 bacillus an
106	26	89.7	453	2	Q6QNG8_9VIRU	Q6qng8 rock bream	179	25	86.2	54	2	Q421B9_PLABE	Q421b9 plasmodium
107	26	89.7	453	2	Q6QNH0_9VIRU	Q6qnh0 rock bream	180	25	86.2	61	2	Q72A11_DESVH	Q72a11 desulfovibr
108	26	89.7	453	2	Q6QNH1_9VIRU	Q6qnh1 rock bream	181	25	86.2	72	2	Q7Y541_BPR69	Q7y541 bacteriopho
109	26	89.7	453	2	Q7T3Y6_9VIRU	Q7t3y6 dwarf goura	182	25	86.2	75	2	Q4KA43_PSEF5	Q4ka43 pseudomonas
110	26	89.7	453	2	Q7T3Y7_9VIRU	Q7t3y7 african lam	183	25	86.2	76	2	Q6MKJ3_BDEBA	Q6mkj3 bdellovibri
111	26	89.7	453	2	Q7T3Z1_RSIV	Q7t3z1 red sea bre	184	25	86.2	76	2	Q72DT7_DESVH	Q72dt7 desulfovibr
112	26	89.7	453	2	Q80M45_RSIV	Q80m45 red sea bre	185	25	86.2	95	2	Q5LDJ7_BACFN	Q5ldj7 bacteroides
113	26	89.7	453	2	Q8VSD9_9VIRU	Q8vsd9 infectious	186	25	86.2	95	2	Q64UL9_BACFR	Q64ul9 bacteroides
114	26	89.7	453	2	Q516L1_9VIRU	Q5i6l1 rock bream	187	25	86.2	100	2	Q8YMU6_ANASP	Q8ymu6 anabaena sp
115	26	89.7	453	2	Q516L2_9VIRU	Q5i6l2 rock bream	188	25	86.2	107	2	Q4U9W4_THEAN	Q4u9w4 thelleria a
116	26	89.7	453	2	Q77ZP6_9VIRU	Q77zp6 sea bass ir	189	25	86.2	109	2	Q650T2_ORYSA	Q650t2 oryza sativ
117	26	89.7	453	2	Q7T3Y4_9VIRU	Q7t3y4 grouper sle	190	25	86.2	119	2	Q650T2_ORYSA	Q650t2 oryza sativ
118	26	89.7	453	2	Q4KSF0_9VIRU	Q4ksf0 orange-spot	191	25	86.2	120	1	Q650T2_ORYSA	Q650t2 oryza sativ
119	26	89.7	457	1	TEME_LISIN	Q926u7 listeria in	192	25	86.2	122	2	Q650T2_ORYSA	Q650t2 oryza sativ
120	26	89.7	458	2	Q4TRD0_9SPHN	Q4trd0 erythrobract	193	25	86.2	122	2	Q650T2_ORYSA	Q650t2 oryza sativ
121	26	89.7	464	1	COAT_IRV1	P18162 tipulia irid	194	25	86.2	128	2	Q4Y2C4_PLABE	Q4y2c4 plasmodium
122	26	89.7	465	2	Q4U3U9_9VIRU	Q4u3u9 trichoplusi	195	25	86.2	128	2	Q4Y2C4_PLABE	Q4y2c4 plasmodium
123	26	89.7	467	1	COAT_IRV6	Q85815 chilo iride	196	25	86.2	129	2	Q4Y2C4_PLABE	Q4y2c4 plasmodium
124	26	89.7	468	2	Q81L75_SHIFL	Q81ly5 shigella fl	197	25	86.2	132	2	Q4Y2C4_PLABE	Q4y2c4 plasmodium
125	26	89.7	472	1	COAT_IRV22	Q831y5 simulum ir	198	25	86.2	134	1	Q650T2_ORYSA	Q650t2 oryza sativ
126	26	89.7	479	2	Q9RFJ8_RHOSH	P22166 simulum ir	199	25	86.2	141	2	Q650T2_ORYSA	Q650t2 oryza sativ
127	26	89.7	479	2	Q9Z5E2_RHOSH	Q9z5e2 rhodobacter	200	25	86.2	141	2	Q650T2_ORYSA	Q650t2 oryza sativ
128	26	89.7	483	2	Q5FQ43_GLUOX	Q5fq43 gluconobact	201	25	86.2	144	2	Q650T2_ORYSA	Q650t2 oryza sativ
129	26	89.7	487	2	Q8BTV9_MOUSE	Q8btv9 mus musculu	202	25	86.2	144	2	Q650T2_ORYSA	Q650t2 oryza sativ
130	26	89.7	494	2	Q6NT77_HUMAN	Q6nt77 homo sapien	203	25	86.2	144	2	Q650T2_ORYSA	Q650t2 oryza sativ
131	26	89.7	496	2	Q6C9A3_YARLI	Q6c9a3 yarrowia li	204	25	86.2	152	2	Q650T2_ORYSA	Q650t2 oryza sativ
132	26	89.7	496	2	Q8D2N2_WIGBR	Q8d2n2 wiggleswort	205	25	86.2	160	2	Q650T2_ORYSA	Q650t2 oryza sativ
133	26	89.7	498	2	Q3YZV4_NOCFA	Q3yzv4 nocardia fa	206	25	86.2	167	2	Q650T2_ORYSA	Q650t2 oryza sativ
134	26	89.7	504	2	Q4H3G7_CIOIN	Q4h3g7 clostridia in	207	25	86.2	167	2	Q650T2_ORYSA	Q650t2 oryza sativ
135	26	89.7	525	2	Q5FVY8_XENTR	Q5fvy8 xenopus tro	208	25	86.2	167	2	Q650T2_ORYSA	Q650t2 oryza sativ
136	26	89.7	539	2	Q5B5V3_EMENI	Q5b5v3 aspergillus	209	25	86.2	172	2	Q650T2_ORYSA	Q650t2 oryza sativ
137	26	89.7	547	2	Q4TC12_TETNG	Q4tc12 tetraodon n	210	25	86.2	174	2	Q650T2_ORYSA	Q650t2 oryza sativ
138	26	89.7	555	2	Q9F103_HUMAN	Q9f103 homo sapien	211	25	86.2	174	2	Q650T2_ORYSA	Q650t2 oryza sativ
139	26	89.7	555	2	Q8NCA4_HUMAN	Q8nca4 homo sapien	212	25	86.2	186	1	Q650T2_ORYSA	Q650t2 oryza sativ
140	26	89.7	556	2	Q8BXN9_MOUSE	Q8bxn9 mus musculu	213	25	86.2	186	2	Q650T2_ORYSA	Q650t2 oryza sativ
141	26	89.7	556	2	Q8R2P9_MOUSE	Q8r2p9 mus musculu	214	25	86.2	190	2	Q650T2_ORYSA	Q650t2 oryza sativ
142	26	89.7	558	2	Q8BU98_MOUSE	Q8bu98 mus musculu	215	25	86.2	190	2	Q650T2_ORYSA	Q650t2 oryza sativ
143	26	89.7	559	2	Q7NSY8_CHRVO	Q7nsy8 chromobacte	216	25	86.2	192	1	Q650T2_ORYSA	Q650t2 oryza sativ
144	26	89.7	564	2	Q8NBN3_HUMAN	Q8nbn3 homo sapien	217	25	86.2	192	1	Q650T2_ORYSA	Q650t2 oryza sativ
145	26	89.7	634	2	Q7RY11_NEUCR	Q7ry11 neurospora	218	25	86.2	192	1	Q650T2_ORYSA	Q650t2 oryza sativ
146	26	89.7	646	2	Q5F565_GLUOX	Q5f565 gluconobact	219	25	86.2	192	1	Q650T2_ORYSA	Q650t2 oryza sativ
147	26	89.7	647	2	Q8WU27_HUMAN	Q8wu27 homo sapien	220	25	86.2	199	2	Q650T2_ORYSA	Q650t2 oryza sativ
148	26	89.7	679	2	Q5YV78_NOCFA	Q5yv78 nocardia fa	221	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
149	26	89.7	715	2	Q5PCX6_SALPA	Q5pcx6 salmonella	222	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
150	26	89.7	715	2	Q8Z4Z0_SALTI	Q8z4z0 salmonella	223	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
151	26	89.7	728	2	Q7NBR7_MYCGA	Q7nbr7 mycoplasma	224	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
152	26	89.7	733	2	Q8KTI9_MYCSY	Q8kti9 mycoplasma	225	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
153	26	89.7	742	2	Q8KTJ1_MYCSY	Q8ktj1 mycoplasma	226	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
154	26	89.7	743	2	Q6KTJ0_MYCSY	Q6ktj0 mycoplasma	227	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
155	26	89.7	844	2	Q6JB32_9BURK	Q6jb32 burkholderi	228	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
156	26	89.7	939	2	Q6AK45_DESPS	Q6ak45 desulfotale	229	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
157	26	89.7	960	2	Q41BE7_GIBZE	Q41be7 gibberella	230	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
158	26	89.7	1041	2	Q5LD76_BACFN	Q5ld76 bacteroides	231	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
159	26	89.7	1041	2	Q6A4U9_BACFR	Q6a4u9 bacteroides	232	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
160	26	89.7	1041	2	Q8A9Y5_BACTN	Q8a9y5 bacteroides	233	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
161	26	89.7	1055	2	Q9A8B7_HUMAN	Q9a8b7 homo sapien	234	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
162	26	89.7	1055	2	Q91VS8_MOUSE	Q91vs8 mus musculu	235	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
163	26	89.7	1139	1	SRBP2_CRIGR	Q60429 cricetus	236	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
164	26	89.7	1411	2	Q73Y53_MYCPA	Q73y53 mycobacteri	237	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
165	26	89.7	1701	2	Q61164_PLAYO	Q61164 plasmodium	238	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
166	26	89.7	1701	2	Q7RC08_PLAYO	Q7rc08 plasmodium	239	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
167	26	89.7	1723	2	Q8WRD0_PLABE	Q8wrd0 plasmodium	240	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
168	26	89.7	1769	2	Q4YQJ3_PLABE	Q4yqj3 plasmodium	241	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
169	26	89.7	1869	2	Q997D0_9COMO	Q997d0 broad bean	242	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
170	26	89.7	2397	1	MOK11_SCHPO	Q09854 schizosacch	243	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
171	26	89.7	2601	2	Q4YQJ3_PLABE	Q4yqj3 plasmodium	244	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
172	26	89.7	3808	2	Q51X35_MAGGR	Q51x35 magnaporthe	245	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
173	26	89.7	4212	2	Q4V218_BURMA	Q4v218 burkholderi	246	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
174	26	89.7	5835	2	Q63LX8_BURPS	Q63lx8 burkholderi	247	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
175	25	86.2	22	2	Q4YG66_PLABE	Q4yg66 plasmodium	248	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
176	25	86.2	42	2	Q7UKA9_RHOBA	Q7uka9 rhodospirell	249	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ
177	25	86.2	46	2	Q73F18_BACCI1	Q73f18 bacillus ce	250	25	86.2	202	2	Q650T2_ORYSA	Q650t2 oryza sativ

251 25 86.2 260 2 P94512 bacillus su  
 252 25 86.2 263 2 Q92VA5 rhizobium m  
 253 25 86.2 268 1 TRUA\_TREDE  
 254 25 86.2 268 2 Q84L48 mirabilis f  
 255 25 86.2 268 2 Q5ZJP4 gallus gall  
 256 25 86.2 270 2 Q4WEP8 aspergillus  
 257 25 86.2 271 2 Q65GA6 bacillus li  
 258 25 86.2 276 2 Q6BFW3 paramecium  
 259 25 86.2 276 2 Q94003 arath  
 260 25 86.2 276 2 Q62RR1 bacld  
 261 25 86.2 282 1 PNMT HUMAN  
 262 25 86.2 282 2 Q6FHD9 HUMAN  
 263 25 86.2 282 2 Q9KMB5 vibrio chol  
 264 25 86.2 291 2 Q87J38 vibrio para  
 265 25 86.2 293 2 Q9Z4F0 plasmid col  
 266 25 86.2 293 2 Q9KY30 streptomyce  
 267 25 86.2 295 2 Q8D6E6 vibrio vuln  
 268 25 86.2 295 2 Q7MD99 vibrio vuln  
 269 25 86.2 297 2 Q8PID6 xanthomonas  
 270 25 86.2 298 2 Q97VK7 sulfolobus  
 271 25 86.2 299 2 Q5NTR3 uncultured  
 272 25 86.2 300 2 Q4ZTF5 pseudomonas  
 273 25 86.2 300 2 Q80B08 orf virus.  
 274 25 86.2 302 2 Q7AGM6 escherichia  
 275 25 86.2 303 2 Q9CLP3 pasteurella  
 276 25 86.2 303 2 Q6TVN6 orf virus.  
 277 25 86.2 303 2 Q6TW16 orf virus.  
 278 25 86.2 307 2 Q6TVAA 9POXV  
 279 25 86.2 313 2 Q71KR8 klebsormidi  
 280 25 86.2 317 2 Q4QEH6 leishmania  
 281 25 86.2 321 2 Q9WZS8 thermotoga  
 282 25 86.2 322 1 Q8JG13 HUMAN  
 283 25 86.2 323 2 Q8X9H6 ECO57  
 284 25 86.2 324 2 Q4IFV0 gibberella  
 285 25 86.2 325 2 Q4TJG6 9SPHN  
 286 25 86.2 326 1 PELA EMENI  
 287 25 86.2 326 2 Q5BFD9 EMENI  
 288 25 86.2 327 2 Q6FKK4 CANGA  
 289 25 86.2 327 2 Q7WS88 BORPA  
 290 25 86.2 327 2 Q7WDB5 BORBR  
 291 25 86.2 327 2 Q7VZ12 BORPE  
 292 25 86.2 331 2 Q4HS16 CAMUP  
 293 25 86.2 331 2 Q821X4 CHLCV  
 294 25 86.2 331 2 Q9Z6V0 CHLPN  
 295 25 86.2 332 2 Q9YCL2 aeropyrum p  
 296 25 86.2 333 2 Q5L571 chlamydophi  
 297 25 86.2 334 2 Q6LH05 PHOPR  
 298 25 86.2 337 2 Q4M1D9 burkholderi  
 299 25 86.2 340 1 YRU3 CAEEL  
 300 25 86.2 340 2 Q63KW3 burkholderi

## ALIGNMENTS

RESULT 1  
 Q91Y69 MESAU  
 ID Q91Y69 MESAU PRELIMINARY; PRT; 143 AA.  
 AC Q91Y69  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Matrix metalloproteinase-2 (Fragment).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Cricetinae; Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Tracheal surface;  
 RA KO K.H., Shin C.Y., Lee W.J., Yoo B.K., Ryu J.R., Park K.H.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF260254; AAK51635.1; -; mRNA.  
 DR HSSP; P08253; 1CK7.  
 DR MEROPS; M10.004; -.  
 DR InterPro; IPR000585; Hemopexin.  
 DR Pfam; PF00045; Hemopexin; 3.  
 DR SMART; SM00120; HK; 3.  
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN\_1.  
 FT NON\_TER 1 1  
 FT NON\_TER 143 143  
 SQ SEQUENCE 143 AA; - 16316 MW; 1B4310F9BE6A023EF CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 21 KAVFFA 26  
 RESULT 2  
 Q9N284 BOVIN  
 ID Q9N284 BOVIN PRELIMINARY; PRT; 162 AA.  
 AC Q9N284;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 MN MMP-2 (Fragment).  
 GN Names=bmp-2;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sato T., Hirata M., Ito A., Hashizume K.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB043994; BAA96387.1; -; mRNA.  
 DR HSSP; P08253; 1CK7.  
 DR MEROPS; M10.003; -.  
 DR InterPro; IPR000585; Hemopexin.  
 DR Pfam; PF00045; Hemopexin; 3.  
 DR SMART; SM00120; HK; 3.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 162 AA; 18351 MW; B8898B49E5E5326A CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 33 KAVFFA 38  
 RESULT 3  
 Q9BGL4 SHEEP  
 ID Q9BGL4 SHEEP PRELIMINARY; PRT; 248 AA.  
 AC Q9BGL4;  
 DT 01-JUN-2001 (TRENBLrel. 17, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Gelatinase A (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Ovary;

```

RX MEDLINE=21858324; PubMed=11870075;
RA Ricke W.A., Smith G.W., Smith M.F.;
RT "Matrix metalloproteinase expression and activity following
RT prostaglandin F(2 alpha)-induced luteolysis.";
RL Biol. Reprod. 66:685-691(2002).
DR EMBL; AF267159; AAG59847.1; -; mRNA.
DR HSSP; P08253; 1GXD.
DR MEROPS; M10.003; -.
DR GO; GO:005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00045; Hemopexin; 3.
DR Pfam; PF00413; Peptidase M10; 1.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00120; HX; 3.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
FT 248 1
FT SEQUENCE 248 AA; 28034 MW; 56F421C2D6DC133E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 184 KAVFFA 189

RESULT 4
Y1086_HAEIN
ID Y1086_HAEIN STANDARD; PRT; 261 AA.
AC P45030;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein H1086.
GN OrderedLocNames=H1086;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA McLennan A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.V., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RA rd.";
RL Science 269:496-512(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the DUF140 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

```

---

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U32788; AAC22742.1; -; Genomic_DNA.
DR TIGR; H11086; -.
DR InterPro; IPR003453; DUF140.
DR Pfam; PF02405; DUF140; 1.
DR TIGRFAMs; TIGR00056; DUF140; 1.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 13
FT TRANSMEM 50 70 Potential.
FT TRANSMEM 90 110 Potential.
FT TRANSMEM 148 168 Potential.
FT TRANSMEM 199 219 Potential.
FT TRANSMEM 239 259 Potential.
FT SEQUENCE 261 AA; 28015 MW; 4BC3695F247A6BF6 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 205 KAVFFA 210

RESULT 5
Q4QLK2_HAE18
ID Q4QLK2_HAE18 PRELIMINARY; PRT; 261 AA.
AC Q4QLK2;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Conserved ABC-type transport system protein, permease component.
GN OrderedLocNames=NTIH1249;
OS Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
[1]
NUCLEOTIDE SEQUENCE.
RP PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RX Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gibson J., Gibson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RL d, strain KW20."
RL J. Bacteriol. 187:4627-4636(2005).
DR EMBL; CP000057; AX88095.1; -; Genomic_DNA.
DR InterPro; IPR003453; DUF140.
DR Pfam; PF02405; DUF140; 1.
DR TIGRFAMs; TIGR00056; DUF140; 1.
KW Complete proteome.
KW SEQUENCE 261 AA; 28075 MW; 0EB1BEEDD2FA133A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 205 KAVFFA 210

RESULT 6
Q73KX6_TREDE
ID Q73KX6_TREDE PRELIMINARY; PRT; 277 AA.
AC Q73KX6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)

```

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Amino acid ABC transporter, amino acid-binding protein, putative.  
 GN OrderedLocusNames=TDE2091;  
 OS Treponema denticola.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
 OX NCBI\_TaxID=158;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 35405 / DSM 14222;  
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;  
 RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,  
 RA Dodson R.J., Davidsen T.M., Tettelin H., Fouts D.E., Haft D.H.,  
 RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,  
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,  
 RA Ghebreorgis E., Geer K., Tsagaye G., Malek J.A., Ayodeji B.,  
 RA Shatman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,  
 RA Vashisth P., McNeill T.Z., Xiang O., Sodergren E., Baca E.,  
 RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;  
 RT "Comparison of the genome of the oral pathogen Treponema denticola  
 with other spirochete genomes";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).  
 DR EMBL; AE017253; AAS12611.1; -; Genomic\_DNA.  
 DR TIGR; TDE2091; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.  
 DR GO; GO:0005215; F:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001311; SBP\_glu receptor.  
 DR InterPro; IPR001638; SBP\_bac\_3.  
 DR Pfam; PF00497; SBP\_bac\_3; 1.  
 DR SMART; SM00062; PBPb; 1.  
 DR PROSITE; PS01039; SBP\_BACTERIAL\_3; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 277 AA; 31013 MW; AC9F1BC5DB10A16E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 DB 8 KAVFFA 13

RESULT 7  
 Q9WY6 ARATH  
 ID Q9WY6 ARATH PRELIMINARY; PRT; 314 AA.  
 AC Q9WY6;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-NAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE F3E22.6 protein.  
 GN Name=F3E22.6;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsia.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,  
 RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,  
 RA Barnstead M.E., Bowman C.L., White O., Niernan W.C., Fraser C.M.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC029912; AAF63818.1; -; Genomic\_DNA.  
 DR InterPro; IPR002575; APH trans.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR Pfam; PF01636; APH; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN\_1.  
 SQ SEQUENCE 314 AA; 34938 MW; B831A6DFA610A5DB CRC64;

Query Match 100.0%; Score 29; DB 2; Length 314;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 282 KAVFFA 287

RESULT 8  
 Q5L1A8 GEOKA  
 ID Q5L1A8 GEOKA PRELIMINARY; PRT; 381 AA.  
 AC Q5L1A8;  
 DT 01-FEB-2005 (TREMBlrel. 29, Created)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE Proton/sodium antiporter.  
 GN OrderedLocusNames=GK0987;  
 OS Geobacillus kaustophilus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
 OX NCBI\_TaxID=1462;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HTA426;  
 RX PubMed=15576355; DOI=10.1093/nar/gkh970;  
 RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,  
 RA Matsui S., Uchiyama I.;  
 RT "Thermoadaptation trait revealed by the genome sequence of  
 thermophilic Geobacillus kaustophilus";  
 RL Nucleic Acids Res. 32:6292-6303 (2004).  
 DR EMBL; BA000043; BAD75272.1; -; Genomic\_DNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.  
 DR GO; GO:0006885; P:regulation of pH; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR006153; Na\_H\_exchanger; 1.  
 DR Pfam; PF00999; Na\_H\_exchanger; 1.  
 KW Complete proteome; Transmembrane; Transport.  
 SQ SEQUENCE 381 AA; 39481 MW; AE3EA4252A7E367B CRC64;

Query Match 100.0%; Score 29; DB 2; Length 381;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 DB 179 KAVFFA 184

RESULT 9  
 Q8KHB6 CLODI  
 ID Q8KHB6 CLODI PRELIMINARY; PRT; 389 AA.  
 AC Q8KHB6;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE S-layer protein variable domain SlpA (fragment).  
 GN Name=slpA;  
 OS Clostridium difficile.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1496;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 43597, 90-111, and 93-136;  
 RX MEDLINE=22083941; PubMed=12089261;  
 RX DOI=10.1128/JCM.40.7.2452-2458.2002;  
 RA Karjalainen T., Saumier N., Barc M.C., Delmee M., Collignon A.;  
 RT "Clostridium difficile genotyping based on slpA variable region in S-  
 layer gene sequence: an alternative to serotyping";  
 RN J. Clin. Microbiol. 40:2452-2458 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 43597, 90-111, and 93-136;

```

RA Karjalainen T.K., Saunier N.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458880; AAM75944.1; -; Genomic DNA.
DR EMBL; AF458881; AAM75945.1; -; Genomic DNA.
DR EMBL; AF458882; AAM75946.1; -; Genomic DNA.
FT NON_TER 1 389
FT NON_TER 389 389
SQ SEQUENCE 389 AA; 41788 MW; C5ED8F4901C18F8C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 340 KAVFFA 345

RESULT 10
Q8S8Q7 ARATH PRELIMINARY; PRT; 469 AA.
AC Q8S8Q7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative selenium-binding protein (Pentatricopeptide repeat-containing protein).
DE NCBI_TaxID=3702;
GN ORFNames=At2g34370;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RA Underwood B.A., Xiao Y., Moskal W., Monaghan E., Wang W., Redman J.,
RA Wu H.C., Utterback T., Town C.D.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004491; AAM14949.1; -; Genomic DNA.
DR EMBL; DQ056566; AAY78716.1; -; mRNA.
DR PIR; T02325; T02325.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF01535; PPR; 4.
DR TIGRFAMs; TIGR00756; PPR; 3.
KW Repeat.
SQ SEQUENCE 469 AA; 53856 MW; FB698FC9C0238437 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 213 KAVFFA 218

RESULT 11
Q9N1P6 CANFA PRELIMINARY; PRT; 632 AA.
ID Q9N1P6 CANFA
AC Q9N1P6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

```

```

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase-2 (Fragment).
GN Name=MMP-2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fibrosarcoma;
RA Jahic H., Faria B., Balkin R., Baxendale V., Fang Y., Kitchell B.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177217; AAF67517.1; -; mRNA.
DR HSSP; P08253; 1GXD.
DR MEROPS; M10_003; -.
DR Ensembl; ENSCAPG0000009421; Canis familiaris.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 632 AA; 70991 MW; D8AE895497E129F3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 632;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 503 KAVFFA 508

RESULT 12
Q6U7G9 MELGA PRELIMINARY; PRT; 654 AA.
ID Q6U7G9 MELGA PRELIMINARY;
AC Q6U7G9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gelatinase A.
OC Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Monsonogo Ornan E., Tong A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY376899; AAQ98971.1; -; mRNA.
DR HSSP; P08254; 1B3D.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

```

DR InterPro; IPR000562; FN\_Type\_II.  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase\_M.  
 DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR Pfam; PF00040; fn2; 3.  
 DR Pfam; PF00045; Hemopexin; 3.  
 DR Pfam; PF00413; Peptidase\_M10; 1.  
 DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
 DR PRINTS; PR00013; FNTYPEII.  
 DR PRINTS; PR00138; MATRIXIN.  
 DR ProDom; PD000995; FN\_Type\_II; 3.  
 DR SMART; SM00059; FN2; 3.  
 DR SMART; SM00120; HX; 4.  
 DR SMART; SM00235; ZnMc; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00023; FIBRONECTIN\_2; 3.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 SQ SEQUENCE 654 AA; 73956 MW; F9B0755F76B6F8DD CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 654;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVPFA 6  
 |||||  
 Db 533 KAVPFA 538

RESULT 13  
 ID MMP2\_HUMAN STANDARD; PRT; 660 AA.  
 AC P08253;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE 72 kDa type IV collagenase precursor (BC 3.4.24.24) (72 kDa  
 DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A) (TBE-  
 DE 1).  
 GN Name=MMP2; Synonyms=CLG4A;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP NUCLEOTIDE SEQUENCE OF 19-660, AND PARTIAL PROTEIN SEQUENCE.  
 RX MEDLINE=86198216; PubMed=2834383;  
 RA Collier I.E., Wilhelm S.M., Eisen A.Z., Marmer B.L., Grant G.A.,  
 RA Seltzer J.L., Kronberger A., He C., Bauer E.A., Goldberg G.I.;  
 RT "H-ras oncogene-transformed human bronchial epithelial cells (TBE-1)  
 RT secrete a single metalloprotease capable of degrading basement  
 RT membrane collagen.";  
 RL J. Biol. Chem. 263:6579-6587(1988).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=91236162; PubMed=1851724;  
 RA Collier I.E., Bruns G.A.P., Goldberg G.I., Gerhard D.S.;  
 RT "On the structure and chromosome location of the 72- and 92-kDa human  
 RT type IV collagenase genes.";  
 RL Genomics 9:429-434(1991).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=90293047; PubMed=2162831;  
 RA Huhtala P., Chow L.T., Tryggvason K.;  
 RT "Structure of the human type IV collagenase gene.";  
 RL J. Biol. Chem. 265:11077-11082(1990).  
 [4]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-447 AND LEU-621.  
 RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,  
 RA Nguyen C.P., Nguyen D.A., Poel C.L., Chambers S.W., Schackwitz W.S.,  
 RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;

RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department  
 of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";  
 Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RP TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Dapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [6]  
 RN NUCLEOTIDE SEQUENCE OF 1-51.  
 RX MEDLINE=90228972; PubMed=2158484;  
 RA Huhtala P., Eddy R.L., Fan Y.S., Byers M.G., Shows T.B.,  
 RA Tryggvason K.;  
 RT "Completion of the primary structure of the human type IV collagenase  
 RT proenzyme and assignment of the gene (CLG4) to the q21 region of  
 RT chromosome 16.";  
 RL Genomics 6:554-559(1990).  
 [7]  
 RN ENZYME REGULATION.  
 RP PubMed=11179305; DOI=10.1128/IAI.69.3.1402-1408.2001;  
 RX Gusman H., Travis J., Helmerhorst E.J., Potempa J., Troxler R.P.,  
 RA Oppenheim F.G.;  
 RT "Salivary histatin 5 is an inhibitor of both host and bacterial  
 RT enzymes implicated in periodontal disease.";  
 RL Infect. Immun. 69:1402-1408(2001).  
 [8]  
 RP PROCESSING OF KISS1.  
 RX MEDLINE=22761370; PubMed=12879005; DOI=10.1038/sj.onc.1206542;  
 RA Takino T., Koehikawa N., Miyamori H., Tanaka M., Sasaki T., Okada Y.,  
 RA Seiki M., Sato H.;  
 RT "Cleavage of metastasis suppressor gene product KiSS-1  
 RT protein/metastin by matrix metalloproteinases.";  
 RN Oncogene 22:4617-4626(2003).  
 [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 443-660.  
 RX MEDLINE=96069777; PubMed=7583664;  
 RA Libson A.M., Gittis A.G., Collier I.E., Marmer B.L., Goldberg G.I.,  
 RA Lattman E.;  
 RT "Crystal structure of the haemopexin-like C-terminal domain of  
 RT gelatinase A.";  
 RL Nat. Struct. Biol. 2:938-942(1995).  
 [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 458-660.  
 RX MEDLINE=96140723; PubMed=8549817; DOI=10.1016/0014-5793(95)01435-7;  
 RA Gohlke U., Gomis-Rueth F.-X., Crabbe T., Murphy G., Docherty A.J.,  
 RA Bode W.;  
 RT "The C-terminal (haemopexin-like) domain structure of human gelatinase  
 RT A (MMP2): structural implications for its function.";  
 RL FEBS Lett. 378:126-130(1996).  
 CC -1- FUNCTION: In addition to gelatin and collagens, it cleaves KiSS1  
 CC at a Glycyl-Leu bond.  
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types  
 CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-  
 CC Ile-Ala-Gly-Gln.

CC -|- COFACTOR: Binds 4 calcium ions per subunit.  
CC -|- COFACTOR: Binds 2 zinc ions per subunit.  
CC -|- ENZYME REGULATION: Inhibited by histatin-3 1/24 (histatin-5).  
CC -|- SUBUNIT: Ligand for integrin alpha-V/beta-3.  
CC -|- TISSUE SPECIFICITY: Produced by normal skin fibroblasts.  
CC -|- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-MMP3).  
CC -|- SIMILARITY: Belongs to the peptidase M10A family.  
CC -|- SIMILARITY: Contains 3 fibronectin type-II domains.  
CC -|- SIMILARITY: Contains 1 hemopexin-like domain.  
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC -----  
DR EMBL; J03210; AAA35701.1; -; mRNA.  
DR EMBL; M33789; AAA52027.1; -; Genomic DNA.  
DR EMBL; M55593; AAA52028.1; -; Genomic DNA.  
DR EMBL; M58552; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55582; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55583; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55584; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55585; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55586; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55587; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55588; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55589; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55590; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55591; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; M55592; AAA52028.1; JOINED; Genomic DNA.  
DR EMBL; AY738117; AAU10089.1; -; Genomic DNA.  
DR EMBL; BC002576; AAH02576.1; -; mRNA.  
DR PIR; A28153; A28153.  
DR PDB; 1CK7; X-ray; A=30-660.  
DR PDB; 1CKW; NMR; A=278-336.  
DR PDB; 1EAK; X-ray; A/B/C/D=32-452.  
DR PDB; 1GEN; X-ray; @=443-660.  
DR PDB; 1GXD; X-ray; A/B=30-660.  
DR PDB; 1HOV; NMR; A=110-214.  
DR PDB; 1J7M; NMR; A=337-394.  
DR PDB; 1KS0; NMR; A=223-282.  
DR PDB; 1QIB; X-ray; A=115-216.  
DR PDB; 1RTG; X-ray; @=451-660.  
DR MEROPS; M10.003; -.  
DR Ensembl; ENSG00000087245; Homo sapiens.  
DR HGNC; HGNC:7186; MMP2.  
DR H-invDB; HIX0013041; -.  
DR MIM; 120360; -.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0004228; F:gelatinase A activity; TAS.  
DR GO; GO:0008270; F:zinc ion binding; TAS.  
DR GO; GO:0006508; F:proteolysis and peptidolysis; TAS.  
DR InterPro; IPR000562; FN\_type2\_col\_bd.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR006026; Peptidase\_M.  
DR Pfam; PF00040; fn2; 3.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase\_M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; PR00013; FNTYPEII.  
DR PRINTS; PR00138; MATRXIN.  
DR ProDom; PD000995; FN\_Type\_II; 3.  
DR SMART; SM00059; FN2; 3.  
DR SMART; SM00120; HX; 4.  
DR SMART; SM00235; ZnMC; 1.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
DR PROSITE; PS00023; FN2\_1; 2.  
DR PROSITE; PS51092; FN2\_2; 3.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
DR Calcium; Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc.  
SQ SEQUENCE 660 AA; 73871 MW; FC7EBB481091C5ED CRC64;

DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW 3D-structure; Calcium; Collagen degradation;  
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;  
KW Hydrolase; Metal-binding; Metalloprotease; Polymorphism; Protease;  
KW Repeat; Signal; Zinc; Zymogen.  
FT SIGNAL 1 29 Potential.  
FT PROPEP 30 109 Activation peptide.  
FT CHAIN 110 660 72 kDa type IV collagenase.  
FT DOMAIN 228 276 Fibronectin type-II 1.  
FT DOMAIN 286 334 Fibronectin type-II 2.  
FT DOMAIN 344 392 Fibronectin type-II 3.  
FT DOMAIN 466 660 Hemopexin-like.  
FT REGION 110 221 Collagenase-like 1.  
  
Query Match 100.0%; Score 29; DB 1; Length 660;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0;  
  
QY 1 KAVFFA 6  
Db 531 KAVFFA 536  
|||||  
  
RESULT 14  
Q5IY21\_TUPGB PRELIMINARY; PRT; 660 AA.  
AC Q5IY21;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Matrix metalloproteinase 2.  
OS Tupaia glis belangeri (Common tree shrew).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaia.  
OX NCBI\_TaxID=37347;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15621657; DOI=10.1080/10425170400012925;  
RA Kenning M.S., Gentle A., McBrien N.A.;  
RT "Expression and cDNA sequence of matrix metalloproteinase-2 (MMP-2) in a mammalian model of human disease processes: Tupaia belangeri.";  
RL DNA Seq. 15:332-337(2004).  
DR EMBL; AY600958; AAT44903.1; -; mRNA.  
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000562; FN\_type2\_col\_bd.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR006026; Peptidase\_M.  
DR Pfam; PF00040; fn2; 3.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase\_M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; PR00013; FNTYPEII.  
DR PRINTS; PR00138; MATRXIN.  
DR ProDom; PD000995; FN\_Type\_II; 3.  
DR SMART; SM00059; FN2; 3.  
DR SMART; SM00120; HX; 4.  
DR SMART; SM00235; ZnMC; 1.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
DR PROSITE; PS00023; FN2\_1; 2.  
DR PROSITE; PS51092; FN2\_2; 3.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Calcium; Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc.  
SQ SEQUENCE 660 AA; 73871 MW; FC7EBB481091C5ED CRC64;

Query Match 100.0%; Score 29; DB 2; Length 660;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0;



```

QY      1 KAVFFA 6
DB      531 KAVFFA 536

RESULT 15
Q95JAA_PIG PRELIMINARY; PRT; 661 AA.
AC Q95JAA;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gelatinase A.
GN Name=MMP-2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sub.
OC NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TSSUE=Tooth enamel organ;
RX MEDLINE=21480581; PubMed=11597028;
RA Caron C., Xue J., Sun X., Simmer J.P., Bartlett J.D.;
RT "Gelatinase A (MMP-2) in developing tooth tissues and amelogenin
RT hydrolysis.";
RL J. Dent. Res. 80:1660-1664 (2001).
DR EMBL; AF295805; AAK97133.1; -; mRNA.
DR HSSP; P08253; IGXD.
DR MEROPS; M10.003; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00013; ENTPEII.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2_3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Metalloprotease; Protease.
SQ SEQUENCE 661 AA; 73776 MW; 90545F7645E5F84D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      532 KAVFFA 537

RESULT 17
MMP2_MOUSE STANDARD; PRT; 662 AA.
AC P33434;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 72 kDa type IV collagenase precursor (BC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN Name=Mmp2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92218452; PubMed=1373140;
RA Reponen P., Sahlberg C., Huhtala P., Hurskainen T., Thesleff I.,
RA Tryggvason K.;
RT "Molecular cloning of murine 72-kDa type IV collagenase and its
RT expression during mouse development.";
RL J. Biol. Chem. 267:7856-7862 (1992).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

```



RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny N.K., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RN DEVELOPMENTAL STAGE.  
RC TISSUE=Embryo;  
RC PubMed:274464;  
RX Brenner C.A., Adler R.R., Rappolee D.A., Pedersen R.A., Werb Z.;  
RA "Genes for extracellular-matrix-degrading metalloproteinases and their  
RT inhibitor, TIMP, are expressed during early mammalian development.";  
RL Genes Dev. 3:848-859 (1989).  
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types  
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-  
CC Ile-Ala-Gly-Gln.  
CC -1- COFACTOR: Binds 4 calcium ions per subunit (By similarity).  
CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).  
CC -1- SUBUNIT: Ligand for integrin alpha-V/beta-3.  
CC -1- DEVELOPMENTAL STAGE: Present in unfertilized eggs and at the  
CC zygote and cleavage stages. Levels increase at the blastocyst  
CC stage and with endoderm differentiation.  
CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-  
CC MMP3) (By similarity).  
CC -1- SIMILARITY: Belongs to the peptidase M10A family.  
CC -1- SIMILARITY: Contains 3 fibronectin type-II domains.  
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; M84324; AAA39338.1; -; mRNA.  
DR EMBL; BC070430; AAH70430.1; -; mRNA.  
DR PIR; A42496; A42496.  
DR HSP; P08253; 1RTG.  
DR MEROPS; M10.003; -.  
DR Ensembl; ENSMUSG0000031740; Mus musculus.  
DR MGI; MGI:97009; Mmp2.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR InterPro; IPR000562; FN\_type2\_col\_bd.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR006026; Peptidase\_M.  
DR Pfam; PF00040; fn2; 3.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase\_M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; PR00013; FNTYPEI.  
DR PRINTS; PR00138; MATRIXIN.  
DR ProDom; PD000995; FN\_Type\_II; 3.  
DR SMART; SM00059; FN2; 3.  
DR SMART; SM00120; HX; 4.  
DR SMART; SM00235; Znmc; 1.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
DR PROSITE; PS00023; FN2\_1; 3.

DR PROSITE; PS51092; FN2\_2; 3.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;  
KW Hydrolase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;  
KW Zinc; Zymogen.  
FT SIGNAL. 1 29 Potential.  
FT PROPEP 30 109 Activation peptide.  
FT CHAIN 110 662 72 kDa type IV collagenase.  
FT DOMAIN 228 276 Fibronectin type-II 1.  
FT DOMAIN 286 334 Fibronectin type-II 2.  
FT DOMAIN 344 392 Fibronectin type-II 3.  
FT DOMAIN 468 662 Hemopexin-like.  
FT REGION 110 221 Collagenase-like 1.  
FT REGION 222 396 Collagen-binding.  
FT REGION 397 467 Collagenase-like 2.  
FT ACT\_SITE 404 404 By similarity.  
FT METAL 134 134 Calcium 1 (By similarity).  
FT METAL 168 168 Calcium 2 (By similarity).  
FT METAL 178 178 Zinc 1 (By similarity).  
FT METAL 180 180 Zinc 1 (By similarity).  
FT METAL 185 185 Calcium 3 (By similarity).  
FT METAL 186 186 Calcium 3 (via carbonyl oxygen) (By similarity).  
FT METAL 193 193 Zinc 1 (By similarity).  
FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By similarity).  
FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By similarity).  
FT METAL 204 204 Calcium 2 (By similarity).  
FT METAL 206 206 Zinc 1 (By similarity).  
FT METAL 208 208 Calcium 3 (By similarity).  
FT METAL 211 211 Calcium 1 (By similarity).  
FT METAL 403 403 Calcium 3 (By similarity).  
FT METAL 407 407 Zinc 2 (catalytic) (By similarity).  
FT METAL 413 413 Zinc 2 (catalytic) (By similarity).  
FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By similarity).  
FT METAL 523 523 Calcium 4 (via carbonyl oxygen) (By similarity).  
FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By similarity).  
FT METAL 620 620 Calcium 4 (via carbonyl oxygen) (By similarity).  
FT SITE 102 102 Cysteine switch (Potential).  
FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 644 644 N-linked (GlcNAc...) (Potential).  
FT DISULFID 471 662 By similarity.  
SQ SEQUENCE 662 AA; 74102 MW; C630AYDBDB272F02 CRC64;  
Query Match 100.0%; Score 29; DB 1; Length 662;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;  
QY 1 KAVPFA 6  
Db 533 KAVPFA 538  
RESULT 18  
MMP2\_RABIT  
ID MMP2\_RABIT STANDARD; PRT; 662 AA.  
AC P50757;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa  
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).  
GN Name=MMP2;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;

OC Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Japanese white; TISSUE=Articular joint;  
 RX MEDLINE=56283805; PubMed=8679695; DOI=10.1016/0167-4781(96)00050-4;  
 RA Matsumoto S.; Kato M.; Watanabe T.; Masuko Y.;  
 RT "Molecular cloning of rabbit matrix metalloproteinase-2 and its broad  
 expression at several tissues.";  
 RL Biochim. Biophys. Acta 1307:137-139 (1996).  
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types  
 IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-  
 Ile-Ala-Gly-Gln.  
 CC -1- COFACTOR: Binds 4 calcium ions per subunit (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).  
 CC -1- SUBUNIT: Ligand for integrin alpha-V/beta-3.  
 CC -1- PFM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-  
 MMP3) (By similarity).  
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.  
 CC -1- SIMILARITY: Contains 3 fibronectin type-II domains.  
 CC -1- SIMILARITY: Contains 1 hemoexin-like domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR EMBL: D63579; BAA09796.1; -; mRNA.  
 DR PIR: S70365; S70365.  
 DR HSP: P08253; 1Q1B.  
 DR MEROPS: M10.003; -.  
 DR InterPro: IPR000562; FN\_type2\_col\_bd.  
 DR InterPro: IPR000585; Hemoexin.  
 DR InterPro: IPR001818; Pept\_M10A\_M12B.  
 DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro: IPR008026; Peptidase\_M.  
 DR Pfam: PF00040; fn2; 3.  
 DR Pfam: PF00045; Hemoexin; 4.  
 DR Pfam: PF00413; Peptidase\_M10; 1.  
 DR Pfam: PF03933; Peptidase\_M10\_N; 1.  
 DR PRINTS: PR00013; FNTYPEII.  
 DR PRINTS: PR00138; MATRXIN.  
 DR ProDom: PD000995; FN\_Type\_II; 3.  
 DR SMART: SM00059; FN2; 3.  
 DR SMART: SM00120; HX; 4.  
 DR SMART: SM00235; ZnMc; 1.  
 DR PROSITE: PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE: PS00023; FN2\_1; 3.  
 DR PROSITE: PS1092; FN2\_2; 3.  
 DR PROSITE: PS00024; HEMOPEXIN; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;  
 KW Hydrolyase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;  
 KW Zinc; Zymogen.  
 FT SIGNAL 1 29 Potential.  
 FT PROPEP 30 109 Activation peptide.  
 FT CHAIN 110 662 72 kDa type IV collagenase.  
 FT DOMAIN 228 276 Fibronectin type-II 1.  
 FT DOMAIN 286 334 Fibronectin type-II 2.  
 FT DOMAIN 344 392 Fibronectin type-II 3.  
 FT DOMAIN 468 662 Hemoexin-like.  
 FT REGION 110 221 Collagenase-like 1.  
 FT REGION 222 396 Collagen-binding.  
 FT REGION 397 467 Collagenase-like 2.  
 FT ACT\_SITE 404 404 By similarity.  
 FT METAL 134 134 Calcium 1 (By similarity).  
 FT METAL 168 168 Calcium 2 (By similarity).  
 FT METAL 178 178 Zinc 1 (By similarity).  
 FT METAL 180 180 Zinc 1 (By similarity).  
 FT METAL 185 185 Calcium 3 (By similarity).  
 FT METAL 186 186 Calcium 3 (via carbonyl oxygen) (By  
 similarity).

FT METAL 193 193 Zinc 1 (By similarity).  
 FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By  
 similarity).  
 FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By  
 similarity).  
 FT METAL 204 204 Calcium 2 (By similarity).  
 FT METAL 206 206 Zinc 1 (By similarity).  
 FT METAL 208 208 Calcium 3 (By similarity).  
 FT METAL 209 209 Calcium 1 (By similarity).  
 FT METAL 211 211 Calcium 3 (By similarity).  
 FT METAL 403 403 Zinc 2 (catalytic) (By similarity).  
 FT METAL 407 407 Zinc 2 (catalytic) (By similarity).  
 FT METAL 413 413 Zinc 2 (catalytic) (By similarity).  
 FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By  
 similarity).  
 FT METAL 523 523 Calcium 4 (via carbonyl oxygen) (By  
 similarity).  
 FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By  
 similarity).  
 FT METAL 620 620 Calcium 4 (via carbonyl oxygen) (By  
 similarity).  
 FT SITE 102 102 Cysteine switch (Potential).  
 FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 644 644 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 471 662 By similarity.  
 SQ SEQUENCE 662 AA; 73803 MW; ICC246B270E440C8 CRC64;  
 Query Match 100.0%; Score 29; DB 1; Length 662;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFPA 6  
 DB 533 KAVFPA 538  
 RESULT 19  
 MMP2\_RAT  
 ID MMP2\_RAT STANDARD; PRT; 662 AA.  
 AC P33436; P97581;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa  
 gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).  
 GN Name=Mmp2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=101116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93249363; PubMed=7916617;  
 RA Marti H.P.; McNeil L.; Davies M.; Martin J.; Lovett D.H.;  
 RT "Homology cloning of rat 72 kDa type IV collagenase: cytokine and  
 second-messenger inducibility in glomerular mesangial cells.";  
 RL Biochem. J. 291:441-446 (1993).  
 CC [2]  
 CC NUCLEOTIDE SEQUENCE.  
 CC STRAIN=Wistar; TISSUE=Skin;  
 CC Okada A.; Basset P.;  
 RT "The cloning of the cDNA encoding rat gelatinase A from a rat skin  
 wound cDNA library.";  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types  
 IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-  
 Ile-Ala-Gly-Gln.  
 CC -1- COFACTOR: Binds 4 calcium ions per subunit (By similarity).  
 CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).  
 CC -1- SUBUNIT: Ligand for integrin alpha-V/beta-3.  
 CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-  
 MMP3) (By similarity).

CC -1- SIMILARITY: Belongs to the peptidase M10A family.  
 CC -1- SIMILARITY: Contains 3 fibronectin type-II domains.  
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: X71466; CAA50583.1; -; mRNA.  
 CC EMBL: U65656; AAB41692.1; -; mRNA.  
 CC PIR: S34780; S34780.  
 CC HSP: P08253; IRTG.  
 CC MEROPS: M10.003; -.  
 CC RGD: 621316; Mmp2.  
 CC GO: GO:0004228; F:gelatinase A activity; IDA.  
 CC GO: GO:0008237; F:metallopeptidase activity; TAS.  
 CC InterPro: IPR000562; FN\_type2\_col\_bd.  
 CC InterPro: IPR000585; Hemopexin.  
 CC InterPro: IPR001818; Pept\_M10A\_M12B.  
 CC InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 CC InterPro: IPR006026; Peptidase\_M.  
 CC Pfam: PF00040; fn2; 3.  
 CC Pfam: PF00045; Hemopexin; 4.  
 CC Pfam: PF00413; Peptidase\_M10; 1.  
 CC Pfam: PF03933; Peptidase\_M10\_N; 1.  
 CC PRINTS: PR00013; FNTYPEII.  
 CC PRINTS: PR00138; MATRXIN.  
 CC ProDom: PD000395; FN\_Type\_II; 3.  
 CC SMART: SM00059; FN2; 3.  
 CC SMART: SM00120; HX; 4.  
 CC SMART: SM00235; ZnMC; 1.  
 CC PROSITE: PS00546; CYSTEINE\_SWITCH; 1.  
 CC PROSITE: PS00023; FN2\_1; 3.  
 CC PROSITE: PS51092; FN2\_2; 3.  
 CC PROSITE: PS00024; HEMOPEXIN; 1.  
 CC PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;  
 KW Hydrolase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;  
 KW Zinc; Zymogen.  
 FT SIGNAL 1 29 Potential.  
 FT PROPEP 30 109 Activation peptide.  
 FT CHAIN 110 662 72 kDa type IV collagenase.  
 FT DOMAIN 228 276 Fibronectin type-II 1.  
 FT DOMAIN 286 334 Fibronectin type-II 2.  
 FT DOMAIN 344 392 Fibronectin type-II 3.  
 FT DOMAIN 468 662 Hemopexin-like.  
 FT REGION 110 221 Collagenase-like 1.  
 FT REGION 222 396 Collagen-binding.  
 FT REGION 397 467 Collagenase-like 2.  
 FT ACT\_SITE 404 404 By similarity.  
 FT METAL 134 134 Calcium 1 (By similarity).  
 FT METAL 168 168 Calcium 2 (By similarity).  
 FT METAL 178 178 Zinc 1 (By similarity).  
 FT METAL 180 180 Zinc 1 (By similarity).  
 FT METAL 185 185 Calcium 3 (By similarity).  
 FT METAL 186 186 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 193 193 Zinc 1 (By similarity).  
 FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 204 204 Calcium 2 (By similarity).  
 FT METAL 206 206 Zinc 1 (By similarity).  
 FT METAL 208 208 Calcium 3 (By similarity).  
 FT METAL 209 209 Calcium 3 (By similarity).  
 FT METAL 211 211 Zinc 2 (catalytic) (By similarity).  
 FT METAL 403 403 Zinc 2 (catalytic) (By similarity).  
 FT METAL 407 407 Zinc 2 (catalytic) (By similarity).  
 FT METAL 413 413 Zinc 2 (catalytic) (By similarity).  
 FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By similarity).

FT METAL 523 523 similarity).  
 FT METAL 523 523 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT METAL 571 571 similarity).  
 FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT METAL 620 620 similarity).  
 FT METAL 620 620 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT SITE 102 102 Cysteine switch (Potential).  
 FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 644 644 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 471 662 By similarity.  
 FT CONFLICT 42 42 A -> S (in Ref. 2).  
 FT CONFLICT 286 286 A -> G (in Ref. 2).  
 FT CONFLICT 369 369 N -> S (in Ref. 2).  
 FT CONFLICT 435 435 H -> N (in Ref. 2).  
 FT CONFLICT 586 586 A -> S (in Ref. 2).  
 SQ SEQUENCE 662 AA; 74182 MW; 7496B34B0A21884B CRC64;  
 Query Match 100.0%; Score 29; DB 1; Length 662;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 533 KAVFFA 538  
 RESULT 20  
 Q6GM9 RAT PRELIMINARY; PRT; 662 AA.  
 ID Q6GM9 RAT PRELIMINARY; PRT; 662 AA.  
 AC Q6GM9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Mmp2 protein.  
 GN Name=Mmp2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL: BC074013; AAH74013.1; -; mRNA.  
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
 DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.



```

FT METAL 572 572 similarity).
FT METAL 621 621 Calcium 4 (via carbonyl oxygen) (By
FT METAL 621 621 Calcium 4 (via carbonyl oxygen) (By
FT SITE 99 99 similarity).
FT DISULFID 472 663 Cysteine switch (Potential).
FT CONFLICT 40 40 By similarity.
FT CONFLICT 116 116 P -> Q (in Ref. 2).
FT CONFLICT 122 122 W -> T (in Ref. 2).
FT CONFLICT 122 122 T -> I (in Ref. 2).
SQ SEQUENCE 663 AA; 74941 MW; 8D6FDA4E67C3EBCA CRC64;

Query Match 100.0%; Score 29; DB 1; Length 663;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 534 KAVFFA 539

RESULT 22
Q8K7W1 CLODI PRELIMINARY; PRT; 767 AA.
AC Q8K7W1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface layer protein A.
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RX MEDLINE=22077258; PubMed=12081960;
RX DOI=10.1128/JB.184.14.3886-3897.2002;
RA Calabi E., Fairweather N.;
RT "Patterns of sequence conservation in the S-Layer proteins and related
RT sequences in Clostridium difficile."
RL J. Bacteriol. 184:3886-3897(2002).
DR EMBL; AF478571; AAM46790.1; -; Genomic_DNA.
DR InterPro; IPR007253; CW binding 2.
DR Pfam; PF04122; CW binding 2; 3.
SQ SEQUENCE 767 AA; 81461 MW; 7280626184495D70 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 767;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 358 KAVFFA 363

RESULT 23
Q7XX63 ORYSA PRELIMINARY; PRT; 770 AA.
AC Q7XX63;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNBa0052P16.14 protein.
GN Name=OSJNBa0052P16.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12447439; DOI=10.1038/nature01183;

```

```

RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL662936; CAD39717.1; -; Genomic_DNA.
DR Gramene; Q7XX63; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth_C; 2.
SQ SEQUENCE 770 AA; 86960 MW; 6CFAB6855D904EE1 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 555 KAVFFA 560

RESULT 24
Q66QH3 ORYSA PRELIMINARY; PRT; 840 AA.
AC Q66QH3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Syn-pimara-7,15-diene synthase.
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15299118; DOI=10.1104/pp.104.045971;
RA Wilderman P.R., Xu M., Jin Y., Coates R.M., Peters R.J.;
RT "Identification of syn-pimara-7,15-diene synthase reveals functional
RT clustering of terpene synthases involved in rice
RT phytoalexin/allicin chemical biosynthesis.";
RL Plant Physiol. 135:2098-2105(2004).
DR EMBL; AY616862; AAU05906.1; -; mRNA.
DR Gramene; Q66QH3; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth_C; 1.
SQ SEQUENCE 840 AA; 94757 MW; B0ECC89323C86ASE CRC64;

Query Match 100.0%; Score 29; DB 2; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 625 KAVFFA 630

```

```
RESULT 25
Q60HB5_ORYSA
ID AC Q60HB5_ORYSA PRELIMINARY; PRT; 842 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 9b-plimara-7,15-diene synthase.
GN Name=OskK34;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15388982; DOI=10.1271/bbb.68.2001;
RA Otsuka K., Kanno Y., Moteji A., Kenmoku H., Yamane H., Mitsuhashi W.,
RA Okawa H., Toshihima H., Itoh H., Matsuo M., Sassa T., Toyomasu T.;
RT "Diterpene cyclases responsible for the biosynthesis of phytoalexins,
RT momilactones A, B, and oryzalexins A-F in rice.";
RL Biosci. Biotechnol. Biochem. 68:2001-2006(2004).
DR EMBL; AB126934; BAD54751.1; -; mRNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
DR SEQUENCE 842 AA; 94868 MW; 928F88F8FCC35497 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 627 KAVFFA 632

RESULT 26
Q69DS7_ORYSA
ID AC Q69DS7_ORYSA PRELIMINARY; PRT; 842 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Ent-kaurene synthase like-4.
GN Name=OskK34;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15668792; DOI=10.1007/s00299-004-0896-6;
RA Margis-Pinheiro M., Zhou X.R., Zhu Q.H., Dennis E.S., Upadhyaya N.M.;
RT "Isolation and characterization of a Ds-tagged rice (Oryza sativa L.)
RT GA-responsive dwarf mutant defective in an early step of the
RT gibberellin biosynthesis pathway.";
RL Plant Cell Rep. 23:819-833(2005).
DR EMBL; AY347880; AAQ72563.1; -; mRNA.
DR Gramene; Q69DS7; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.

Query Match 100.0%; Score 29; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 627 KAVFFA 632

RESULT 27
Q9N175_SHEEP
ID AC Q9N175_SHEEP PRELIMINARY; PRT; 945 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22168784; PubMed=12181148;
RA Merhoun J.L., Baker R.S., Clark K.R.;
RT "Estrogen increases iNOS expression in the ovine coronary artery.";
RL Am. J. Physiol. Heart Circ. Physiol. 283:H1169-H1180(2002).
DR EMBL; AF223942; AAF34710.1; -; mRNA.
DR HSSP; P35228; INSI.
DR SNR; Q9N175; 1-326.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001709; PPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxired_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PFIRS; PFIRS000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; PFNCR.
DR PROSITE; PS0902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 945 AA; 108001 MW; 9A5ACFD40440A74P CRC64;

Query Match 100.0%; Score 29; DB 2; Length 945;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 344 KAVFFA 349

RESULT 28
NOS2_RAT
```

ID NOS2\_RAT STANDARD; PRT; 1147 AA.  
AC Q06518; Q35765; Q35766; Q60591; Q60604; P97774; Q63267; Q64005;  
AC Q64558;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-OCT-1995 (Rel. 34, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)  
DE (Inducible NOS) (iNOS).  
DE Name=Nos2;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Vascular smooth muscle;  
RX MEDLINE=93191721; PubMed=7680561;  
RA Nunokawa Y., Ishida N., Tanaka S.;  
RT "Cloning of inducible nitric oxide synthase in rat vascular smooth  
muscle cells.";  
RL Biochem. Biophys. Res. Commun. 191:89-94(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Pancreatic islets;  
RX MEDLINE=95309542; PubMed=7540573;  
RA Karlsson A.E., Andersen H.U., Viessing H., Larsen P.M., Fey S.J.,  
RA Cuatrecasas B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,  
RA Mandrup-Poulsen T., Boel E., Nerup J.;  
RT "Cloning and expression of cytokine-inducible nitric oxide synthase  
cDNA from rat islets of Langerhans.";  
RL Diabetes 44:753-758(1995).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Astocytes;  
RX MEDLINE=94231594; PubMed=7513745;  
RA Galea E., Reis D.J., Feinstein D.L.;  
RT "Cloning and expression of inducible nitric oxide synthase from rat  
astocytes.";  
RL J. Neurosci. Res. 37:406-414(1994).  
RN [4]  
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=94039059; PubMed=7693462;  
RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,  
RA Kawasaki H., Sugimura T., Esumi H.;  
RT "Molecular cloning of a cDNA encoding an inducible calmodulin-  
dependent nitric-oxide synthase from rat liver and its expression in  
COS 1 cells.";  
RL Eur. J. Biochem. 217:37-43(1993).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Hepatocyte;  
RX MEDLINE=93221515; PubMed=7682072;  
RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;  
RT "Hepatocytes and macrophages express an identical cytokine inducible  
nitric oxide synthase gene.";  
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Aorta;  
RX MEDLINE=94325351; PubMed=7519448; DOI=10.1016/0167-4781(94)90196-1;  
RA Geng Y.J., Almqvist M., Hansson G.K.;  
RT "cDNA cloning and expression of inducible nitric oxide synthase from  
rat vascular smooth muscle cells.";  
RL Biochim. Biophys. Acta 1218:421-424(1994).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RA Kosuga K., Yui Y., Hattori R., Sase K., Bizawa H., Aoyama T.,  
RA Inoue R., Sasayama S.;  
RT "Cloning of an inducible nitric oxide synthase from rat  
polymorphonuclear neutrophils.";  
RL Endothelium 2:217-221(1994).

RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97070590; PubMed=8913516;  
RA Tezumi-shita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,  
RA Putaki S., Niwa M.;  
RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,  
lung, and uterus.";  
RL Biol. Pharm. Bull. 19:1374-1376(1996).  
RN [9]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99066690; PubMed=9851365; DOI=10.1006/niox.1998.0184;  
RA Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Giesen S.,  
RA Schuler G., Hambrecht R.;  
RT "Complete coding sequence of inducible nitric oxide synthase from  
human heart and skeletal muscle of patients with chronic heart  
failure.";  
RL Nitric Oxide 2:242-249(1998).  
RN [10]  
RP NUCLEOTIDE SEQUENCE OF 426-788.  
RC STRAIN=Dahl/Rapp salt sensitive strain; TISSUE=Vascular smooth muscle;  
RX MEDLINE=98195092; PubMed=9535415;  
RA Chen P.Y., Gladish R.D., Sanders P.W.;  
RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp  
salt-sensitive rats.";  
RL Hypertension 31:918-924(1998).  
RN [11]  
RP NUCLEOTIDE SEQUENCE OF 509-740.  
RC STRAIN=Wistar; TISSUE=Renal glomerulus;  
RA Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;  
RT "Advances in the studies of NO synthesis regulation in mesangial  
cells.";  
RL Nefrologia 16:35-39(1996).  
RN [12]  
RP NUCLEOTIDE SEQUENCE OF 479-655.  
RC STRAIN=Sprague-Dawley; TISSUE=Renal glomerulus;  
RX MEDLINE=94276509; PubMed=7516453;  
RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,  
RA Klahr S.;  
RT "Location of an inducible nitric oxide synthase mRNA in the normal  
kidney.";  
RL Kidney Int. 45:998-1005(1994).  
RN [13]  
RP NUCLEOTIDE SEQUENCE OF 420-479.  
RC TISSUE=Myocardium;  
RA Michel T., Balligand J.-L.;  
RT "Isolation and characterization of iNOS from rat cardiocytes.";  
Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule  
with diverse functions throughout the body.  
CC -!- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline +  
nitric oxide + n NADP(+).  
CC -!- COFACTOR: Heme.  
CC -!- COFACTOR: FAD. Binds 1 mole of FAD.  
CC -!- COFACTOR: FMN. Binds 1 mole of FMN.  
CC -!- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric  
form of the enzyme.  
CC -!- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin  
inhibits expression and function of this enzyme and effects may be  
exerted at the level of translational/posttranslational  
modification and directly on the catalytic activity (By  
similarity).  
CC -!- SUBUNIT: Homodimer. Binds SLC9A3R1 (By similarity).  
CC -!- TISSUE SPECIFICITY: In normal kidney, expressed primarily in the  
medullary thick ascending limb, with minor amounts in the  
medullary collecting duct and vasa recta bundle.  
CC -!- INDUCTION: By interferon gamma and lipopolysaccharides (LPS).  
CC -!- SIMILARITY: Belongs to the NOS family.  
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.  
CC -!- CAUTION: Ref.9 sequence was originally thought to originate from  
human but appears to be from rat.  
-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -



CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

```

-----
DR EMBL; D14051; BAA03138.1; -; mRNA.
DR EMBL; U26686; AAC85861.1; -; mRNA.
DR EMBL; U03699; AAC13747.1; -; mRNA.
DR EMBL; D12520; BAA02090.1; -; mRNA.
DR EMBL; L12562; AAA41720.1; -; mRNA.
DR EMBL; X76881; CAA54208.1; -; mRNA.
DR EMBL; D44591; BAA07994.1; -; mRNA.
DR EMBL; D83661; BAA12035.1; -; mRNA.
DR EMBL; AF049656; AAC83553.1; -; mRNA.
DR EMBL; AF051164; AAC83554.1; -; mRNA.
DR EMBL; AF006619; AAC16401.1; -; mRNA.
DR EMBL; AF006620; AAC16402.1; -; mRNA.
DR EMBL; U48829; AAB18620.1; -; mRNA.
DR EMBL; S71597; AAB31028.2; -; mRNA.
DR EMBL; L36063; AAC02242.1; -; mRNA.
DR PIR; I53165; I53165.
DR PIR; I56575; I56575.
DR PIR; JC5027; JC5027.
DR PIR; S38253; S38253.
DR PIR; S47647; S47647.
DR HSSP; P29477; INOS.
DR SMR; Q06518; 80-499.
DR Ensembl; ENSRNOG00000011023; Rattus norvegicus.
DR RGD; 3185; Nos2.
DR GO; GO:0005829; Cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0008603; F:calmodulin-dependent protein kinase regulator act. .; IDA.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.
DR GO; GO:00042742; P:defense response to bacteria; ISS.
DR GO; GO:0007199; P:G-protein signaling, coupled to GMP nucleo. .; IDA.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006809; P:nitric oxide biosynthesis; TAS.
DR GO; GO:0007165; P:signal transduction; IDA.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD bd.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR012144; NOS.
DR PANTHER; PTHR19386; NO synthase; 1.
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.

Query Match 100.0%; Score 29; DB 1; Length 1147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 517 KAVFFA 522

RESULT 29
Q6XS76 RAT PRELIMINARY; PRT; 1147 AA.
AC Q6XS76;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Inducible nitric oxide synthase (fragment).
GN Name=Nos2;

Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar; TISSUE=Aortic smooth muscle;
RC Cui Z., Tulladhar R., Hart S., Marber M., Pearson J., Baydoun A.R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY211532; AAP43670.1; -; mRNA.
DR HSSP; P29477; 1JWK.
DR SMR; Q6XS76; 80-499.
DR GO; GO:0005516; F:calmodulin binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0010181; F:FMN binding; IEA.
DR GO; GO:0004517; F:nitric-oxide synthase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IEA.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN nitox synth.
DR InterPro; IPR0012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN_1.
DR NON_TER 1147 1147
SQ SEQUENCE 1147 AA; 130673 MW; 204484F2231D9ECA CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 517 KAVFFA 522

RESULT 30
Q9QW28 9MURI PRELIMINARY; PRT; 1147 AA.
AC Q9QW28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytokine inducible nitric oxide synthase, iNOS.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=93221515; PubMed=7682072;
RC Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
RT "Hepatocytes and macrophages express an identical cytokine inducible
RT nitric oxide synthase gene."
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
DR HSSP; P29477; INOS.
DR SMR; Q9QW28; 80-499.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:00020037; F:heme binding; ISS.

```



DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.  
 DR GO; GO:0042742; P:defense response to bacteria; ISS.  
 DR GO; GO:0006954; P:inflammatory response; ISS.  
 DR GO; GO:0045855; P:positive regulation of cytotoxic T-cell dif. . . ; ISS.  
 DR GO; GO:0006801; P:superoxide metabolism; ISS.  
 DR InterPro; IPR003097; FAD binding.  
 DR InterPro; IPR001094; Flavodoxin like.  
 DR InterPro; IPR008254; Flav nitox synth.  
 DR InterPro; IPR001709; FPN cyt redctse.  
 DR InterPro; IPR012144; NOS.  
 DR InterPro; IPR004030; NO synthase.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00667; FAD binding\_1; 1.  
 DR Pfam; PF00258; Flavodoxin\_1; 1.  
 DR Pfam; PF00175; NAD binding\_1; 1.  
 DR Pfam; PF02898; NO synthase; 1.  
 DR PIRSF; PIRSF000333; NOS; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 DR PROSITE; PS00902; FLAVODOXIN LIKE; 1.  
 DR PROSITE; PS60001; NOS; UNKNOWN 1.  
 DR PROSITE; PS60001; NOS; UNKNOWN 1.  
 SQ SEQUENCE 1147 AA; 130625 MW; 2CARB983E56F651A CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 1147;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 Db 517 KAVFFA 522  
 ID Q9ROW4\_RAT PRELIMINARY; PRT; 1147 AA.  
 AC Q9ROW4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Inducible nitric oxide synthase.  
 GN Name=INOS;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Wistar Kyoto;  
 RX MEDLINE=93326503; PubMed=10395902; DOI=10.1016/S0378-1119(99)00196-1;  
 RA Keinänen R.A., Vartiainen N., Koistinaho J.;  
 RT "Molecular cloning and characterization of the rat inducible nitric  
 oxide synthase (INOS) gene";  
 RL Gene 234:297-305(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed=8647111;  
 RA Iwashina M., Hirata Y., Imai T., Sato K., Marumo F.;  
 RT "Molecular cloning of endothelial, inducible nitric oxide synthase  
 gene from rat aortic endothelial cell.";  
 RL Eur. J. Biochem. 237:668-673(1996).  
 DR EMBL; AJ230462; CAB46089.1; -; Genomic DNA.  
 DR EMBL; AJ230463; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230465; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230464; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230467; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230469; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230471; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230473; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230475; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230484; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230483; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230482; CAB46089.1; JOINED; Genomic DNA.

DR EMBL; AJ230481; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230480; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230479; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230478; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230477; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230476; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230487; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230486; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230485; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230474; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230472; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230470; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230468; CAB46089.1; JOINED; Genomic DNA.  
 DR EMBL; AJ230466; CAB46089.1; JOINED; Genomic DNA.  
 DR PIR; JCS028; JCS028.  
 DR PIR; JCS029; JCS029.  
 DR PIR; S65440; S65440.  
 DR HSP; F29477; INOS.  
 DR SMR; Q9ROW4; 80-499.  
 DR GO; GO:0005829; C:cytosol; ISS.  
 DR GO; GO:0005516; F:calmodulin binding; ISS.  
 DR GO; GO:0020037; F:heme binding; ISS.  
 DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.  
 DR GO; GO:0042742; P:defense response to bacteria; ISS.  
 DR GO; GO:0006954; P:inflammatory response; ISS.  
 DR GO; GO:0006801; P:superoxide metabolism; ISS.  
 DR InterPro; IPR003097; FAD bd.  
 DR InterPro; IPR008254; Flav nitox synth.  
 DR InterPro; IPR001094; Flavodoxin like.  
 DR InterPro; IPR001709; FPN cyt redctse.  
 DR InterPro; IPR004030; NO synthase.  
 DR InterPro; IPR012144; NOS.  
 DR InterPro; IPR001433; Oxred\_FAD NAD bd.  
 DR Pfam; PF00667; FAD binding\_1; 1.  
 DR Pfam; PF00258; Flavodoxin\_1; 1.  
 DR Pfam; PF00175; NAD binding\_1; 1.  
 DR Pfam; PF02898; NO synthase; 1.  
 DR PIRSF; PIRSF000333; NOS; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 DR PROSITE; PS00902; FLAVODOXIN LIKE; 1.  
 DR PROSITE; PS60001; NOS; UNKNOWN 1.  
 DR PROSITE; PS60001; NOS; UNKNOWN 1.  
 SQ SEQUENCE 1147 AA; 130614 MW; E76B3F8407D54CF6 CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 1147;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 Db 517 KAVFFA 522  
 ID Q8YIS2\_RALSO PRELIMINARY; PRT; 118 AA.  
 AC Q8YIS2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE PROBABLE SIGNAL PEPTIDE PROTEIN.  
 OS OrderedLocustNames=RSC0617; ORFNames=RS01518;  
 OC Ralstonia solanacearum (Pseudomonas solanacearum).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GMT1000;  
 RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;  
 RA Salanoubat M., Genin S., Artiguenave P., Gouzy J., Mangenot S.,  
 RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,  
 RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

```

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguler P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646060; CAD14147.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 118 AA; 12054 MW; 955D9DEA2C16CF42 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 118;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 8 KAIFFA 13

RESULT 33
Q8UI59_AGR75
ID Q8UI59_AGR75 PRELIMINARY; PRT; 169 AA.
AC Q8UI59;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Atu0441.
GN OrderedLocuNames=Atu0441;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58."
RL Science 294:2317-2323(2001).
DR EMBL; AB009014; AAU41460.1; -; Genomic_DNA.
DR PIR; AF2630; AF2630.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 169 AA; 19428 MW; F8DBB80BAC5D38EB CRC64;

Query Match          96.6%; Score 28; DB 2; Length 169;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 114 KAIFFA 119

RESULT 34
Q19334_CABEL
ID Q19334_CABEL PRELIMINARY; PRT; 283 AA.
AC Q19334; Q21599;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein W79.2.
GN ORFNames=W79.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

```

```

OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RT "The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z50857; CAA90720.1; -; Genomic DNA.
DR EMBL; Z50806; CAA90692.1; -; Genomic DNA.
DR EMBL; Z50806; CAA90720.1; JOINED; Genomic DNA.
DR EMBL; Z50857; CAA90692.1; JOINED; Genomic DNA.
DR PIR; T20734; T20734.
DR Ensemble; M79.2; Caenorhabditis elegans.
DR WormBase; WBGene00010902; M79.2.
DR WormPep; M79.2; CR03507.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 283 AA; 32582 MW; 51638B43CB266860 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 157 KAIFFA 162

RESULT 35
Q8EM92_OCEIH
ID Q8EM92_OCEIH PRELIMINARY; PRT; 305 AA.
AC Q8EM92;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical conserved protein.
GN OrderedLocuNames=OB2966;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HT831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC14922.1; -; Genomic DNA.
DR InterPro; IPR003507; Peptidase U61.
DR Pfam; PF02016; Peptidase U61.
DR KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 305 AA; 33528 MW; 6A7F3E282B5580 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 305;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 75 KAIFFA 80

RESULT 36
Q6LJY6_PROPR
ID Q6LJY6_PROPR PRELIMINARY; PRT; 355 AA.
AC Q6LJY6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

```

DE Hypothetical protein.
GN OrderedLocusNames=PBPRB0521;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Castaro A., Malacrida G., Simonati B., Cannata N.,
RA Romaldi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis.";
RL Science 307:1459-1461(2005).
DR EMBL; CR378676; CAG22394.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 355 AA; 40056 MW; 6A3C866307079447 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 355;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 316 KAIFFA 321

RESULT 37
QXINS_CLOPE
ID Q8XIN5_CLOPE PRELIMINARY; PRT; 1044 AA.
AC Q8XIN5;
DT 01-WAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-mannosidase.
GN OrderedLocusNames=CPE2080;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; BA000016; BAB81786.1; -; Genomic DNA.
DR GO; GO:0004559; F:alpha-mannosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006013; P:mannose metabolism; IEA.
DR InterPro; IPR000602; Glyco_hydro_38.
DR InterPro; IPR011682; Glyco_hydro_38.
DR Pfam; PF01074; Glyco_hydro_38; 1_38C.
DR Pfam; PF07748; Glyco_hydro_38C; 1.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 1044 AA; 121432 MW; 3CABB79447D42B6F CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1044;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 666 KAIFFA 671

RESULT 38
Q19641_CABEL

```

```

ID Q19641_CABEL PRELIMINARY; PRT; 85 AA.
AC Q19641;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein F20D12.5.
GN ORFNames=F20D12.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SIMILARITY: Contains 1 LIM zinc-binding domain.
DR EMBL; U40933; AAL27241.1; -; Genomic_DNA.
DR HSSP; P04006; LIML.
DR SMR; Q19641; 2-77.
DR Ensembl; F20D12.5; Caenorhabditis elegans.
DR WormBase; WBGene00017644; F20D12.5.
DR WormPep; F20D12.5; CE29767.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001781; LIM_Zn_bd.
DR Pfam; PF00412; LIM; 1.
DR ProDom; PD0000094; LIM; 1.
DR SMART; SM00132; LIM; 1.
DR PROSITE; PS50023; LIM DOMAIN 2; 1.
KW Complete proteome; Hypothetical protein; LIM domain; Metal-binding;
KW Zinc.
SQ SEQUENCE 85 AA; 9479 MW; 83B934A0C82AE849 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 85;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 9 KAVFFA 14

RESULT 39
Q731J0_WOLP
ID Q731J0_WOLP PRELIMINARY; PRT; 99 AA.
AC Q731J0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Oxidoreductase, putative.
GN OrderedLocusNames=WD0173;
OS Wolbachia pipientis wMel.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachieae; Wolbachia.
OX NCBI_TaxID=66077;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15024419; DOI=10.1371/journal.pbio.0020069;
RA Wu M., Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,
RA Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
RA Wiegand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA Durkin A.S., Kolonay J.F., Nelson W.C., Mohamoud Y., Lee P.,
RA Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,
RA Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.E., Eisen J.A.;
RT "Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
RT a streamlined genome overrun by mobile genetic elements.";
RL PLOS Biol. 2:327-341(2004).
DR EMBL; AE017256; AAS13922.1; -; Genomic_DNA.
DR TIGR; WD0173; -.

```

```

DR GO; GO:0016651; F:oxidoreductase activity, acting on NADH or . . . ; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006885; ETC CI 21.
DR PANTHER; PTHR12219; ETC CI 21; 1.
DR Pfam; PF04800; ETC_C1_NDUF4; 1.
DR Complete proteome.
SQ SEQUENCE 99 AA; 11504 MW; FFB301D34D6C8F84 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 99;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 65 KAVFFA 70

RESULT 40
Q8XQ19_RALSO
ID Q8XQ19_RALSO PRELIMINARY; PRT; 109 AA.
AC Q8XQ19;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PUTATIVE TRANSMEMBRANE PROTEIN.
GN OrderedLocuNames=RSPI467; ORFNames=RS03077;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OC NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangenot S.,
RA Aliat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646085; CAD18618.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR Complete proteome; Plasmid; Transmembrane.
KW Complete proteome; Plasmid; Transmembrane.
SQ SEQUENCE 109 AA; 11658 MW; BEDB6D1DBFF1EB13 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 109;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 10 KSVFFA 15

RESULT 41
Q6G347_BARHE
ID Q6G347_BARHE PRELIMINARY; PRT; 126 AA.
AC Q6G347;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=BH09610;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OC NCBI_TaxID=38323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 49882 / Houston 1;

```

```

RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scola B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF27754.1; -; Genomic DNA.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 126 AA; 14027 MW; 7A632D838151FFAE CRC64;

Query Match      89.7%; Score 26; DB 2; Length 126;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 34 RAVFFA 39

RESULT 42
Q6C1M8_YARLI
ID Q6C1M8_YARLI PRELIMINARY; PRT; 131 AA.
AC Q6C1M8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to w|NCU06209.1 Neurospora crassa NCU06209.1 hypothetical
DE protein.
GN OrderedLocuNames=VALI0P14905g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OC NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Geoffaut N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumaszet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Svennen D., Tekaa F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382132; CAG78243.1; -; Genomic DNA.
DR Complete proteome; Hypothetical protein.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 131 AA; 14843 MW; 5D7F9328DBC87E19 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 131;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 126 KAVFFS 131

RESULT 43
Q6G346_BARHE
ID Q6G346_BARHE PRELIMINARY; PRT; 131 AA.
AC Q6G346;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

```

DE Hypothetical protein.
GN OrderedLocusNames=BH09620;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 49882 / Houston 1;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alenmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scala B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF27755.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 131 AA; 14730 MW; 48D91F115B667439 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 131;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
Db 34 RAVFFA 39

RESULT 44
QSKK3_THET8
ID Q5SKK3_THET8 PRELIMINARY; PRT; 137 AA.
AC Q5SKK3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein TTHA0640.
GN OrderedLocusNames=TTHA0640;
OS Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=300852;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HB8;
RA Masui R., Kurokawa K., Nakagawa N., Tokunaga F., Koyama Y.,
RA Shibata T., Oshima T., Yokoyama S., Yasunaga T., Kuramitsu S.;
RT "Complete genome sequence of Thermus thermophilus HB8.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008226; BAD70463.1; -; Genomic_DNA.
DR InterPro; IPR007842; HEPN.
DR Pfam; PF05168; HEPN; 1.
DR PROSITE; PS0910; HEPN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 137 AA; 15304 MW; 37D01C6D9C3287FA CRC64;

Query Match 89.7%; Score 26; DB 2; Length 137;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
Db 43 KAVFFA 48

RESULT 45
QAJC95_SULAC
ID QAJC95_SULAC PRELIMINARY; PRT; 142 AA.
AC QAJC95;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Conserved membrane protein.

```

```

GN OrderedLocusNames=Saci_0164;
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
RX PubMed=1595215; DOI=10.1128/JB.187.14.4992-4999.2005;
RA Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarinsson E.,
RA Greve B., Awavez M., Zibat A., Klenk H.-P., Garrett R.A.;
RT "The genome of Sulfolobus acidocaldarius, a model organism of the
RT Crenarchaeota.";
RL J. Bacteriol. 187:4992-4999(2005).
DR EMBL; CP000077; AAY79584.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 142 AA; 16221 MW; 5E922483FA7F664C4 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 142;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
Db 82 KSVFFA 87

RESULT 46
QSWU01_LEGPL
ID QSWU01_LEGPL PRELIMINARY; PRT; 149 AA.
AC QSWU01;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lp12372;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR628337; CAH16612.1; -; Genomic_DNA.
DR LegiOList; lp12372; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16274 MW; F698CECE732B0837 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
Db 37 KSVFFA 42

RESULT 47
Q5X274_LEGPA
ID Q5X274_LEGPA PRELIMINARY; PRT; 149 AA.
AC Q5X274;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lp2519;
OS Legionella pneumophila (strain Paris).

```

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaeser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR289336; CH13672.1; -; Genomic_DNA.
DR Legionellist; lpp2519; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16323 MW; 8489CE2861AD3D5A CRC64;

Query Match      89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 37 KSVFFA 42

RESULT 48
Q5ZSR4 LEGPH
ID Q5ZSR4 LEGPH PRELIMINARY; PRT; 149 AA.
AC Q5ZSR4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=lpq2453;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Stechenko V., Park S.H., Zhao B., Teplickaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cavanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila.";
RL Science 305:1966-1968(2004).
DR EMBL; AB017354; AAU28513.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16374 MW; 76C1CB2C5D08BDF23 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 37 KSVFFA 42

RESULT 49
Q51314 9NOSO
ID Q51314 9NOSO PRELIMINARY; PRT; 150 AA.
AC Q51314;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

```

DE SdNA replicating plasmid encoding a replication-associated protein
DE (repA) and three ORFs, complete cds.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=1180;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Walton D.K., Gendel S.M., Atherly A.G.;
RL Submitted (F88-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M81381; AAA25514.1; -; Genomic_DNA.
DR PIR; S27597; S27597.
SQ SEQUENCE 150 AA; 16660 MW; 7C34D00291E436A6 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 150;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 36 KALFFA 41

RESULT 50
GUAD BACSU
ID GUAD BACSU STANDARD; PRT; 156 AA.
AC C34598;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Guanine deaminase (EC 3.5.4.3) (Guanase) (Guanine aminase) (Guanine
DE aminohydrolase) (GAH) (GDEase).
GN Name=guad; Synonyms=gde; OrderedLocustNames=BSU13170;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=168;
RC Devine K.M.;
RT "Sequence of the Bacillus subtilis genome between xlyA and ykoR.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=168;
MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Betero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dueterhoeft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Gim S.-Y., Glaeser P., Goffeau A., Gough J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.-P., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasehara Y., Klaer-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Fujic P., Furnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone P., Sekiguchi J., Sekowska A., Szor S.J., Serror P.,
RA Shin B.-S., Soldo B., Sorokin A., Taccioni E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Waitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,

```

RA Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.";  
RL Nature 390:249-256(1997).  
RN [3]  
RP FUNCTION.  
RC STRAIN=168;  
RX MEDLINE=20553169; PubMed=11101664;  
RA Nygaard P., Basted S.M., Andersen K.A.K., Saxild H.H.;  
RT "Bacillus subtilis guanine deaminase is encoded by the ykna gene and is induced during growth with purines as the nitrogen source.";  
RL Microbiology 146:3061-3069(2000).  
CC -!- FUNCTION: Catalyzes the hydrolytic deamination of guanine, producing xanthine and ammonia.  
CC -!- CATALYTIC ACTIVITY: Guanine + H(2)O = xanthine + NH(3).  
CC -!- COFACTOR: Zinc (By similarity).  
CC -!- PATHWAY: Purine catabolism  
CC -!- INDUCTION: Expressed only during limited or partially limited nitrogen conditions. Can be induced to high levels in the presence of purines or intermediates of the purine catabolic pathway.  
CC Expression seems indirectly controlled by trnA and glnR.  
CC -!- SIMILARITY: Belongs to the cytidine and deoxycytidylate deaminase family.  
CC -----  
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC -----  
DR EMBL; AJ002571; CA005596.1; -; Genomic DNA.  
DR EMBL; Z99110; CAB13174.1; -; Genomic DNA.  
DR PIR; F69857; F69857.  
DR PDB; 1TV; X-ray; A/B=1-156.  
DR PDB; 1WQ; X-ray; A/B=1-156.  
DR Subtilist; BG13240; Guad.  
DR InterPro; IPR002125; dCMP\_cyt\_deam; 1.  
DR Pfam; PF00383; dCMP\_cyt\_deam; 1.  
DR PROSITE; PS00903; CYT\_DCMP\_DEAMINASES; 1.  
KW 3D-structure; Complete proteome; Hydrolase; Metal-binding;  
KW Purine metabolism; Zinc.  
FT METAL 53 53 Zinc (By similarity).  
FT METAL 83 83 Zinc (By similarity).  
FT METAL 86 86 Zinc (By similarity).  
SQ SEQUENCE 156 AA; 17156 MW; B6498345A98BC214 CRC64;  
  
Query Match 89.7%; Score 26; DB 1; Length 156;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KAVFFA 6  
DB 96 KAVFYA 101  
|||||  
- - - - -  
  
RESULT 51  
QSWBB0\_BACSK PRELIMINARY; PRT; 156 AA.  
ID Q5WBB0\_BACSK PRELIMINARY;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Guanine deaminase (EC 3.5.4.3).  
GN Name=gde; OrderedLocusNames=ABC3819;  
OS Bacillus clausii (strain KSM-K16).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=66692;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=KSM-K16;  
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,  
RA Kawai S., Ito S., Horikoshi K.;  
RT "The complete genome sequence of the alkaliphilic *Bacillus clausii*

RT KSM-K16.";  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP006627; BAD66350.1; -; Genomic DNA.  
DR GO; GO:000892; F:guanine deaminase activity; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR InterPro; IPR002125; dCMP\_cyt\_deam; 1.  
DR Pfam; PF00383; dCMP\_cyt\_deam; 1.  
DR PROSITE; PS00903; CYT\_DCMP\_DEAMINASES; UNKNOWN\_1.  
KW Complete proteome; Hydrolase.  
SQ SEQUENCE 156 AA; 17287 MW; F2BFFFF2FB4B28A1 CRC64;  
  
Query Match 89.7%; Score 26; DB 2; Length 156;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KAVFFA 6  
DB 96 KAVFYA 101  
|||||  
- - - - -  
  
RESULT 52  
OS9317\_PVRHO PRELIMINARY; PRT; 166 AA.  
ID OS9317\_PVRHO PRELIMINARY;  
AC OS9317;  
DT 01-AUG-1998 (TReMBLrel. 07, Created)  
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE 166aa long hypothetical L(+)-tartrate dehydratase.  
GN OrderedLocusNames=PH1684;  
OS Pyrococcus horikoshii.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=53953;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=OT3;  
RX MEDLINE=98344137; PubMed=9679194;  
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
RA Funahashi T., Tanaka T., Kudo H. Y., Yamazaki J., Kishida N., Oguchi A.,  
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
RA Masuchi Y., Shizuya H., Kikuchi H.;  
RT "Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";  
RL DNA Res. 5:55-76(1998).  
DR EMBL; BA000001; BAA30796.1; -; Genomic DNA.  
DR PIR; D71049; D71049.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR InterPro; IPR004647; TtdB\_fumA\_fumB.  
DR Pfam; PF05683; Fumerase\_C; 1.  
DR TIGRFAMs; TIGR00723; ttdB\_fumA\_fumB; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 166 AA; 18250 MW; A2A70CF533DD166 CRC64;  
  
Query Match 89.7%; Score 26; DB 2; Length 166;  
Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KAVFFA 6  
DB 107 KAVFYA 112  
|||||  
- - - - -  
  
RESULT 53  
O67590\_AQUAE PRELIMINARY; PRT; 185 AA.  
ID O67590\_AQUAE PRELIMINARY;  
AC O67590;  
DT 01-AUG-1998 (TReMBLrel. 07, Created)  
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE C-terminal fumarate hydratase, class I.



```

GN Name=fumX; OrderedLocusNames=AQ_1679;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
[1]
RN STRAIN=VPS; PubMed=9537320; DOI=10.1038/32831;
RX MEDLINE=96196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeck R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus";
RL Nature 392:353-358(1998).
DR EMBL; AE000750; AAC07546.1; -; Genomic_DNA.
DR PIR; B44358; E70445.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR004647; TtdB_fumA_fumB.
DR Pfam; PF05683; Fumerase_C_1.
DR TIGRPFAMs; TIGR00723; ttdB_fumA_fumB; 1.
KW Complete proteome.
SQ SEQUENCE 185 AA; 20441 MW; CBA8320A226E2558 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 185;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KAVPFA 6
Db 117 KAVYFA 122
|||:|
|||:|

RESULT 54
CSRPI CHICK STANDARD; PRT; 191 AA.
AC P6796f; P32965;
AT 01-OCT-1993 (Rel. 27, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cysteine-rich protein 1 (CRP1) (CRP).
GN Name=CSRPI; Synonyms=CRSP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryonic fibroblast;
RX MEDLINE=94124603; PubMed=8294495; DOI=10.1083/jcb.124.1.117;
RA Crawford A.W., Pino J.D., Beckerle M.C.;
RT "Biochemical and molecular characterization of the chicken cysteine-
RT rich protein, a developmentally regulated LIM-domain protein that is
RT associated with the actin cytoskeleton.";
RL J. Cell Biol. 124:117-127(1994).
[2]
RN PROTEIN SEQUENCE OF 1-49; 69-83; 111-129 AND 177-188.
RX MEDLINE=93107157; PubMed=1469049; DOI=10.1083/jcb.119.6.1573;
RA Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
RT "Zyxin and cCRP: two interactive LIM domain proteins associated with
RT the cytoskeleton.";
RL J. Cell Biol. 119:1573-1587(1992).
[3]
RN ZINC-BINDING.
RX MEDLINE=93281587; PubMed=8506279;
RA Michelsen J.W., Schmeichel K.L., Beckerle M.C., Winge D.R.;
RT "The LIM motif defines a specific zinc-binding protein domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4404-4408(1993).
[4]
RN MUTAGENESIS.
RX MEDLINE=94209279; PubMed=8157637;
RA Michelsen J.W., Sewell A.K., Louis H.A., Olsen J.I., Davis D.R.,
RA Winge D.R., Beckerle M.C.;
RT "Mutational analysis of the metal sites in an LIM domain.";
J. Biol. Chem. 269:11108-11113(1994).
[5]
RN STRUCTURE BY NMR OF C-TERMINAL LIM DOMAIN.
RX MEDLINE=95393167; PubMed=7664053;
RA Perez-Alvarado G.C., Miles C., Michelsen J.W., Louis H.A., Winge D.R.;
RT "Structure of the carboxy-terminal LIM domain from the cysteine rich
RT protein CRP.";
RL Nat. Struct. Biol. 1:388-398(1994).
CC -1- FUNCTION: Heat stable protein, that interacts with zyxin. May be a
CC component of a signal transduction pathway that mediates adhesion-
CC stimulated changes in gene expression.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Associates with the actin cytoskeleton.
CC -1- TISSUE SPECIFICITY: Most prominent in tissues that are enriched in
CC smooth muscle cells, such as gizzard, stomach, and intestine.
CC Lower level in the heart, no expression in liver, skeletal muscle,
CC or brain.
CC -1- DEVELOPMENTAL STAGE: Expression levels increase dramatically
CC during smooth muscle maturation.
CC -1- DOMAIN: Glycine-rich repeats mediate the association with the
CC actin cytoskeleton (Probable).
CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; X73831; CAA52053.1; -; mRNA.
DR PIR; A49648; A49648.
DR PIR; B44358; B44358.
DR PIR; C44358; C44358.
DR PDB; 1B8T; NMR; A=1-191.
DR PDB; 1CTU; NMR; @=107-191.
DR InterPro; IPR001781; LIM_zn_bd.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
KW 3D-structure; Direct protein sequencing; LIM domain; Metal-binding;
KW Nuclear protein; Repeat; Zinc.
FT INIT MET 0 0
FT DOMAIN 9 60 LIM zinc-binding 1.
FT DOMAIN 117 168 LIM zinc-binding 2.
FT MOTIF 63 68 Nuclear localization signal (Potential).
FT COMPBIAS 62 77 Gly-rich.
FT COMPBIAS 174 185 Gly-rich.
FT STRAND 7 8
FT TURN 10 12
FT STRAND 15 16
FT STRAND 22 24
FT TURN 25 26
FT STRAND 27 29
FT TURN 31 33
FT STRAND 35 35
FT TURN 37 39
FT STRAND 42 42
FT STRAND 48 51
FT TURN 52 53
FT STRAND 54 57
FT HELIX 58 65
FT STRAND 115 116
FT TURN 118 120
FT STRAND 123 124
FT STRAND 130 132
FT TURN 133 134
FT STRAND 135 137
FT TURN 139 141
FT STRAND 143 143
FT TURN 145 147

```



FT STRAND 150 150  
 FT TURN 156 159  
 FT TURN 160 161  
 FT STRAND 162 165  
 FT HELIX 166 172  
 FT TURN 173 173  
 SQ SEQUENCE 191 AA; 20254 MW; BC1A45013C7BDA38 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 191;  
 Best Local Similarity 83.3%; Pred. No. 5.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||:|  
 Db 14 KAVYFA 19

## RESULT 55

CSRP1\_COTJUA STANDARD; PRT; 191 AA.  
 AC P67967; P32965;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Cysteine-rich protein 1 (CRP1) (CRP).  
 GN Name=CSRP1; Synonyms=CSR1;  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Coturnix.  
 OC NCBI\_TaxID=93934;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryonic fibroblast;  
 RX MEDLINE=96081967; PubMed=7499425; DOI=10.1074/jbc.270.48.28946;  
 RA Weiskirchen R., Pino J.D., Macalima T., Bister K., Beckerle M.C.;  
 RT "The cysteine-rich protein family of highly related LIM domain proteins";  
 RL J. Biol. Chem. 270:28946-28954(1995).  
 CC -!- FUNCTION: Heat stable protein, that interacts with zyxin. May be a component of a signal transduction pathway that mediates adhesion-stimulated changes in gene expression.  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Associates with the actin cytoskeleton (By similarity).  
 CC -!- DOMAIN: Glycine-rich repeats mediate the association with the actin cytoskeleton (Probable).  
 CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.

-----  
 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

DR EMBL; Z28333; CAA82187.1; -; mRNA.  
 DR PIR; S38879; S38879.  
 DR InterPro; IPR001781; LIM\_Zn\_bd.  
 DR Pfam; PF00412; LIM; 2.  
 DR ProDom; PD000094; LIM; 2.  
 DR SMART; SM00132; LIM; 2.  
 DR PROSITE; PS00478; LIM DOMAIN 1; 2.  
 DR PROSITE; PS50023; LIM DOMAIN 2; 2.  
 KW LIM domain; Metal-binding; Nuclear protein; Repeat; Zinc.  
 FT INIT\_MET 0 0 By similarity.  
 FT DOMAIN 9 60 LIM zinc-binding 1.  
 FT DOMAIN 117 168 LIM zinc-binding 2.  
 FT MOTIF 63 68 Nuclear localization signal (Potential).  
 FT COMPIAS 62 77 Gly-rich.  
 FT COMPIAS 174 185 Gly-rich.  
 SQ SEQUENCE 191 AA; 20254 MW; BC1A45013C7BDA38 CRC64;

Query Match

89.7%; Score 26; DB 1; Length 191;

Best Local Similarity 83.3%; Pred. No. 5.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||:|  
 Db 14 KAVYFA 19

## RESULT 56

Q9RR88\_DEIRA PRELIMINARY; PRT; 229 AA.  
 AC Q9RR88;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Molybdenum cofactor biosynthesis protein D/E.  
 GN OrderedLocusNames=DR2607;  
 OS Deinococcus radiodurans.  
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;  
 OC Deinococcaceae; Deinococcus.  
 OC NCBI\_TaxID=1299;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;  
 RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1";  
 RL Science 286:1571-1577(1999).  
 DR EMBL; AE002090; AAF12145.1; -; Genomic\_DNA.  
 DR PIR; E75252; E75252.  
 DR HSSP; P30748; 1NVI.  
 DR TIGR; DR2607; -.  
 DR GO; GO:0006777; P-Mo-molybdopterin cofactor biosynthesis; IEA.  
 DR GO; GO:0006790; P-sulfur metabolism; IEA.  
 DR InterPro; IPR003448; Mb\_biosynth\_MoaE.  
 DR InterPro; IPR010034; MoaD.  
 DR InterPro; IPR003749; This.  
 DR PANTHER; PTHR10311; Mb\_biosynth\_MoaE; 1.  
 DR Pfam; PF02391; MoaE; 1.  
 DR Pfam; PF02597; ThisS; 1.  
 DR TIGRFAMs; TIGR01682; moaD; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 229 AA; 25311 MW; CD0F8B7060118B38 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 229;  
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 :|||  
 Db 4 RAVFFA 9

## RESULT 57

Q67QUL\_SYTH PRELIMINARY; PRT; 232 AA.  
 AC Q67QUL;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocusNames=STH967;  
 OS Symbiobacterium thermophilum.  
 OC Bacteria; Actinobacteria; Symbiobacterium.  
 OC NCBI\_TaxID=2734;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=IAMI4863; DOI=10.1093/nar/gkh830;  
RX PubMed=15383646; DOI=10.1093/nar/gkh830;  
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,  
RA Morimura K., Ikeda H., Hattori M., Beppu T.;  
RT "Genome sequence of *Symbiobacterium thermophilum*, an uncultivable  
RT bacterium that depends on microbial commensalism.";  
RL Nucleic Acids Res. 32:4937-4944(2004).  
DR EMBL; AP006840; BAD39952.1; -; Genomic\_DNA.  
DR InterPro; IPR005834; Dehal\_like\_hydro.  
DR Pfam; PF00702; Hydrolase; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 232 AA; 24811 MW; D630F748FD4D67B CRC64;

Query Match 89.7%; Score 26; DB 2; Length 232;  
Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
DB 3 KALFFA 8  
|||||

RESULT 58  
Q527F8\_MAGGR PRELIMINARY; PRT; 233 AA.  
AC Q527F8;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=MG05732.4;  
OS Magnaporthe grisea 70-15.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.  
OX NCBI\_TaxID=242507;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
RA Arachchi H., Armbruster J., Bachanteang P., Baldwin J., Barry A.,  
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,  
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,  
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,  
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
RA Darjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,  
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,  
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvasselis M., Karlsson E.,  
RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,  
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
RA Lindblad-toh K., Liu X., Lokitysang T., Lokitysang Y., Lucien O.,  
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,  
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,  
RA McCarthy M., McDonough S., McGhee T., Meldrim J., Meneus L.,  
RA Mesirov J., Mihalov A., Minova T., Mikkelsen T., Mienga V., Moru K.,  
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Onotosho B.,  
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,  
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schupbach R., Seaman C., Settippalli S., Sharpe T.,  
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,  
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
RA Stetson K., Stone S., Stone S., Stubbs M., Talamas J., Tchuinga P.,  
RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,  
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,

RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
RA Zimmer A., Zody M., Zander E.;  
RT "The genome sequence of *Magnaporthe grisea*.";  
RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Zhu H., Blackmon B.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL; AACU01000565; EAA54941.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 233 AA; 25744 MW; C25C02486B86B34C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 233;  
Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
DB 192 RAVFFA 197  
|||||

RESULT 59  
O30760 RHOSH PRELIMINARY; PRT; 233 AA.  
AC O30760;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Autoinducer synthesis regulator.  
GN Names=cerR;  
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1063;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX MEDLINE=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT *Rhodobacter sphaeroides*.";  
RL J. Bacteriol. 179:7530-7537(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX STRAIN=2.4.1T;  
RA Cogez V., Puskas A., Gak E., Kaplan S., Bohin J.-P.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RA Puskas A., Cogez V., Gak E., Bohin J.-P., Kaplan S.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF016298; AAC46021.1; -; Genomic\_DNA.  
DR HSP; P11470; 1FSK.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR005143; Autoind bd.  
DR InterPro; IPR000792; HTH LuxR.  
DR InterPro; IPR011991; Wing hlx DNA\_bd.  
DR Pfam; PF03472; Autoind\_bind; 1.  
DR Pfam; PF00196; GcrB; 1.

```

DR PRINTS; PR00038; HTHLUXR.
DR ProDom; PD000307; HTH LuxR; 1.
DR SMART; SM00421; HTH LUXR; 1.
SQ SEQUENCE 233 AA; 26080 MW; 127DDEDE86DB8D48 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 233;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
   :|||||
Db 92 RAVFFPA 97

RESULT 60
Q9N2Y5 CAEEL PRELIMINARY; PRT; 235 AA.
AC Q9N2Y5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Y71G10AR.3.
GN ORFNames=Y71G10AR.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=981916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AC024856; AAF60868.4; -; Genomic_DNA.
DR Ensembl; Y71G10AR.3; Caenorhabditis elegans.
DR WormBase; WBGene0022137; Y71G10AR.3.
DR WormPep; Y71G10AR.3; CE36900.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 235 AA; 27638 MW; 206BEC3C9570D089 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 235;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
   :|||||
Db 47 KAVFFS 52

RESULT 61
Q5UEW2 9PROT PRELIMINARY; PRT; 266 AA.
AC Q5UEW2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative sulfatase (fragment).
GN ORFNames=Red2C11_75;
OS uncultured alpha proteobacterium EBAC2C11.
OC Bacteria; Proteobacteria; Alphaproteobacteria; SAR116 cluster;
OC environmental samples.
OX NCBI_TaxID=295349;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sabeni G., Beja O.;
RT "SAR116.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY744399; AAV31659.1; -; Genomic DNA.
DR GO; GO:0008484; P:sulfuric ester hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000917; Sulfatase.

DR PFam; PF00884; Sulfatase; 1.
FT NON_TER 266 266
SQ SEQUENCE 266 AA; 29908 MW; 518924D95F9043A7 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
   :|||||
Db 232 KALFFPA 237

RESULT 62
Q5GU79 XANOR PRELIMINARY; PRT; 268 AA.
AC Q5GU79;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=XO04490;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KACC10331 / KX085;
RX PubMed=15673718; DOI=10.1093/nar/gki206;
RA Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W., Kim J.-G., Song E.-S.,
RA Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S., Lee G.-B., Kim H.,
RA Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H., Koh N.-H., Seo J.-S.,
RA Go S.-J.;
RT "The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
RT the bacterial blight pathogen of rice.";
RL Nucleic Acids Res. 33:577-586(2005).
DR EMBL; AE013598; AAW77744.1; -; Genomic_DNA.
DR InterPro; IPR005184; DUF306_MetA_HslJ.
DR PFam; PF03724; META; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 268 AA; 28691 MW; 7757E113FF1816E9 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
   :|||||
Db 2 RAVFFPA 7

RESULT 63
Q7QS35 GIALA PRELIMINARY; PRT; 276 AA.
AC Q7QS35;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_661_5852_6682.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

```

DR EMBL; AACB01000125; EAA37819.1; -; Genomic\_DNA.  
 DR InterPro; IPR001498; UPF0029.  
 DR Pfam; PF01205; UPF0029; 1.  
 DR PROSITE; PS00910; UPF0029; UNKNOWN 1.  
 SQ SEQUENCE 276 AA; 30612 MW; 09078636BA1D9667 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 276;  
 Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 Db 155 KSVFFA 160  
 |||:|

## RESULT 64

O48777 ARATH  
 ID O48777 ARATH PRELIMINARY; PRT; 285 AA.

AC O48777;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein At2g32880.  
 GN NameAt2g32880;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.J.,  
 RA Wu D., Maiti R., Roming C.M., Koo H., Fujii C.Y., Utterback T.R.,  
 RA Barnstead M.B., Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

## [2]

## NUCLEOTIDE SEQUENCE.

RA Town C.D., Kaul S.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC003033; AAB91985.1; -; Genomic\_DNA.

PIR; T01119; T01119.

PIR; T01119; T01119.

InterPro; IPR002083; MATH.

Pfam; PF00917; MATH; 1.

SMART; SM0061; MATH; 2.

PROSITE; PS0144; MATH; 2.

Hypothetical protein.

SQ SEQUENCE 285 AA; 32882 MW; 192157DB0D30FE27 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 285;  
 Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 Db 137 KAVFYA 142  
 |||:|

## RESULT 65

## Q5ASP9 CANAL

ID Q5ASP9 CANAL PRELIMINARY; PRT; 290 AA.

## AC Q5ASP9;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Hypothetical protein CTK3.

GN Name=CTK3; ORFNames=CA019.12810, CA019.5350;

OS Candida albicans SC5314.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI\_TaxID=237561;

## [1]

## NUCLEOTIDE SEQUENCE.

RP STRAIN=SC5314;

RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
 RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,  
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,  
 RA Davis R.W., Scherer S.;  
 RT "The diploid genome sequence of *Candida albicans*.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=SC5314;  
 RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,  
 RA Roberts J., Persson K., Donnelly S., Favoreto S., Tsung K.-W.,  
 RA Jones T., Scherer S., Agabian N.;  
 RT "Annotation of the Genome of *Candida albicans*.";   
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AACQ01000059; EAK98097.1; -; Genomic\_DNA.  
 DR EMBL; AACQ01000058; EAK98178.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 290 AA; 34139 MW; 41D96D679D453249 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 290;  
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 Db 26 KAVFYA 31  
 |||:|

## RESULT 66

## Q751V7 ORYZA

ID Q751V7 ORYZA PRELIMINARY; PRT; 296 AA.

## AC Q751V7;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Putative 6-phosphogluconolactonase (With alternative splicing).

GN Names=OSUNB0059G13.23;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI\_TaxID=39947;

## [1]

## NUCLEOTIDE SEQUENCE.

RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,  
 RA Overton II L.L., Taitzin T., Kim M.M., Bera J.J., Jin S.S.,  
 RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Haiao J., Blunt S.,  
 RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,  
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,  
 RA White O., Salzberg S.L., Fraser C.M.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

## [2]

## NUCLEOTIDE SEQUENCE.

RA Buell R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC120538; AAS07092.1; -; Genomic\_DNA.

Gramene; Q751V7; -;

DR GO; GO:0017057; F16-phosphogluconolactonase activity; IEA.

DR GO; GO:0016787; F16-phosphatase activity; IEA.

DR GO; GO:0005975; P-carbohydrate metabolism; IEA.

DR GO; GO:0006098; P-pentose-phosphate shunt; IEA.

DR InterPro; IPR006148; Gluc gal isom.

DR InterPro; IPR005900; Phosphogluconolac.

DR Pfam; PF01182; Glucosamine iso; 1.

DR TIGRFAMs; TIGR01198; pgl; 1.

SQ SEQUENCE 296 AA; 33270 MW; 36B72EAB4C2FE65A CRC64;

Query Match 89.7%; Score 26; DB 2; Length 296;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||:|

Db 240 KAVYFA 245

RESULT 67  
VG12 ICHV1  
ID VG12 ICHV1 STANDARD; PRT; 299 AA.  
AC Q00165;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Hypothetical gene 12 zinc-binding protein.  
GN Name=12;  
OS Ictalurid herpesvirus 1 (ICHV-1) (Channel catfish herpesvirus).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Ictalurivirus.  
OX NCBI\_TaxID=10401;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Auburn 1;  
RX MEDLINE=92087490; PubMed=1727613;  
RA Davison A.J.;  
RT "Channel catfish virus: a new type of herpesvirus.";  
RL Virology 186:9-14(1992).  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; W75136; AAA88193.1; -; Genomic DNA.  
CC EMBL; M75136; AAA88115.1; -; Genomic DNA.  
CC PIR; D36787; ZBBE13.  
CC DR InterPro; IPR001841; Znf\_RING.  
CC DR SMART; SM00184; RING\_1.  
CC KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.  
SQ SEQUENCE 299 AA; 33108 MW; B78295A904A647EB CRC64;  
  
Query Match 89.7%; Score 26; DB 1; Length 299;  
Best Local Similarity 83.3%; Pred. No. 7.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KAVYFA 6  
:|||||  
39 RAVYFA 44  
  
Db 318 AA.  
  
RESULT 68  
Q8GX90 ARATH  
ID Q8GX90 ARATH PRELIMINARY; PRT; 318 AA.  
AC Q8GX90;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein At5g32880.  
GN Name=At5g32880;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,  
RA Hayashizaki Y., Shinozaki K.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK118361; BAC42975.1; -; mRNA.  
DR InterPro; IPR002083; MATH.  
DR Pfam; PF00917; MATH; 2.  
DR SMART; SM00061; MATH; 2.  
DR PROSITE; PS0144; MATH; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 318 AA; 36701 MW; 14B0D9BF9BE0C7BD CRC64;

Query Match 89.7%; Score 26; DB 2; Length 318;  
Best Local Similarity 83.3%; Pred. No. 8.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KAVYFA 6  
|||||:  
137 KAVYFA 142  
  
RESULT 69  
Q6ASCI DESPS  
ID Q6ASCI DESPS PRELIMINARY; PRT; 321 AA.  
AC Q6ASCI;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Related to glycosyltransferase involved capsular polysaccharide  
DE biosynthesis.  
GN OrderedLocusNames=DP0013;  
OS Desulfotalea psychrophila.  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;  
OC Desulfobulbaceae; Desulfotalea.  
OX NCBI\_TaxID=84980;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=LSV54 / DSM 12343;  
RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;  
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,  
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,  
RA Teeling H., Leuschner W.D., Gloeckner P.-O., Lupas A.N., Amann R.,  
RA Klenk H.-P.;  
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium  
RT from permanently cold Arctic sediments.";  
RL Environ. Microbiol. 6:887-902(2004).  
DR EMBL; CR522870; CAG34742.1; -; Genomic DNA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR InterPro; IPR001173; Glyco trans 2.  
DR Pfam; PF00535; Glycos transf 2; I.  
KW Complete proteome; Transferase.  
SQ SEQUENCE 321 AA; 37861 MW; B3DEC2F91FB040BD CRC64;  
  
Query Match 89.7%; Score 26; DB 2; Length 321;  
Best Local Similarity 83.3%; Pred. No. 8.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KAVYFA 6  
|||||  
190 KAVYFA 195  
  
RESULT 70  
Q9EZ99 ZYMO  
ID Q9EZ99 ZYMO PRELIMINARY; PRT; 340 AA.  
AC Q9EZ99; Q5NLZ6;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Tryptophanyl-tRNA synthase (EC 6.1.1.2).  
GN Name=trpS; OrderedLocusNames=ZMO1640;  
OS Zymomonas mobilis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
OC Sphingomonadaceae; Zymomonas.  
OX NCBI\_TaxID=542;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ZM4;  
RA Shin I.S., Kang H.S.;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 31821 / ZM4 / CP4;  
RX PubMed=15592456; DOI=10.1038/ndt1045;

```

RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J.,
RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y.,
RA Kang H.L., Lee S.Y., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZM4."
RL Nat. Biotechnol. 23:63-68(2005).
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA (Trp) = AMP +
CC diphosphate + L-tryptophyl-tRNA(Trp).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AF300471; AAG2413.1; -; Genomic DNA.
DR EMBL; AE008632; AAV90284.1; -; Genomic DNA.
DR HSSP; P00953; IMAU.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004830; F:tryptophan-tRNA ligase activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1b.
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR PRINTS; PR01039; TRNASYNTRP.
DR TIGRFAMs; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA TRNA LIGASE I; 1.
DR ATP-binding; Aminoacyl-tRNA synthetase; Complete proteome; Ligase;
KW Nucleotide-binding; Protein biosynthesis.
FT DOMAIN 3 237 ABC transporter.
FT NP BIND 35 42 ATP (By similarity).
SQ SEQUENCE 340 AA; 37475 MW; 363EACB6A6EB883 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 340;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 81 RAVFFA 86

RESULT 71
CYSA METCA STANDARD; PRT; 348 AA.
ID Q609Q1;
AC Q609Q1;
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Sulfate/thiosulfate import ATP-binding protein cysA (EC 3.6.3.25)
DE (Sulfate-transporting ATPase).
GN Name=cysA; OrderedLocNames=MCAL181;
OS Methylococcus capsulatus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylococcus.
OX NCBI_TaxID=414;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bath / NCIMB 11132;
RC PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
RA Ward N.L., Larsen O., Sakwa J., Bruseeth L., Khouri H.M., Durkin A.S.,
RA Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.F., Fouts D.E.,
RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,
RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
RA Grindhaug S.H., Holt I.B., Eidhammer I., Jonassen I., Vanaken S.,
RA Utterback T.R., Feldblyum T.V., Fraser C.M., Lillehaug J.R.,
RA Eisen J.A.;
RT "Genomic insights into methanotrophy: the complete genome sequence of
RT Methylococcus capsulatus (Bath).";
RL PLOS Biol. 2:1616-1628(2004).
CC -1- FUNCTION: Part of the ABC transporter complex cysAATP involved in
CC sulfate/thiosulfate import. Responsible for energy coupling to the
CC transport system (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + sulfate(Out) = ADP + phosphate +
CC sulfate(In).

```

---

```

CC -1- SUBUNIT: The complex is composed of two ATP-binding proteins
CC (cysA), two transmembrane proteins (cysT and cysW) and a solute-
CC binding protein (cysP) (Probable).
CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC Sulfate/thiosulfate importer (TC 3.A.1.6) subfamily.
CC -1- SIMILARITY: Contains 1 ABC transporter domain.
CC
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC -----
DR EMBL; AE017282; AAU92758.1; -; Genomic DNA.
DR TIGR; MCAL181; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR InterPro; IPR005666; Sulph_transptl.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR00968; 3a0106s01; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Hydrolase; Inner membrane; Membrane;
KW Nucleotide-binding; Sulfate transporter; Transport.
FT DOMAIN 3 237 ABC transporter.
FT NP BIND 35 42 ATP (By similarity).
SQ SEQUENCE 348 AA; 38768 MW; 05FEEF976A11895 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 348;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 271 KALFFA 276

RESULT 72
Q83MJ3_SHIFL PRELIMINARY; PRT; 352 AA.
ID Q83MJ3; SHIFL; Q7UB67;
AC Q83MJ3; Q7UB67;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative resistance protein.
GN Name=yihN; OrderedLocNames=S3802, SF3944;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=301 / Serotype 2a;
RC MEDLINE=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RC MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786-2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

```

```

RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RL flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AS005674; AAN45379.2; -; Genomic_DNA.
DR EMBL; AS016990; AAP18819.1; -; Genomic_DNA.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
KW Complete proteome.
SQ SEQUENCE 352 AA; 38913 MW; 2CEA79CE6252270B CRC64;

Query Match      89.7%; Score 26; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 332 RAVFFPA 337
:|||||

RESULT 73
ID Q72FT5_DESVH PRELIMINARY; PRT; 352 AA.
AC Q72FT5_2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane protein, putative.
GN OrderedLocusNames=DVU0128;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heideberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RA "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.";
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AS017309; AAS94612.1; -; Genomic_DNA.
DR TIGR; DVU0128; -.
DR InterPro; IPR002549; UPF0118.
DR Pfam; PF01594; UPF0118; 1.
KW Complete proteome.
SQ SEQUENCE 352 AA; 36026 MW; 787856A87410B493 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 23 KALFFPA 28
:|||||

RESULT 74
ID Q6MI90_BDEBA PRELIMINARY; PRT; 383 AA.
AC Q6MI90_2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative polysaccharide deacetylase precursor (EC 3.5.1.-).
GN OrderedLocusNames=Bd3279;
OS Bdellovibrio bacteriovorus.

```

```

OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RT Science 303:689-692(2004).
RL EMBL; BX842655; CAE78090.1; -; Genomic_DNA.
DR GO; GO:0016810; F:hydrolase activity, acting on carbon-nitrog. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR002509; Poly8ac deacet.
DR Pfam; PF01522; Poly8ac_deac_1; 1.
KW Complete proteome; Hydrolase; Signal.
FT SIGNAL 1 11 Potential.
SQ SEQUENCE 383 AA; 42819 MW; 7A1A4BF645C565BC CRC64;

Query Match      89.7%; Score 26; DB 2; Length 383;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 197 KAMFFPA 202
:|||||

RESULT 75
ID Q4HML6_CAMLA PRELIMINARY; PRT; 390 AA.
AC Q4HML6_2
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Cytochrome P-450, putative.
GN ORFNames=CLA1389;
OS Campylobacter lari RM2100.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306263;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM2100;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAPK0100001; EAL55536.1; -; Genomic_DNA.
SQ SEQUENCE 390 AA; 42990 MW; 29E9CF925C147383 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 390;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 75 KALFFPA 80
:|||||

Search completed: December 29, 2005, 17:47:28
Job time : 78.1936 secs

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.83871 Seconds  
(without alignments)  
13.656 Million cell updates/sec

Title: US-10-009-122-18  
Perfect score: 34  
Sequence: 1 KLVFFPAQ 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Published Applications AA New.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	91.2	19	6	US-10-923-605-5
2	31	91.2	19	6	US-10-934-818-5
3	31	91.2	40	7	US-11-016-706-36
4	31	91.2	40	7	US-11-098-674-12
5	31	91.2	42	6	US-10-923-605-1
6	31	91.2	42	6	US-10-934-818-1
7	31	91.2	42	7	US-11-016-706-37
8	31	91.2	43	6	US-10-934-818-6
9	31	91.2	43	6	US-10-250-581-1
10	31	91.2	43	6	US-10-250-581-1
11	31	91.2	770	6	US-10-982-545-15
12	31	91.2	770	6	US-10-789-273-38
13	26	76.5	525	7	US-11-082-369-350
14	26	76.5	858	6	US-10-613-744-6
15	25	73.5	5	7	US-11-098-674-1
16	25	73.5	179	6	US-10-467-657-306
17	25	73.5	179	6	US-10-467-657-6422
18	25	73.5	325	6	US-10-454-437-142
19	25	73.5	485	6	US-10-204-029-7
20	25	73.5	528	6	US-10-793-626-1930
21	25	73.5	721	6	US-10-467-962B-49
22	24	70.6	71	7	US-11-000-463-765
23	24	70.6	197	5	US-09-940-308-3
24	24	70.6	211	6	US-10-467-657-6932
25	24	70.6	215	6	US-10-131-826A-4
26	24	70.6	215	6	US-10-131-826A-4
27	24	70.6	215	6	US-10-131-826A-4
28	24	70.6	215	6	US-10-131-826A-4
29	24	70.6	215	6	US-10-131-826A-4
30	24	70.6	215	6	US-10-131-826A-4
31	24	70.6	215	6	US-10-131-826A-4
32	24	70.6	215	6	US-10-131-826A-4
33	24	70.6	215	6	US-10-131-826A-4
34	24	70.6	215	6	US-10-131-826A-4
35	24	70.6	215	6	US-10-131-826A-4
36	24	70.6	215	6	US-10-131-826A-4
37	24	70.6	215	6	US-10-131-826A-4
38	24	70.6	215	6	US-10-131-826A-4
39	24	70.6	215	6	US-10-131-826A-4
40	24	70.6	215	6	US-10-131-826A-4
41	24	70.6	215	6	US-10-131-826A-4
42	24	70.6	215	6	US-10-131-826A-4
43	24	70.6	215	6	US-10-131-826A-4
44	23	67.6	47	6	US-10-467-657-5436
45	23	67.6	57	6	US-10-467-657-5448
46	23	67.6	104	6	US-10-689-742-206
47	23	67.6	143	6	US-10-793-626-370
48	23	67.6	155	6	US-10-467-657-2420
49	23	67.6	194	6	US-10-467-657-3978
50	23	67.6	195	7	US-11-019-955-24
51	23	67.6	211	6	US-10-821-234-1372
52	23	67.6	216	6	US-10-467-657-8102
53	23	67.6	223	7	US-11-112-882-88
54	23	67.6	241	7	US-11-019-955-27
55	23	67.6	258	6	US-10-793-626-2360
56	23	67.6	268	7	US-11-019-955-28
57	23	67.6	269	6	US-10-467-657-330
58	23	67.6	272	6	US-10-632-150-46
59	23	67.6	272	7	US-11-073-457-46
60	23	67.6	272	7	US-11-073-460-46
61	23	67.6	370	6	US-10-821-234-1105
62	23	67.6	400	6	US-10-793-626-1056
63	23	67.6	463	6	US-10-467-657-6352
64	23	67.6	463	6	US-10-467-657-7604
65	23	67.6	522	6	US-10-995-561-1030
66	23	67.6	582	7	US-11-090-439-58
67	23	67.6	585	6	US-10-967-457-18
68	23	67.6	585	6	US-10-939-890-500
69	23	67.6	585	7	US-11-078-663-18
70	23	67.6	585	7	US-11-078-914-18
71	23	67.6	615	6	US-10-995-561-943
72	23	67.6	662	6	US-10-995-561-943
73	23	67.6	690	6	US-10-939-890-501
74	23	67.6	702	6	US-10-995-561-942
75	23	67.6	754	6	US-10-995-561-941
76	22	64.7	35	6	US-10-821-234-1704
77	22	64.7	50	6	US-10-467-657-7892
78	22	64.7	106	7	US-11-064-174-50
79	22	64.7	117	6	US-10-467-657-2282
80	22	64.7	122	6	US-10-467-657-606
81	22	64.7	127	6	US-10-467-657-3152
82	22	64.7	134	6	US-10-467-657-6860
83	22	64.7	150	6	US-10-467-657-2040
84	22	64.7	175	6	US-10-873-528-90
85	22	64.7	183	6	US-10-980-388-89
86	22	64.7	183	6	US-10-467-657-8825
87	22	64.7	189	6	US-10-467-657-6854
88	22	64.7	189	6	US-10-467-657-7856
89	22	64.7	204	6	US-10-980-388-102
90	22	64.7	208	6	US-10-467-657-3098
91	22	64.7	220	6	US-10-467-657-8734
92	22	64.7	239	6	US-10-467-657-8743
93	22	64.7	271	6	US-10-793-626-1156
94	22	64.7	276	6	US-10-873-528-134
95	22	64.7	347	6	US-10-467-657-2014
96	22	64.7	352	7	US-11-191-072-4
97	22	64.7	358	6	US-10-467-657-7030
98	22	64.7	362	6	US-10-467-657-6880

Sequence 290, App  
Sequence 5750, App  
Sequence 568, App  
Sequence 4838, App  
Sequence 1322, App  
Sequence 3128, App  
Sequence 19, Appl  
Sequence 376, App  
Sequence 6, Appl  
Sequence 198, App  
Sequence 959, App  
Sequence 120, App  
Sequence 87, Appl  
Sequence 19, Appl  
Sequence 1137, App  
Sequence 2, Appl  
Sequence 125, App  
Sequence 917, App  
Sequence 5436, App  
Sequence 5448, App  
Sequence 206, App  
Sequence 370, App  
Sequence 2420, App  
Sequence 3978, App  
Sequence 24, Appl  
Sequence 1372, App  
Sequence 8102, App  
Sequence 88, Appl  
Sequence 27, Appl  
Sequence 2360, App  
Sequence 28, Appl  
Sequence 330, App  
Sequence 46, Appl  
Sequence 46, Appl  
Sequence 1105, App  
Sequence 1056, App  
Sequence 6352, App  
Sequence 7604, App  
Sequence 1030, App  
Sequence 58, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 500, App  
Sequence 18, Appl  
Sequence 940, App  
Sequence 943, App  
Sequence 501, App  
Sequence 942, App  
Sequence 941, App  
Sequence 1704, App  
Sequence 7892, App  
Sequence 50, Appl  
Sequence 2282, App  
Sequence 606, App  
Sequence 3152, App  
Sequence 6860, App  
Sequence 2040, App  
Sequence 90, Appl  
Sequence 89, Appl  
Sequence 8825, App  
Sequence 6854, App  
Sequence 7856, App  
Sequence 102, App  
Sequence 3098, App  
Sequence 8734, App  
Sequence 8743, App  
Sequence 1156, App  
Sequence 134, App  
Sequence 2014, App  
Sequence 4, Appl  
Sequence 7030, App  
Sequence 6880, App



99	22	64.7	366	6	US-10-467-657-7024	Sequence 7024, Ap	172	21	61.8	433	6	US-10-821-234-1429	Sequence 1429, Ap
100	22	64.7	366	6	US-10-467-657-7964	Sequence 7964, Ap	173	21	61.8	446	6	US-10-467-657-930	Sequence 930, Ap
101	22	64.7	392	6	US-10-467-657-2726	Sequence 2726, Ap	174	21	61.8	447	7	US-11-112-882-4	Sequence 4, Appl
102	22	64.7	402	6	US-10-467-657-9070	Sequence 9070, Ap	175	21	61.8	448	6	US-10-467-657-1096	Sequence 1096, Ap
103	22	64.7	409	6	US-10-821-234-1425	Sequence 1425, Ap	176	21	61.8	460	6	US-10-467-657-3136	Sequence 3136, Ap
104	22	64.7	413	6	US-10-467-657-1858	Sequence 1858, Ap	177	21	61.8	475	7	US-11-174-150-45	Sequence 45, Appl
105	22	64.7	425	7	US-11-055-822-1104	Sequence 1104, Ap	178	21	61.8	476	6	US-10-763-712A-107	Sequence 107, Appl
106	22	64.7	426	6	US-10-467-657-2120	Sequence 2120, Ap	179	21	61.8	481	6	US-10-467-657-3292	Sequence 3292, Ap
107	22	64.7	444	6	US-10-467-657-2414	Sequence 2414, Ap	180	21	61.8	481	6	US-10-467-657-4660	Sequence 4660, Ap
108	22	64.7	445	6	US-10-873-528-30	Sequence 30, Appl	181	21	61.8	489	6	US-10-793-626-2632	Sequence 2632, Ap
109	22	64.7	524	6	US-10-689-743-13	Sequence 13, Appl	182	21	61.8	522	7	US-11-080-991-104	Sequence 104, Appl
110	22	64.7	525	7	US-11-112-882-27	Sequence 27, Appl	183	21	61.8	525	6	US-10-763-712A-108	Sequence 108, Appl
111	22	64.7	576	6	US-10-508-442-2	Sequence 2, Appl	184	21	61.8	529	7	US-11-174-150-46	Sequence 46, Appl
112	22	64.7	616	6	US-10-131-826A-206	Sequence 206, App	185	21	61.8	533	6	US-10-467-657-2868	Sequence 2868, Ap
113	22	64.7	672	6	US-10-467-657-8280	Sequence 8280, Ap	186	21	61.8	554	7	US-11-000-463-240	Sequence 240, Appl
114	22	64.7	677	6	US-10-131-826A-230	Sequence 230, App	187	21	61.8	554	7	US-11-080-991-62	Sequence 62, Appl
115	22	64.7	708	7	US-11-174-150-25	Sequence 25, Appl	188	21	61.8	592	6	US-10-467-657-4888	Sequence 4888, Ap
116	22	64.7	710	7	US-11-078-189-18	Sequence 18, Appl	189	21	61.8	594	6	US-10-467-657-3952	Sequence 3952, Ap
117	22	64.7	736	7	US-11-174-150-26	Sequence 26, Appl	190	21	61.8	602	7	US-11-055-822-74	Sequence 74, Appl
118	22	64.7	736	7	US-11-078-189-9	Sequence 9, Appl	191	21	61.8	626	6	US-10-512-184-49	Sequence 49, Appl
119	22	64.7	739	7	US-11-078-189-12	Sequence 12, Appl	192	21	61.8	707	7	US-11-186-284-132	Sequence 132, Appl
120	22	64.7	856	6	US-11-147-109-2	Sequence 2, Appl	193	21	61.8	738	7	US-11-147-047-48	Sequence 48, Appl
121	22	64.7	856	6	US-10-467-657-8534	Sequence 8534, Ap	194	21	61.8	747	7	US-11-018-018-1	Sequence 1, Appl
122	22	64.7	989	6	US-10-821-234-975	Sequence 975, App	195	21	61.8	747	7	US-11-047-757-1	Sequence 1, Appl
123	22	64.7	1167	6	US-10-601-368-8	Sequence 8, Appl	196	21	61.8	823	6	US-10-467-657-2526	Sequence 2526, Ap
124	22	64.7	2504	6	US-10-647-956A-8	Sequence 8, Appl	197	21	61.8	1016	7	US-11-103-957-41	Sequence 41, Appl
125	21	61.8	26	6	US-10-986-501-303	Sequence 303, App	198	21	61.8	1070	7	US-11-147-047-49	Sequence 49, Appl
126	21	61.8	45	6	US-10-467-657-8626	Sequence 8626, Ap	199	21	61.8	1113	7	US-11-067-811-4	Sequence 4, Appl
127	21	61.8	50	6	US-10-467-657-9144	Sequence 9144, Ap	200	21	61.8	1196	6	US-10-613-744-9	Sequence 9, Appl
128	21	61.8	101	6	US-10-467-657-6722	Sequence 6722, Ap	201	21	61.8	1259	6	US-10-467-657-5510	Sequence 5510, Ap
129	21	61.8	104	6	US-10-793-626-2312	Sequence 2312, Ap	202	21	61.8	1510	7	US-11-055-822-72	Sequence 72, Appl
130	21	61.8	105	6	US-10-467-657-9209	Sequence 9209, Ap	203	21	61.8	1766	7	US-11-075-185-10	Sequence 10, Appl
131	21	61.8	133	7	US-11-069-834-2	Sequence 2, Appl	204	21	61.8	2261	6	US-10-995-561-600	Sequence 600, App
132	21	61.8	147	7	US-11-000-463-758	Sequence 758, App	205	21	61.8	2261	7	US-11-055-309A-9	Sequence 9, Appl
133	21	61.8	179	6	US-10-793-626-3052	Sequence 3052, Ap	206	21	61.8	2261	7	US-11-055-309A-10	Sequence 10, Appl
134	21	61.8	183	7	US-11-000-463-286	Sequence 286, App	207	21	61.8	2333	7	US-11-096-281-13	Sequence 13, Appl
135	21	61.8	190	6	US-10-467-657-3436	Sequence 3436, Ap	208	21	61.8	2339	7	US-11-096-281-11	Sequence 11, Appl
136	21	61.8	193	6	US-10-467-657-8294	Sequence 8294, Ap	209	21	61.8	3623	6	US-10-995-561-593	Sequence 593, App
137	21	61.8	194	7	US-11-103-957-57	Sequence 57, Appl	210	20	58.8	11	7	US-11-074-176-377	Sequence 377, App
138	21	61.8	199	6	US-10-467-657-4532	Sequence 4532, Ap	211	20	58.8	19	6	US-10-467-657-8712	Sequence 8712, Ap
139	21	61.8	204	6	US-10-467-657-8687	Sequence 8687, Ap	212	20	58.8	28	6	US-10-250-581-14	Sequence 14, Appl
140	21	61.8	205	6	US-10-873-528-52	Sequence 52, Appl	213	20	58.8	28	6	US-10-250-581-17	Sequence 17, Appl
141	21	61.8	207	6	US-10-858-730-136	Sequence 196, App	214	20	58.8	28	6	US-10-250-581-14	Sequence 14, Appl
142	21	61.8	208	6	US-10-467-657-2658	Sequence 2658, Ap	215	20	58.8	28	6	US-10-250-581-17	Sequence 17, Appl
143	21	61.8	210	6	US-10-793-626-972	Sequence 972, App	216	20	58.8	28	6	US-10-250-581-15	Sequence 15, Appl
144	21	61.8	213	6	US-10-467-657-1194	Sequence 1194, Ap	217	20	58.8	40	6	US-10-250-581-18	Sequence 18, Appl
145	21	61.8	220	6	US-10-467-657-3154	Sequence 3154, Ap	218	20	58.8	40	6	US-10-250-581-15	Sequence 15, Appl
146	21	61.8	224	6	US-10-793-626-2684	Sequence 2684, Ap	219	20	58.8	40	6	US-10-250-581-18	Sequence 18, Appl
147	21	61.8	229	6	US-10-131-826A-410	Sequence 410, App	220	20	58.8	42	6	US-10-250-581-16	Sequence 16, Appl
148	21	61.8	231	6	US-10-467-657-7406	Sequence 7406, Ap	221	20	58.8	42	6	US-10-250-581-19	Sequence 19, Appl
149	21	61.8	248	6	US-10-793-626-3218	Sequence 3218, Ap	222	20	58.8	42	6	US-10-250-581-16	Sequence 16, Appl
150	21	61.8	249	7	US-11-113-424-30	Sequence 30, Appl	223	20	58.8	42	6	US-10-250-581-19	Sequence 19, Appl
151	21	61.8	258	6	US-10-467-657-6180	Sequence 6180, Ap	224	20	58.8	44	7	US-11-000-463-372	Sequence 372, App
152	21	61.8	258	6	US-10-467-657-7572	Sequence 7572, Ap	225	20	58.8	47	6	US-10-467-657-9186	Sequence 9186, Ap
153	21	61.8	259	6	US-10-512-184-34	Sequence 34, Appl	226	20	58.8	52	6	US-10-467-657-2216	Sequence 2216, Ap
154	21	61.8	269	6	US-10-821-234-1683	Sequence 1683, Ap	227	20	58.8	53	6	US-10-467-657-6120	Sequence 6120, Ap
155	21	61.8	267	6	US-10-467-657-2198	Sequence 2198, Ap	228	20	58.8	54	6	US-10-467-657-4978	Sequence 4978, Ap
156	21	61.8	298	6	US-10-793-626-1298	Sequence 1298, Ap	229	20	58.8	54	6	US-10-467-657-8560	Sequence 8560, Ap
157	21	61.8	311	6	US-10-793-626-2450	Sequence 2450, Ap	230	20	58.8	56	6	US-10-467-657-1050	Sequence 1050, Ap
158	21	61.8	327	6	US-10-793-626-1104	Sequence 1104, Ap	231	20	58.8	56	6	US-10-467-657-5386	Sequence 5386, Ap
159	21	61.8	348	6	US-10-467-657-6602	Sequence 6602, Ap	232	20	58.8	76	6	US-10-467-657-5690	Sequence 5690, Ap
160	21	61.8	348	6	US-10-467-657-7662	Sequence 7662, Ap	233	20	58.8	80	7	US-11-123-896-89	Sequence 89, Appl
161	21	61.8	349	6	US-10-515-419-2	Sequence 2, Appl	234	20	58.8	90	7	US-11-020-772-33	Sequence 33, Appl
162	21	61.8	352	6	US-10-515-419-3	Sequence 3, Appl	235	20	58.8	92	6	US-10-467-657-2378	Sequence 2378, Ap
163	21	61.8	355	6	US-10-467-657-7996	Sequence 7996, Ap	236	20	58.8	98	6	US-10-467-657-4746	Sequence 4746, Ap
164	21	61.8	355	7	US-11-055-822-162	Sequence 162, App	237	20	58.8	100	7	US-11-123-896-137	Sequence 137, App
165	21	61.8	371	6	US-10-512-184-71	Sequence 71, Appl	238	20	58.8	104	6	US-10-467-657-6866	Sequence 6866, Ap
166	21	61.8	373	6	US-10-858-730-20	Sequence 20, Appl	239	20	58.8	105	7	US-11-155-775-12	Sequence 12, Appl
167	21	61.8	378	6	US-10-467-657-1796	Sequence 1796, Ap	240	20	58.8	106	6	US-10-467-657-3052	Sequence 3052, Ap
168	21	61.8	395	6	US-10-793-626-664	Sequence 664, Appl	241	20	58.8	107	7	US-11-064-174-36	Sequence 36, Appl
169	21	61.8	417	6	US-10-467-657-2112	Sequence 2112, Ap	242	20	58.8	112	7	US-11-054-669-113	Sequence 113, Appl
170	21	61.8	428	6	US-10-821-234-997	Sequence 997, App	243	20	58.8	114	6	US-10-467-657-9012	Sequence 9012, Ap
171	21	61.8	433	6	US-10-652-893-4	Sequence 4, Appl	244	20	58.8	115	6	US-10-793-626-1554	Sequence 1554, Ap

Sequence 23, Appl  
Sequence 38, Appl  
Sequence 38, Appl  
Sequence 38, Appl  
Sequence 354, App  
Sequence 1528, Ap  
Sequence 5166, Ap  
Sequence 2766, Ap  
Sequence 10, Appl  
Sequence 432, App  
Sequence 530, App  
Sequence 1980, Ap  
Sequence 2928, Ap  
Sequence 28, Appl  
Sequence 8188, Ap  
Sequence 5104, Ap  
Sequence 18, Appl  
Sequence 97, Appl  
Sequence 4, Appl  
Sequence 5942, Ap  
Sequence 2836, Ap  
Sequence 6906, Ap  
Sequence 818, App  
Sequence 2700, Ap  
Sequence 72, Appl  
Sequence 172, App  
Sequence 6318, Ap  
Sequence 5460, Ap  
Sequence 5, Appl  
Sequence 7608, Ap  
Sequence 5212, Ap  
Sequence 228, App  
Sequence 59, Appl  
Sequence 432, App  
Sequence 1073, Ap  
Sequence 5676, Ap  
Sequence 23, Appl  
Sequence 48, Appl  
Sequence 4742, Ap  
Sequence 1027, Ap  
Sequence 6188, Ap  
Sequence 2500, Ap  
Sequence 1419, Ap  
Sequence 1, Appl  
Sequence 1272, Ap  
Sequence 24, Appl  
Sequence 7686, Ap  
Sequence 2190, Ap  
Sequence 106, App  
Sequence 5794, Ap  
Sequence 3982, Ap  
Sequence 8140, Ap  
Sequence 424, App  
Sequence 2504, Ap

245 20 58.8 119 7 US-11-084-508-23  
246 20 58.8 122 6 US-10-632-150-38  
247 20 58.8 122 7 US-11-073-457-38  
248 20 58.8 122 7 US-11-073-460-38  
249 20 58.8 123 6 US-10-793-626-354  
250 20 58.8 123 6 US-10-467-657-1528  
251 20 58.8 123 6 US-10-467-657-5166  
252 20 58.8 126 6 US-10-793-626-2766  
253 20 58.8 127 7 US-11-106-796-10  
254 20 58.8 129 6 US-10-501-039-8  
255 20 58.8 134 6 US-10-793-626-432  
256 20 58.8 137 6 US-10-793-626-530  
257 20 58.8 137 6 US-10-793-626-1980  
258 20 58.8 138 6 US-10-467-657-2928  
259 20 58.8 139 6 US-10-467-657-28  
260 20 58.8 139 6 US-10-467-657-8188  
261 20 58.8 167 6 US-10-467-657-5104  
262 20 58.8 167 7 US-11-210-316-18  
263 20 58.8 175 6 US-10-873-528-97  
264 20 58.8 178 6 US-10-892-379-4  
265 20 58.8 179 6 US-10-467-657-5942  
266 20 58.8 182 6 US-10-793-626-2836  
267 20 58.8 183 6 US-10-467-657-6906  
268 20 58.8 191 6 US-10-467-657-818  
269 20 58.8 193 6 US-10-467-657-2700  
270 20 58.8 205 6 US-10-689-742-72  
271 20 58.8 208 6 US-10-510-386-172  
272 20 58.8 210 6 US-10-467-657-6318  
273 20 58.8 215 6 US-10-467-657-5460  
274 20 58.8 215 7 US-11-008-331-5  
275 20 58.8 222 6 US-10-467-657-7608  
276 20 58.8 223 6 US-10-467-657-5212  
277 20 58.8 229 6 US-10-510-386-228  
278 20 58.8 230 7 US-11-170-653-59  
279 20 58.8 239 6 US-10-467-657-432  
280 20 58.8 242 6 US-10-821-234-1073  
281 20 58.8 242 6 US-10-467-657-5676  
282 20 58.8 243 6 US-10-512-109-23  
283 20 58.8 243 6 US-10-512-109-48  
284 20 58.8 245 6 US-10-467-657-4742  
285 20 58.8 256 7 US-11-054-515-1027  
286 20 58.8 263 6 US-10-467-657-6188  
287 20 58.8 265 6 US-10-793-626-2500  
288 20 58.8 271 6 US-10-821-234-1419  
289 20 58.8 274 7 US-11-132-142-1  
290 20 58.8 288 6 US-10-467-657-1272  
291 20 58.8 291 7 US-11-102-883-22  
292 20 58.8 292 7 US-11-102-883-24  
293 20 58.8 294 6 US-10-467-657-7686  
294 20 58.8 299 6 US-10-467-657-2190  
295 20 58.8 299 6 US-10-873-528-106  
296 20 58.8 302 6 US-10-467-657-5794  
297 20 58.8 313 6 US-10-467-657-3982  
298 20 58.8 313 6 US-10-467-657-8140  
299 20 58.8 320 6 US-10-467-657-424  
300 20 58.8 321 6 US-10-467-657-2504

## ALIGNMENTS

RESULT 1  
US-10-923-605-5  
; Sequence 5, Application US/10923605  
; Publication No. US20050245727A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004740US  
; CURRENT APPLICATION NUMBER: US/10/923,605  
; CURRENT FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: US/09/322,289

; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)\_RES  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-10-923-605-5

Query Match 91.2%; Score 31; DB 6; Length 19;  
Best Local Similarity 85.7%; Pred. No. 0.32;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 4 KLVFFAE 10

## RESULT 2

US-10-934-818-5  
; Sequence 5, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)\_RES  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-10-934-818-5

Query Match 91.2%; Score 31; DB 6; Length 19;  
Best Local Similarity 85.7%; Pred. No. 0.32;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 4 KLVFFAE 10

## RESULT 3

US-11-016-706-36  
; Sequence 36, Application US/11016706  
; Publication No. US20050244334A1  
; GENERAL INFORMATION:  
; APPLICANT: CASTILLO, GERARDO  
; APPLICANT: LAKE, THOMAS P.

; APPLICANT: NGUYEN, BETH P.  
 ; APPLICANT: SANDERS, VIRGINIA J.  
 ; APPLICANT: SNOW, ALAN D.  
 ; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
 ; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS  
 ; FILE REFERENCE: PROTEO.P03C13  
 ; CURRENT APPLICATION NUMBER: US/11/016,706  
 ; CURRENT FILING DATE: 2004-12-16  
 ; PRIOR APPLICATION NUMBER: 09/962,955  
 ; PRIOR FILING DATE: 2001-09-24  
 ; PRIOR APPLICATION NUMBER: 09/938,275  
 ; PRIOR FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 08/947,057  
 ; PRIOR FILING DATE: 1997-10-08  
 ; NUMBER OF SEQ ID NOS: 89  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO 36  
 ; LENGTH: 40  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-11-016-706-36

```

Query Match          91.2%; Score 31; DB 7; Length 40;
Best Local Similarity 85.7%; Pred.No. 0.66;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
        |||||:
Db      16 KLVFFAE 22

RESULT 4
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION: John B.
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

```

```

Query Match      91.2% Score 31; DB 7; Length 40;
Best Local Similarity 85.7% Pred. No. 0.66;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVEFFAQ 7
Db      16 KLVEFFAE 22

```

RESULT 5  
US-10-923-605-1  
; Sequence 1, Application US/10923605  
; Publication No. US20050249727A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004740US  
; CURRENT APPLICATION NUMBER: US/10/923.605

```

; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-
US-10-923-605-1

```

```

Query Match      31.2%; Score 31; DB 6; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7
Db 16 KLVFFFAE 22

```

```

RESULT 6
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

```

```

Query Match      91.2%; Score 31; DB 6; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFFAQ 7
        |||||:
Db      16 KLVFFFAE 22

```

```

RESULT 7
US-11-016-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES
; TITLE OF INVENTION: OTHER BETA-AMY
; FILE REFERENCE: PROTO. P03C13
; CURRENT APPLICATION NUMBER: US/11/0
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,95
; PRIOR FILING DATE: 2001-09-24

```

; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 37  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-016-706-37

Query Match 91.2%; Score 31; DB 7; Length 42;  
Best Local Similarity 85.7%; Pred. No. 0.69;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||||:  
Db 16 KLVFFPAE 22

## RESULT 8

US-10-934-818-6  
; Sequence 6, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide  
US-10-934-818-6

Query Match 91.2%; Score 31; DB 6; Length 43;  
Best Local Similarity 85.7%; Pred. No. 0.71;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||||:  
Db 16 KLVFFPAE 22

## RESULT 9

US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 91.2%; Score 31; DB 6; Length 43;  
Best Local Similarity 85.7%; Pred. No. 0.71;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||||:  
Db 16 KLVFFPAE 22

## RESULT 10

US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 91.2%; Score 31; DB 6; Length 43;  
Best Local Similarity 85.7%; Pred. No. 0.71;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||||:  
Db 16 KLVFFPAE 22

## RESULT 11

US-10-982-545-15  
; Sequence 15, Application US/10982545  
; Publication No. US20050244890A1  
; GENERAL INFORMATION:

; APPLICANT: Davies, Huw Alun  
; APPLICANT: McGuire, James  
; APPLICANT: Simonsen, Anja Hviid  
; APPLICANT: Blennow, Kaj  
; APPLICANT: Podust, Vladimir  
; APPLICANT: CIPHERGEN Biosystems, Inc.  
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease  
; FILE REFERENCE: 016866-011550US  
; CURRENT APPLICATION NUMBER: US/10/982,545  
; CURRENT FILING DATE: 2004-11-06  
; PRIOR APPLICATION NUMBER: US 60/518,360  
; PRIOR FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US 60/526,753  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: US 60/546,423  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/547,250  
; PRIOR FILING DATE: 2004-02-23  
; PRIOR APPLICATION NUMBER: US 60/558,896  
; PRIOR FILING DATE: 2004-04-02  
; PRIOR APPLICATION NUMBER: US 60/572,617  
; PRIOR FILING DATE: 2004-05-18  
; PRIOR APPLICATION NUMBER: US 60/586,503  
; PRIOR FILING DATE: 2004-07-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

```
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; OTHER INFORMATION: C31
US-10-982-545-15
```

```
Query Match          91.2%; Score 31; DB 6; Length 770;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 KLVFFPAQ 7

Db 687 KLVFFFAE 693

RESULT 12

```
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saidanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-38
```

```
Query Match          91.2%; Score 31; DB 6; Length 770;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 KLVFFPAQ 7

Db 687 KLVFFFAE 693

RESULT 13

```
US-11-082-389-350
; Sequence 350, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
```

```
; SEQ ID NO 350
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-350

Query Match          76.5%; Score 26; DB 7; Length 525;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      230 KYVFAQ 236
      |||||

RESULT 14
US-10-613-744-6
; Sequence 6, Application US/10613744
; Publication No. US2005027093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-6

Query Match          76.5%; Score 26; DB 6; Length 858;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFAQ 7
Db      348 LVFFAQ 353
      |||||

RESULT 15
US-11-098-674-1
; Sequence 1, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; TITLE OF INVENTION: Compounds Which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTO-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match          73.5%; Score 25; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFF 5
Db      1 KLVFF 5
      |||||

RESULT 16
US-10-467-657-306
; Sequence 306, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 306
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-306

Query Match          73.5%; Score 25; DB 6; Length 179;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      30 KLVFFAQ 36
      ||::||

RESULT 17
US-10-467-657-6422
; Sequence 6422, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6422
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6422

Query Match          73.5%; Score 25; DB 6; Length 179;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
   ||:|
Db 30 KLLYYAQ 36

RESULT 18
US-10-454-437-142
; Sequence 142, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128PCPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 142
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-142

Query Match 73.5%; Score 25; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VFFAQ 7
   ||||
Db 55 VFFAQ 59

RESULT 19
US-10-204-029-7
; Sequence 7, Application US/10204029
; Publication No. US20050261487A1
; GENERAL INFORMATION:
; APPLICANT: Cully, Doris F.
; APPLICANT: Priest, Birgit
; APPLICANT: Yuan, Jeffrey
; APPLICANT: Zheng, Yingcong
; TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND-GATED ION
; TITLE OF INVENTION: CHANNELS FROM DROSOPHILA MELANOGASTER
; FILE REFERENCE: 20615P
; CURRENT APPLICATION NUMBER: US/10/204,029
; CURRENT FILING DATE: 2002-08-15
```

```
; PRIOR APPLICATION NUMBER: PCT/US01/06096
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/186645
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-204-029-7

Query Match 73.5%; Score 25; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VFFAQ 7
   ||||
Db 78 VFFAQ 82

RESULT 20
US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930

Query Match 73.5%; Score 25; DB 6; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFF 5
   ||||
Db 477 KLVFF 481

RESULT 21
US-10-467-962B-49
; Sequence 49, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 49
; LENGTH: 721
; TYPE: PRT
```

```

; ORGANISM: Arabidopsis thaliana
US-10-467-962B-49

Query Match      73.5%; Score 25; DB 6; Length 721;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVFFAQ 7
   |||||
Db 286 LVFFAQ 290

RESULT 22
US-11-000-463-765
; Sequence 765, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radjoe T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 765
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-765

Query Match      70.6%; Score 24; DB 7; Length 71;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 LVFFAQ 7
   |||||
Db 44 LVFFLQ 49

RESULT 23
US-09-940-308-3
; Sequence 3, Application US/09940308
; Publication No. US20040092437A1
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Retoprotein as
; FILE REFERENCE: an Immunosuppressive Agent
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308

; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-940-308-3

Query Match      70.6%; Score 24; DB 5; Length 197;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVFFAQ 7
   |||||
Db 30 LVFFAQ 34

RESULT 24
US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

Query Match      70.6%; Score 24; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFFA 6
   |||||
Db 19 LVFFFA 23

RESULT 25
US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.

```



```
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match          70.6%; Score 24; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFFA 6
Db      166 LVFFFA 170

RESULT 26
US-10-467-657-290
; Sequence 290, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 290
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-290

Query Match          70.6%; Score 24; DB 6; Length 221;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFFA 6
Db      156 LVFFFA 160

RESULT 29
US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

Query Match          70.6%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFFA 6
Db      156 LVFFFA 160

RESULT 29
```

```
QY      2 LVFFFAQ 7
Db      41 LIFFFAR 46

RESULT 27
US-10-467-657-5750
; Sequence 5750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5750
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5750

Query Match          70.6%; Score 24; DB 6; Length 221;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFFAQ 7
Db      41 LIFFFAR 46

RESULT 28
US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

Query Match          70.6%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFFA 6
Db      156 LVFFFA 160

RESULT 29
```

```
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match      70.6%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFPA 6
Db      156 LVFFPA 160

RESULT 30
US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US2005025511A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match      70.6%; Score 24; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFPA 6
Db      166 LVFFPA 170

RESULT 31
US-10-467-657-3128
; Sequence 3128, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

US-10-467-657-3128
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3128
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3128

Query Match      70.6%; Score 24; DB 6; Length 252;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KLVFFPA 7
Db      202 KLVFFPA 208

RESULT 32
US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19

Query Match      70.6%; Score 24; DB 6; Length 338;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFP 5
Db      76 KLVFFP 80

RESULT 33
US-10-131-826A-376
; Sequence 376, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
```

```
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match          70.6%; Score 24; DB 6; Length 344;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFF 5
        |||||
Db       279 KLIFP 283

RESULT 34
US-09-940-308-6
; Sequence 6, Application US/09940308
; Publication No. US20040092437A1
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-940-308-6

Query Match          70.6%; Score 24; DB 5; Length 389;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 VFPPA 7
```

```
Db       30 IFFAQ 34
        :|||||
        30 IFFAQ 34

RESULT 35
US-11-082-389-198
; Sequence 198, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 198
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-198

Query Match          70.6%; Score 24; DB 7; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFA 6
        |||||
Db       401 LVFFA 405

RESULT 36
US-10-995-561-959
; Sequence 959, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 959
; LENGTH: 481
```

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-959

Query Match 70.6%; Score 24; DB 6; Length 481;  
Best Local Similarity 66.7%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
Db 275 KLVFFA 280

RESULT 37  
US-10-873-528-120  
; Sequence 120, Application US/10873528  
; Publication No. US20050276814A1  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129W0  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; PRIOR FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 120  
; LENGTH: 505  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-120

Query Match 70.6%; Score 24; DB 6; Length 505;  
Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VFFAQ 7  
Db 241 IFFAQ 245

RESULT 38  
US-10-770-726-87  
; Sequence 87, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 87  
; LENGTH: 547  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-770-726-87

Query Match 70.6%; Score 24; DB 6; Length 547;  
Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 537 KLIGFAQ 543

RESULT 39  
US-11-078-189-19  
; Sequence 19, Application US/11078189  
; Publication No. US20050277167A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachinger, Hans Peter  
; APPLICANT: Vranka, Janice  
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES  
; FILE REFERENCE: 08062-020001 US/11/078,189  
; CURRENT APPLICATION NUMBER: US/11/078,189  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: US 60/552,409  
; PRIOR FILING DATE: 2004-03-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 558  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
US-11-078-189-19

Query Match 70.6%; Score 24; DB 7; Length 558;  
Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 278 ELLFFAE 284

RESULT 40  
US-10-821-234-1137  
; Sequence 1137, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: Pt\_SEQ\_genes Version 1.0  
; SEQ ID NO 1137  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1137

Query Match 70.6%; Score 24; DB 6; Length 588;  
Best Local Similarity 71.4%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 578 KLIGFAQ 584

RESULT 41  
US-09-940-308-2  
; Sequence 2, Application US/09940308  
; Publication No. US20040092437A1

```
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; FILE OF INVENTION: an Immunosuppressive Agent
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-940-308-2
```

```
Query Match          70.6%; Score 24; DB 5; Length 590;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 VFFAQ 7
Db      30 IFFAQ 34
```

```
RESULT 42
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125
```

```
Query Match          70.6%; Score 24; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
Db      531 KAVFFA 536
```

RESULT 43

```
US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917
```

```
Query Match          70.6%; Score 24; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
Db      579 KAVFFA 584
```

```
RESULT 44
US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436
```

```
Query Match          67.6%; Score 23; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 41;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFF 5
Db      36 KLVFF 40
```

```
RESULT 45
US-10-467-657-5448
; Sequence 5448, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
```

```
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5448
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5448
```

```
Query Match 67.6%; Score 23; DB 6; Length 57;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 LVFFAQ 7
Db 51 LVFYAE 56
```

```
RESULT 46
US-10-689-742-206
; Sequence 206, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Ragie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-206
```

```
Query Match 67.6%; Score 23; DB 6; Length 104;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 LVFFAQ 7
Db 21 LMFFSQ 26
```

```
RESULT 47
US-10-793-626-370
; Sequence 370, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 370
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-370
```

```
Query Match 67.6%; Score 23; DB 6; Length 143;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 2 LVFFAQ 7
Db 101 LVFLAQ 106
```

```
RESULT 48
US-10-467-657-2420
; Sequence 2420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2420
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2420
```

```
Query Match 67.6%; Score 23; DB 6; Length 155;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 LVFFAQ 7
Db 18 MVFFAK 23
```

```
RESULT 49
US-10-467-657-3978
; Sequence 3978, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3978
; LENGTH: 194
; TYPE: PRT
```

; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3978

Query Match 67.6%; Score 23; DB 6; Length 194;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
; : |||||  
Db 13 REAFFAQ 19

RESULT 50

US-11-019-955-24  
; Sequence 24, Application US/11019955  
; Publication No. US20050282763A1  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS  
; FILE REFERENCE: 08191-022001  
; CURRENT APPLICATION NUMBER: US/11/019,955  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US/10/074,956  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/268,175  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-019-955-24

Query Match 67.6%; Score 23; DB 7; Length 195;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
: : |||||  
Db 153 ELLFFAK 159

RESULT 51

US-10-821-234-1372  
; Sequence 1372, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1372  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1372

Query Match 67.6%; Score 23; DB 6; Length 211;  
Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| : |||||  
Db 33 KTVYFAE 39

RESULT 52

US-10-467-657-8102  
; Sequence 8102, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8102  
; LENGTH: 216  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8102

Query Match 67.6%; Score 23; DB 6; Length 216;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFA 6  
| : |||||  
Db 18 LVFFA 22

RESULT 53

US-11-112-882-88  
; Sequence 88, Application US/11112882  
; Publication No. US20050273885A1  
; GENERAL INFORMATION:  
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation  
; TITLE OF INVENTION: Synthesis of Long-Chain Polyunsaturated Fatty Acids in Recombinant  
; FILE REFERENCE: 503244  
; CURRENT APPLICATION NUMBER: US/11/112,882  
; CURRENT FILING DATE: 2005-04-22  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Melosira sp.  
US-11-112-882-88

Query Match 67.6%; Score 23; DB 7; Length 223;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LVFFAQ 7  
| : |||||  
Db 199 LVLFAQ 204

RESULT 54

US-11-019-955-27  
; Sequence 27, Application US/11019955  
; Publication No. US20050282763A1  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS  
; FILE REFERENCE: 08191-022001  
; CURRENT APPLICATION NUMBER: US/11/019,955  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US/10/074,956

```
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,175
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-955-27

Query Match      67.6%; Score 23; DB 7; Length 241;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
DB      177 ELLFFAK 183

RESULT 55
US-10-793-626-2360
; Sequence 2360, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2360
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2360

Query Match      67.6%; Score 23; DB 6; Length 258;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFAQ 7
DB      158 LVFFSE 163

RESULT 56
US-11-019-955-28
; Sequence 28, Application US/11019955
; Publication No. US20050282763A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
; FILE REFERENCE: 08191-022001
; CURRENT APPLICATION NUMBER: US/11/019,955
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US/10/074,956
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,175
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-955-28

Query Match      67.6%; Score 23; DB 7; Length 268;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
DB      177 ELLFFAK 183

RESULT 57
US-10-467-657-330
; Sequence 330, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 330
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-330

Query Match      67.6%; Score 23; DB 6; Length 269;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFF 5
DB      11 KLVFF 15

RESULT 58
US-10-632-150-46
; Sequence 46, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chlaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-46

Query Match      67.6%; Score 23; DB 6; Length 272;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
```



```
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 211 KLMYFA 216

RESULT 59
US-11-073-457-46
; Sequence 46, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; PRIOR FILING DATE: 2005-03-04
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-46

Query Match 67.6%; Score 23; DB 7; Length 272;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 211 KLMYFA 216

RESULT 60
US-11-073-460-46
; Sequence 46, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; PRIOR FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-46

Query Match 67.6%; Score 23; DB 7; Length 272;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 211 KLMYFA 216

RESULT 61
US-10-821-234-1105
```

```
; Sequence 1105, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1105
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1105

Query Match 67.6%; Score 23; DB 6; Length 370;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 115 RLLFFA 120

RESULT 62
US-10-793-626-1056
; Sequence 1056, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1056

Query Match 67.6%; Score 23; DB 6; Length 400;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFF 5
Db 7 KLVFF 11

RESULT 63
US-10-467-657-6352
; Sequence 6352, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

```
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 6352
/ LENGTH: 463
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6352

Query Match      67.6%; Score 23; DB 6; Length 463;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFA 6
Db      369 LIFFA 373

RESULT 64
US-10-467-657-7604
/ Sequence 7604, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 7604
/ LENGTH: 463
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7604

Query Match      67.6%; Score 23; DB 6; Length 463;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFA 6
Db      369 LIFFA 373

RESULT 65
US-10-995-561-1030
/ Sequence 1030, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1030
/ LENGTH: 522
/ TYPE: PRT
/ ORGANISM: Homo sapiens

US-10-995-561-1030

Query Match      67.6%; Score 23; DB 6; Length 522;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFA 6
Db      353 LIFFA 357

RESULT 66
US-11-090-439-58
/ Sequence 58, Application US/11090439
/ Publication No. US20050266442A1
/ GENERAL INFORMATION:
/ APPLICANT: Squillace, Rachel P.
/ APPLICANT: Weiner, Michael P.
/ TITLE OF INVENTION: Immortalized Human Tuberos Sclerosis Null
/ TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
/ FILE REFERENCE: 24318-502
/ CURRENT APPLICATION NUMBER: US/11/090,439
/ CURRENT FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: 60/556,344
/ PRIOR FILING DATE: 2004-03-25
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 58
/ LENGTH: 582
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-090-439-58

Query Match      67.6%; Score 23; DB 7; Length 582;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFAQ 7
Db      178 MIFFAE 183

RESULT 67
US-10-967-457-18
/ Sequence 18, Application US/10967457
/ Publication No. US20050244931A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.
/ TITLE OF INVENTION: Albumin Fusion Proteins
/ FILE REFERENCE: PF545PCT
/ CURRENT APPLICATION NUMBER: US/10/967,457
/ CURRENT FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: US/09/833,041
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/229,358
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: 60/256,931
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/199,384
/ PRIOR FILING DATE: 2000-04-25
/ NUMBER OF SEQ ID NOS: 90
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 18
/ LENGTH: 585
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-967-457-18

Query Match      67.6%; Score 23; DB 6; Length 585;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
```

```
; :|:|:|:
Db      153 ELLFFAK 159

RESULT 68
US-10-939-890-500
; Sequence 500, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617-70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 500
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo sapiens
US-10-939-890-500

Query Match      67.6%; Score 23; DB 6; Length 585;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      153 ELLFFAK 159

RESULT 69
US-11-078-663-18
; Sequence 18, Application US/11078663
; Publication No. US20050266532A1
; GENERAL INFORMATION:
; APPLICANT: Rozen, Craig A.
; APPLICANT: Sadeghi, Homa
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF543
; CURRENT APPLICATION NUMBER: US/11/078,663
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US/09/833,117
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-078-663-18

Query Match      67.6%; Score 23; DB 7; Length 585;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      153 ELLFFAK 159

RESULT 70
US-11-078-914-18
; Sequence 18, Application US/11078914
; Publication No. US20050268533A1
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J.
; APPLICANT: Sleep, Darrell
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homa
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF542
; CURRENT APPLICATION NUMBER: US/11/078,914
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US/09/832,501
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-078-914-18

Query Match      67.6%; Score 23; DB 7; Length 585;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      153 ELLFFAK 159

RESULT 71
US-10-995-561-940
; Sequence 940, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: PF543
; CURRENT APPLICATION NUMBER: US/11/078,663
```

```
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 940
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-940

Query Match      67.6%; Score 23; DB 6; Length 615;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFA 6
Db      502 LIFFA 506

RESULT 72
US-10-995-561-943
; Sequence 943, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 943
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-943

Query Match      67.6%; Score 23; DB 6; Length 662;
Best Local Similarity 80.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFA 6
Db      547 LIFFA 551

RESULT 73
US-10-939-890-501
; Sequence 501, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.

; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 501
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HSA-Linked Dimer
US-10-939-890-501

Query Match      67.6%; Score 23; DB 6; Length 690;
Best Local Similarity 57.1%; Pred. No. 5.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      205 ELLFFAK 211

RESULT 74
US-10-995-561-942
; Sequence 942, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 942
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-942

Query Match      67.6%; Score 23; DB 6; Length 702;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFA 6
Db      587 LIFFA 591

RESULT 75
US-10-995-561-941
; Sequence 941, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
```

```
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 941
; LENGTH: 754
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)---(754)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-995-561-941

Query Match      67.6%; Score 23; DB 6; Length 754;
Best Local Similarity 80.0%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFA 6
Db      587 LVFFA 591
```

Search completed: December 29, 2005, 18:50:22  
Job time : 4.83871 secs

1

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 77.3387 Seconds  
(without alignments)  
37.818 Million cell updates/sec

Title: US-10-009-122-18  
Perfect score: 34  
Sequence: 1 KLVFFAQ 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Published\_applications AA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	3	US-09-867-847-27
2	34	100.0	7	3	US-09-867-847-28
3	34	100.0	7	3	US-09-915-092-17
4	34	100.0	7	3	US-09-915-092-18
5	34	100.0	7	3	US-09-747-408-18
6	34	100.0	7	3	US-09-747-408-19
7	34	100.0	7	5	US-10-728-028-17
8	34	100.0	7	5	US-10-728-028-18
9	34	100.0	10	3	US-09-867-847-29
10	34	100.0	10	3	US-09-915-092-19
11	34	100.0	10	5	US-10-728-028-19
12	34	100.0	35	6	US-11-066-697-979
13	34	100.0	35	6	US-11-066-697-1006
14	34	100.0	42	4	US-10-217-584-8
15	34	100.0	42	5	US-10-853-593-1
16	34	100.0	42	5	US-10-969-898-1
17	34	100.0	100	4	US-10-275-025-7
18	34	100.0	108	4	US-10-275-025-15
19	31	91.2	7	5	US-10-825-558-25
20	31	91.2	7	5	US-10-825-558-26
21	31	91.2	8	4	US-10-235-483-1
22	31	91.2	8	4	US-10-281-092-42
23	31	91.2	8	5	US-10-810-881A-125
24	31	91.2	8	5	US-10-817-979-73
25	31	91.2	9	3	US-09-899-815-2
26	31	91.2	9	4	US-10-235-483-64
27	31	91.2	9	4	US-10-619-454-3
28	31	91.2	9	4	US-10-619-454-25
29	31	91.2	9	4	US-10-619-454-57
30	31	91.2	10	5	US-10-889-999-21
31	31	91.2	10	5	US-10-889-999-22
32	31	91.2	10	5	US-10-889-999-23
33	31	91.2	10	5	US-10-889-999-24
34	31	91.2	10	5	US-10-890-070-21
35	31	91.2	10	5	US-10-890-070-22
36	31	91.2	10	5	US-10-890-070-23
37	31	91.2	10	5	US-10-890-070-24
38	31	91.2	10	5	US-10-890-000-21
39	31	91.2	10	5	US-10-890-000-22
40	31	91.2	10	5	US-10-890-000-23
41	31	91.2	10	5	US-10-890-000-24
42	31	91.2	10	5	US-10-823-463-21
43	31	91.2	10	5	US-10-823-463-22
44	31	91.2	10	5	US-10-823-463-23
45	31	91.2	10	5	US-10-823-463-24
46	31	91.2	10	5	US-10-822-968-21
47	31	91.2	10	5	US-10-822-968-22
48	31	91.2	10	5	US-10-822-968-23
49	31	91.2	10	5	US-10-822-968-24
50	31	91.2	10	5	US-10-777-792-21
51	31	91.2	10	5	US-10-777-792-22
52	31	91.2	10	5	US-10-777-792-23
53	31	91.2	10	5	US-10-777-792-24
54	31	91.2	10	5	US-10-890-071-21
55	31	91.2	10	5	US-10-890-071-22
56	31	91.2	10	5	US-10-890-071-23
57	31	91.2	10	5	US-10-890-024-21
58	31	91.2	10	5	US-10-890-024-22
59	31	91.2	10	5	US-10-890-024-23
60	31	91.2	10	5	US-10-890-024-24
61	31	91.2	10	5	US-10-828-926-21
62	31	91.2	10	5	US-10-828-926-22
63	31	91.2	10	5	US-10-828-926-23
64	31	91.2	10	5	US-10-828-926-24
65	31	91.2	10	5	US-10-558-757-21
66	31	91.2	10	5	US-10-558-757-22
67	31	91.2	10	5	US-10-558-757-23
68	31	91.2	10	5	US-10-558-757-24
69	31	91.2	10	5	US-09-888-842-9
70	31	91.2	10	5	US-10-235-483-14
71	31	91.2	10	5	US-10-237-673-20
72	31	91.2	10	5	US-10-464-117-13
73	31	91.2	10	5	US-10-772-230-9
74	31	91.2	10	5	US-10-772-230-25
75	31	91.2	10	5	US-10-810-881A-117
76	31	91.2	10	5	US-10-281-458-1
77	31	91.2	10	5	US-10-625-854-140
78	31	91.2	10	5	US-09-592-800-5
79	31	91.2	10	5	US-09-992-994-5
80	31	91.2	10	5	US-10-385-065-5
81	31	91.2	10	5	US-10-810-881A-114
82	31	91.2	10	5	US-10-505-313-2
83	31	91.2	10	5	US-10-625-854-128
84	31	91.2	10	5	US-10-625-854-141
85	31	91.2	10	5	US-10-625-854-142
86	31	91.2	10	5	US-09-972-475-14
87	31	91.2	10	5	US-09-972-475-15
88	31	91.2	10	5	US-10-235-483-56
89	31	91.2	10	5	US-10-235-483-57
90	31	91.2	10	5	US-10-235-483-58
91	31	91.2	10	5	US-10-235-483-59
92	31	91.2	10	5	US-10-235-483-60
93	31	91.2	10	5	US-10-235-483-61
94	31	91.2	10	5	US-10-235-483-62
95	31	91.2	10	5	US-10-235-483-63
96	31	91.2	10	5	US-10-235-483-64
97	31	91.2	10	5	US-10-235-483-65
98	31	91.2	10	5	US-10-463-729-14
99	31	91.2	10	5	US-10-625-854-116
100	31	91.2	10	5	US-10-625-854-129

101	31	91.2	15	5	US-10-625-854-142	Sequence 142, App	174	31	91.2	28	6	US-11-066-697-992	Sequence 992, App
102	31	91.2	16	5	US-10-625-854-104	Sequence 104, App	175	31	91.2	28	6	US-11-066-697-1003	Sequence 1003, App
103	31	91.2	16	5	US-10-625-854-117	Sequence 117, App	176	31	91.2	30	3	US-09-861-847-1	Sequence 1, Appli
104	31	91.2	16	5	US-10-625-854-130	Sequence 130, App	177	31	91.2	30	4	US-10-301-488A-1	Sequence 1, Appli
105	31	91.2	16	5	US-10-625-854-143	Sequence 143, App	178	31	91.2	30	4	US-10-666-423-1	Sequence 1, Appli
106	31	91.2	17	3	US-09-992-800-3	Sequence 3, Appli	179	31	91.2	30	4	US-10-617-876-9	Sequence 9, Appli
107	31	91.2	17	3	US-09-992-994-3	Sequence 3, Appli	180	31	91.2	30	4	US-10-619-454-24	Sequence 24, Appli
108	31	91.2	17	3	US-09-998-491-8	Sequence 8, Appli	181	31	91.2	30	4	US-10-301-448-1	Sequence 1, Appli
109	31	91.2	17	4	US-10-385-065-3	Sequence 3, Appli	182	31	91.2	30	5	US-10-775-562-5	Sequence 5, Appli
110	31	91.2	17	4	US-10-475-281-8	Sequence 8, Appli	183	31	91.2	32	4	US-10-732-862A-99	Sequence 99, Appli
111	31	91.2	17	4	US-10-810-915-3	Sequence 3, Appli	184	31	91.2	33	3	US-09-930-915A-295	Sequence 295, App
112	31	91.2	17	5	US-10-684-346-24	Sequence 24, Appli	185	31	91.2	33	4	US-10-082-014-84	Sequence 84, Appli
113	31	91.2	17	5	US-10-997-078-46	Sequence 46, Appli	186	31	91.2	33	4	US-10-372-076-85	Sequence 85, Appli
114	31	91.2	17	5	US-10-997-700-19	Sequence 19, Appli	187	31	91.2	33	4	US-10-732-862A-98	Sequence 98, Appli
115	31	91.2	17	6	US-11-063-350-3	Sequence 3, Appli	188	31	91.2	33	4	US-10-806-006-295	Sequence 295, App
116	31	91.2	17	6	US-11-066-697-950	Sequence 950, App	189	31	91.2	33	4	US-10-677-074-85	Sequence 85, Appli
117	31	91.2	17	6	US-11-066-697-993	Sequence 983, App	190	31	91.2	33	4	US-10-805-913-295	Sequence 295, App
118	31	91.2	19	3	US-09-825-242-5	Sequence 5, Appli	191	31	91.2	35	3	US-09-867-847-3	Sequence 3, Appli
119	31	91.2	19	4	US-10-429-216-5	Sequence 5, Appli	192	31	91.2	35	3	US-09-972-475-16	Sequence 16, Appli
120	31	91.2	19	4	US-10-816-022-5	Sequence 5, Appli	193	31	91.2	35	4	US-10-463-729-16	Sequence 16, Appli
121	31	91.2	19	4	US-10-816-529-5	Sequence 5, Appli	194	31	91.2	35	5	US-10-825-958-3	Sequence 3, Appli
122	31	91.2	19	4	US-10-815-353-5	Sequence 5, Appli	195	31	91.2	36	3	US-09-861-847-6	Sequence 6, Appli
123	31	91.2	19	4	US-10-815-391-5	Sequence 5, Appli	196	31	91.2	36	3	US-09-861-847-11	Sequence 11, Appli
124	31	91.2	19	5	US-10-828-548-5	Sequence 5, Appli	197	31	91.2	36	4	US-10-301-488A-6	Sequence 6, Appli
125	31	91.2	19	5	US-10-816-380-5	Sequence 5, Appli	198	31	91.2	36	4	US-10-301-488A-11	Sequence 11, Appli
126	31	91.2	19	5	US-10-889-999-75	Sequence 75, Appli	199	31	91.2	36	4	US-10-666-423-6	Sequence 6, Appli
127	31	91.2	19	5	US-10-890-070-75	Sequence 75, Appli	200	31	91.2	36	4	US-10-666-423-11	Sequence 11, Appli
128	31	91.2	19	5	US-10-890-000-75	Sequence 75, Appli	201	31	91.2	36	4	US-10-301-448-6	Sequence 6, Appli
129	31	91.2	19	5	US-10-788-666-5	Sequence 5, Appli	202	31	91.2	36	4	US-10-301-448-11	Sequence 11, Appli
130	31	91.2	19	5	US-10-923-471-5	Sequence 5, Appli	203	31	91.2	36	4	US-10-732-862A-436	Sequence 436, App
131	31	91.2	19	5	US-10-823-463-75	Sequence 75, Appli	204	31	91.2	38	6	US-11-066-697-975	Sequence 975, App
132	31	91.2	19	5	US-10-923-469-5	Sequence 5, Appli	205	31	91.2	38	6	US-11-066-697-1002	Sequence 1002, Ap
133	31	91.2	19	5	US-10-933-559-5	Sequence 5, Appli	206	31	91.2	39	4	US-10-051-496-5	Sequence 5, Appli
134	31	91.2	19	5	US-10-815-404-5	Sequence 5, Appli	207	31	91.2	39	4	US-10-190-548A-5	Sequence 5, Appli
135	31	91.2	19	5	US-10-934-609-5	Sequence 5, Appli	208	31	91.2	40	3	US-09-861-847-7	Sequence 7, Appli
136	31	91.2	19	5	US-10-923-474-5	Sequence 5, Appli	209	31	91.2	40	3	US-09-861-847-8	Sequence 8, Appli
137	31	91.2	19	5	US-10-884-892-5	Sequence 5, Appli	210	31	91.2	40	3	US-09-867-842-2	Sequence 2, Appli
138	31	91.2	19	5	US-10-822-968-75	Sequence 75, Appli	211	31	91.2	40	3	US-09-988-842-3	Sequence 3, Appli
139	31	91.2	19	5	US-10-777-792-75	Sequence 75, Appli	212	31	91.2	40	3	US-09-851-071-3	Sequence 3, Appli
140	31	91.2	19	5	US-10-890-071-75	Sequence 75, Appli	213	31	91.2	40	3	US-09-962-955C-36	Sequence 36, Appli
141	31	91.2	19	5	US-10-890-024-75	Sequence 75, Appli	214	31	91.2	40	3	US-09-792-079-12	Sequence 12, Appli
142	31	91.2	19	5	US-10-934-819-5	Sequence 5, Appli	215	31	91.2	40	4	US-10-007-779A-1	Sequence 1, Appli
143	31	91.2	19	5	US-10-923-267-5	Sequence 5, Appli	216	31	91.2	40	4	US-10-051-496-4	Sequence 4, Appli
144	31	91.2	19	6	US-11-058-757-75	Sequence 75, Appli	217	31	91.2	40	4	US-10-217-580-3	Sequence 3, Appli
145	31	91.2	19	6	US-11-058-757-75	Sequence 75, Appli	218	31	91.2	40	4	US-10-169-580-1	Sequence 1, Appli
146	31	91.2	20	3	US-11-108-102-5	Sequence 5, Appli	219	31	91.2	40	4	US-10-143-534-3	Sequence 3, Appli
147	31	91.2	20	3	US-09-908-943A-75	Sequence 25, Appli	220	31	91.2	40	4	US-10-190-548A-4	Sequence 4, Appli
148	31	91.2	20	5	US-10-801-487-25	Sequence 25, Appli	221	31	91.2	40	4	US-10-051-663-3	Sequence 3, Appli
149	31	91.2	20	5	US-10-801-938-25	Sequence 25, Appli	222	31	91.2	40	4	US-10-151-614-1	Sequence 1, Appli
150	31	91.2	20	5	US-10-801-509-25	Sequence 25, Appli	223	31	91.2	40	4	US-10-159-279-12	Sequence 12, Appli
151	31	91.2	20	5	US-10-801-486-25	Sequence 25, Appli	224	31	91.2	40	4	US-10-301-488A-7	Sequence 7, Appli
152	31	91.2	20	5	US-10-801-486-25	Sequence 25, Appli	225	31	91.2	40	4	US-10-301-488A-8	Sequence 8, Appli
153	31	91.2	24	5	US-10-801-493-25	Sequence 5, Appli	226	31	91.2	40	4	US-10-455-218-1	Sequence 1, Appli
154	31	91.2	24	5	US-10-728-246-5	Sequence 5, Appli	227	31	91.2	40	4	US-10-366-125-27	Sequence 27, Appli
155	31	91.2	26	3	US-09-792-079-11	Sequence 11, Appli	228	31	91.2	40	4	US-10-337-261-1	Sequence 1, Appli
156	31	91.2	26	4	US-10-159-279-11	Sequence 11, Appli	229	31	91.2	40	4	US-10-666-423-7	Sequence 7, Appli
157	31	91.2	28	3	US-09-867-847-4	Sequence 4, Appli	230	31	91.2	40	4	US-10-666-423-8	Sequence 8, Appli
158	31	91.2	28	3	US-09-865-294-66	Sequence 66, Appli	231	31	91.2	40	4	US-10-301-448-7	Sequence 7, Appli
159	31	91.2	28	3	US-09-792-079-5	Sequence 5, Appli	232	31	91.2	40	4	US-10-301-448-8	Sequence 8, Appli
160	31	91.2	28	4	US-10-159-279-5	Sequence 5, Appli	233	31	91.2	40	4	US-10-683-815-1	Sequence 1, Appli
161	31	91.2	28	4	US-10-363-082-2	Sequence 2, Appli	234	31	91.2	40	4	US-10-683-815-14	Sequence 14, Appli
162	31	91.2	28	4	US-10-433-385-7	Sequence 7, Appli	235	31	91.2	40	4	US-10-683-815-15	Sequence 15, Appli
163	31	91.2	28	4	US-10-390-472-4	Sequence 4, Appli	236	31	91.2	40	4	US-10-683-815-16	Sequence 16, Appli
164	31	91.2	28	4	US-10-741-205-36	Sequence 36, Appli	237	31	91.2	40	4	US-10-683-815-17	Sequence 17, Appli
165	31	91.2	28	4	US-10-416-262B-7	Sequence 7, Appli	238	31	91.2	40	4	US-10-683-815-18	Sequence 18, Appli
166	31	91.2	28	4	US-10-478-308-4	Sequence 4, Appli	239	31	91.2	40	4	US-10-810-919-1	Sequence 1, Appli
167	31	91.2	28	4	US-10-478-307-4	Sequence 4, Appli	240	31	91.2	40	5	US-10-864-107-1	Sequence 1, Appli
168	31	91.2	28	5	US-10-861-614-66	Sequence 66, Appli	241	31	91.2	40	5	US-10-485-310-18	Sequence 18, Appli
169	31	91.2	28	5	US-10-825-958-4	Sequence 4, Appli	242	31	91.2	40	5	US-10-481-387-1	Sequence 1, Appli
170	31	91.2	28	6	US-11-091-309-3	Sequence 3, Appli	243	31	91.2	40	5	US-10-481-954-5	Sequence 5, Appli
171	31	91.2	28	6	US-11-066-697-959	Sequence 959, App	244	31	91.2	40	5	US-10-698-259A-1	Sequence 1, Appli
172	31	91.2	28	6	US-11-066-697-965	Sequence 965, App	245	31	91.2	40	5	US-10-884-729-1	Sequence 1, Appli
173	31	91.2	28	6	US-11-066-697-976	Sequence 976, App	246	31	91.2	40	5	US-10-728-246-4	Sequence 4, Appli

```
247 31 91.2 40 5 US-10-772-230-3 Sequence 3, Appli
248 31 91.2 40 5 US-10-933-206-36 Sequence 36, Appl
249 31 91.2 40 5 US-10-825-958-2 Sequence 2, Appli
250 31 91.2 40 5 US-10-775-562-2 Sequence 2, Appli
251 31 91.2 40 5 US-10-296-168-1 Sequence 1, Appli
252 31 91.2 40 6 US-11-004-053-36 Sequence 36, Appl
253 31 91.2 40 6 US-11-007-643-36 Sequence 36, Appl
254 31 91.2 40 6 US-11-007-644-36 Sequence 36, Appl
255 31 91.2 40 6 US-11-007-669-36 Sequence 36, Appl
256 31 91.2 40 6 US-11-066-697-956 Sequence 956, App
257 31 91.2 40 6 US-11-066-697-962 Sequence 962, App
258 31 91.2 40 6 US-11-066-697-968 Sequence 968, App
259 31 91.2 40 6 US-11-066-697-978 Sequence 978, App
260 31 91.2 40 6 US-11-066-697-989 Sequence 989, App
261 31 91.2 40 6 US-11-066-697-995 Sequence 995, App
262 31 91.2 40 6 US-11-066-697-1005 Sequence 1005, App
263 31 91.2 41 4 US-10-051-496-3 Sequence 3, Appli
264 31 91.2 41 4 US-10-190-548A-3 Sequence 3, Appli
265 31 91.2 41 4 US-10-683-815-13 Sequence 13, Appl
266 31 91.2 42 2 US-08-922-930-2 Sequence 2, Appli
267 31 91.2 42 2 US-08-923-055-2 Sequence 2, Appli
268 31 91.2 42 3 US-09-867-847-1 Sequence 1, Appli
269 31 91.2 42 3 US-09-956-625-26 Sequence 26, Appl
270 31 91.2 42 3 US-09-731-460-1 Sequence 1, Appli
271 31 91.2 42 3 US-09-962-955C-37 Sequence 37, Appl
272 31 91.2 42 3 US-09-848-616-174 Sequence 174, App
273 31 91.2 42 3 US-09-865-294-65 Sequence 65, Appl
274 31 91.2 42 3 US-09-792-079-13 Sequence 13, Appl
275 31 91.2 42 3 US-09-825-242-1 Sequence 1, Appli
276 31 91.2 42 3 US-09-930-915A-293 Sequence 293, App
277 31 91.2 42 4 US-10-051-496-2 Sequence 2, Appli
278 31 91.2 42 4 US-10-082-804-7 Sequence 7, Appli
279 31 91.2 42 4 US-10-217-584-2 Sequence 2, Appli
280 31 91.2 42 4 US-10-217-584-11 Sequence 11, Appl
281 31 91.2 42 4 US-10-169-580-2 Sequence 2, Appli
282 31 91.2 42 4 US-10-278-181-1 Sequence 1, Appli
283 31 91.2 42 4 US-10-143-534-2 Sequence 2, Appli
284 31 91.2 42 4 US-10-190-548A-1 Sequence 1, Appli
285 31 91.2 42 4 US-10-051-663-2 Sequence 2, Appli
286 31 91.2 42 4 US-10-159-279-13 Sequence 13, Appl
287 31 91.2 42 4 US-10-318-302-4 Sequence 4, Appli
288 31 91.2 42 4 US-10-050-902-220 Sequence 220, App
289 31 91.2 42 4 US-10-050-998-220 Sequence 220, App
290 31 91.2 42 4 US-10-082-014-81 Sequence 81, Appl
291 31 91.2 42 4 US-10-372-076-82 Sequence 82, Appl
292 31 91.2 42 4 US-10-455-218-2 Sequence 2, Appli
293 31 91.2 42 4 US-10-231-298B-15 Sequence 15, Appl
294 31 91.2 42 4 US-10-231-470C-15 Sequence 15, Appl
295 31 91.2 42 4 US-10-231-063C-15 Sequence 15, Appl
296 31 91.2 42 4 US-10-366-125-28 Sequence 28, Appl
297 31 91.2 42 4 US-10-411-544-2 Sequence 2, Appli
298 31 91.2 42 4 US-10-231-213D-15 Sequence 15, Appl
299 31 91.2 42 4 US-10-231-114C-15 Sequence 15, Appl
300 31 91.2 42 4 US-10-337-261-2 Sequence 2, Appli

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match 100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 1 KLVFFAQ 7

RESULT 2
US-09-867-847-28
; Sequence 28, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-867-847-28

Query Match 100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 1 KLVFFAQ 7

RESULT 3
US-09-915-092-17
; Sequence 17, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
```

## ALIGNMENTS

```
RESULT 1
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
```



```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-17
```

```
Query Match      100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFAQ 7
      |||||
Db      1 KLVFFAQ 7
```

```
RESULT 4
US-09-915-092-18
; Sequence 18, Application US/09915092
; Publication No. US2002011517A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-18
```

```
Query Match      100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFAQ 7
      |||||
Db      1 KLVFFAQ 7
```

```
RESULT 5
US-09-747-408-18
; Sequence 18, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18
```

```
Query Match      100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFAQ 7
      |||||
Db      1 KLVFFAQ 7
```

```
RESULT 6
US-09-747-408-19
; Sequence 19, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19
```

```
Query Match      100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFAQ 7
      |||||
Db      1 KLVFFAQ 7
```

```
RESULT 7
US-10-728-028-17
; Sequence 17, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-17

Query Match      100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 1 KLVFFPAQ 7

RESULT 8
US-10-728-028-18
; Sequence 18, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: US THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-18

Query Match      100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 1 KLVFFPAQ 7

RESULT 9
US-09-867-847-29
; Sequence 29, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 29

; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-19

Query Match      100.0%; Score 34; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 4 KLVFFPAQ 10

RESULT 10
US-09-915-092-19
; Sequence 19, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneaault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: US THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Synthetic Construct
US-09-915-092-19

Query Match      100.0%; Score 34; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 4 KLVFFPAQ 10

RESULT 11
US-10-728-028-19
; Sequence 19, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: US THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
```

```

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-19
Query Match      100.0%; Score 34; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      4 KLVFFAQ 10

RESULT 12
US-11-066-697-979
; Sequence 979, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 979
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-979
Query Match      100.0%; Score 34; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      11 KLVFFAQ 17

RESULT 13
US-11-066-697-1006
; Sequence 1006, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697

```

```

; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1006
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1006
Query Match      100.0%; Score 34; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      11 KLVFFAQ 17

RESULT 14
US-10-217-584-8
; Sequence 8, Application US/10217584
; Publication No. US20030077261A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Daniel
; APPLICANT: Mullan, Michael
; TITLE OF INVENTION: Modulation of Angiogenesis by A-Beta Peptides
; FILE REFERENCE: USF-T161XC1
; CURRENT APPLICATION NUMBER: US/10/217,584
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,656
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 22Q-A-beta 1-42 (Dutch) mutant
US-10-217-584-8
Query Match      100.0%; Score 34; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      16 KLVFFAQ 22

RESULT 15
US-10-853-593-1
; Sequence 1, Application US/10853593
; Publication No. US20040250302A1
; GENERAL INFORMATION:
; APPLICANT: Envivo Pharmaceuticals
; APPLICANT: Lowe, David
; APPLICANT: Cummings, Christopher
; APPLICANT: Koenig, Gerhard
; TITLE OF INVENTION: Transgenic Flies Expressing AB42Dutch
; FILE REFERENCE: 9000-2202
; CURRENT APPLICATION NUMBER: US/10/853,593
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 60/512,972

```

```
; PRIOR FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-853-593-1

Query Match      100.0%; Score 34; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 16 KLVFFPAQ 22

RESULT 16
US-10-969-898-1
; Sequence 1, Application US/10969898
; Publication No. US2005013242A1
; GENERAL INFORMATION:
; APPLICANT: EnVivo Pharmaceuticals
; APPLICANT: Lowe, David
; APPLICANT: Cummings, Christopher
; APPLICANT: Koenig, Gerhard
; TITLE OF INVENTION: Transgenic Flies Expressing AB42Dutch
; FILE REFERENCE: 9000-2202
; CURRENT APPLICATION NUMBER: US/10/969,898
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/512,972
; PRIOR FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-969-898-1

Query Match      100.0%; Score 34; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 16 KLVFFPAQ 22

RESULT 17
US-10-275-025-7
; Sequence 7, Application US/10275025
; Publication No. US20030215896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yueming
; APPLICANT: Huang, Qian
; APPLICANT: Gardell, Stephen J.
; TITLE OF INVENTION: GAMMA SECRETASE SUBSTRATES AND IN VITRO
; FILE REFERENCE: 20507P
; CURRENT APPLICATION NUMBER: US/10/275,025
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US01/13332
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/201,053
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-275-025-7

Query Match      100.0%; Score 34; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 17 KLVFFPAQ 23

RESULT 18
US-10-275-025-15
; Sequence 15, Application US/10275025
; Publication No. US20030215896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yueming
; APPLICANT: Xu, Min
; APPLICANT: Huang, Qian
; APPLICANT: Gardell, Stephen J.
; TITLE OF INVENTION: GAMMA SECRETASE SUBSTRATES AND IN VITRO
; FILE REFERENCE: 20507P
; CURRENT APPLICATION NUMBER: US/10/275,025
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US01/13332
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/201,053
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gamma-secretase substrate
US-10-275-025-15

Query Match      100.0%; Score 34; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 17 KLVFFPAQ 23

RESULT 19
US-10-825-958-25
; Sequence 25, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 7
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-25

Query Match          91.2%; Score 31; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
   |||||:
Db 1 KLVFFAE 7

RESULT 20
US-10-825-958-26
; Sequence 26, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangdi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (7)_
; OTHER INFORMATION: AMIDATION
US-10-825-958-26

Query Match          91.2%; Score 31; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
   |||||:
Db 1 KLVFFAE 7

RESULT 21
US-10-235-483-1
; Sequence 1, Application US/10235483
; Publication No. US20030087407A1
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; BAUMANN, Marc
; FRANGIONE, Bias
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIK
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
```

```
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-235-483-1

Query Match          91.2%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
   |||||:
Db 1 KLVFFAE 7

RESULT 22
US-10-281-092-42
; Sequence 42, Application US/10281092
; Publication No. US20040121947A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Arun K.
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Bilcer, Geoffrey
; APPLICANT: Chang, Wainpin
; APPLICANT: Hong, Lin
; APPLICANT: Koelsch, Gerald E.
; APPLICANT: Loy, Jeffrey A.
; APPLICANT: Turner, Robert T., III
; APPLICANT: Devasumadrum, Thippeswamy
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT BETA-SECRETASE
; FILE REFERENCE: 2932.1001-004
; CURRENT APPLICATION NUMBER: US/10/281,092
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/032,818
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: PCT US01/50826
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
```

```
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/335,952
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/333,545
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/348,464
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/348,615
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/390,804
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/397,557
; PRIOR FILING DATE: 2002-07-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-10-281-092-42

Query Match          91.2%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 23
US-10-810-881A-125
; Sequence 125, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Mercken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5021 NP
; CURRENT APPLICATION NUMBER: US/10/810,881A
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PEPTIDE
US-10-810-881A-125

Query Match          91.2%; Score 31; DB 5; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 24
US-10-817-979-73
; Sequence 73, Application US/10817979
```

```
; Publication No. US20050196398A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 29915/40065
; CURRENT APPLICATION NUMBER: US/10/817,979
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 09/668,314
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-817-979-73

Query Match          91.2%; Score 31; DB 5; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 25
US-09-899-815-2
; Sequence 2, Application US/09899815
; Patent No. US20020162129A1
; GENERAL INFORMATION:
; APPLICANT: LANNFELT, Lars
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: LANNFELT-1A
; CURRENT APPLICATION NUMBER: US/09/899,815
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,098
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: EP 00202387.7
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (16-24 of SEQ ID NO:1)
US-09-899-815-2

Query Match          91.2%; Score 31; DB 3; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7
```

RESULT 26  
US-10-235-483-64  
; Sequence 64, Application US/10235483  
; Publication No. US20030087407A1  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; BAUMANN, Marc  
; BAUMANN, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/235,483  
; FILING DATE: 06-Sep-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:  
US-10-235-483-64

Query Match 91.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 2 KLVFFAE 8

RESULT 27  
US-10-619-454-3  
; Sequence 3, Application US/10619454  
; Publication No. US20040091945A1  
; GENERAL INFORMATION:  
; APPLICANT: Mindset  
; APPLICANT: Fitzer Attas, Cheryl  
; APPLICANT: Chain, Daniel  
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A  
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED

; FILE REFERENCE: P-5202-US  
; CURRENT APPLICATION NUMBER: US/10/619,454  
; CURRENT FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: US 60/396,245  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 187  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: algorithm generated  
US-10-619-454-3

Query Match 91.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 1 KLVFFAE 7

RESULT 28  
US-10-619-454-25  
; Sequence 25, Application US/10619454  
; Publication No. US20040091945A1  
; GENERAL INFORMATION:  
; APPLICANT: Mindset  
; APPLICANT: Fitzer Attas, Cheryl  
; APPLICANT: Chain, Daniel  
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A  
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED  
; FILE REFERENCE: P-5202-US  
; CURRENT APPLICATION NUMBER: US/10/619,454  
; CURRENT FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: US 60/396,245  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 187  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 25  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: algorithm generated  
US-10-619-454-25

Query Match 91.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 1 KLVFFAE 7

RESULT 29  
US-10-619-454-57  
; Sequence 57, Application US/10619454  
; Publication No. US20040091945A1  
; GENERAL INFORMATION:  
; APPLICANT: Mindset  
; APPLICANT: Fitzer Attas, Cheryl  
; APPLICANT: Chain, Daniel  
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A  
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED  
; FILE REFERENCE: P-5202-US  
; CURRENT APPLICATION NUMBER: US/10/619,454  
; CURRENT FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: US 60/396,245  
; PRIOR FILING DATE: 2002-07-17

; NUMBER OF SEQ ID NOS: 187  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: algorithm generated  
; US-10-619-454-57

Query Match 91.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
Db 1 KLVFFAE 7

## RESULT 30

US-10-619-454-157

; Sequence 157, Application US/10619454

; Publication No. US20040091945A1

; GENERAL INFORMATION:

; APPLICANT: Mindset

; APPLICANT: Fitzer Attas, Cheryl

; APPLICANT: Chain, Daniel

; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES

; FILE REFERENCE: AD IN WHICH T-CELL EPITOPES ARE REDUCED

; CURRENT APPLICATION NUMBER: US/10/619,454

; PRIOR FILING DATE: 2003-07-16

; PRIOR APPLICATION NUMBER: US 60/396,245

; PRIOR FILING DATE: 2002-07-17

; NUMBER OF SEQ ID NOS: 187

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 157

; LENGTH: 9

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: algorithm generated

; US-10-619-454-157

Query Match 91.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
Db 1 KLVFFAE 7

## RESULT 31

US-10-889-999-21

; Sequence 21, Application US/10889999

; Publication No. US20040247590A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/889,999

; CURRENT FILING DATE: 2004-07-13

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 10

; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

; US-10-889-999-21

Query Match 91.2%; Score 31; DB 5; Length 10;

Best Local Similarity 85.7%; Pred. No. 4.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
Db 4 KLVFFAE 10

## RESULT 32

US-10-889-999-22

; Sequence 22, Application US/10889999

; Publication No. US20040247590A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/889,999

; CURRENT FILING DATE: 2004-07-13

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

; US-10-889-999-22

Query Match 91.2%; Score 31; DB 5; Length 10;

Best Local Similarity 85.7%; Pred. No. 4.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
Db 3 KLVFFAE 9

## RESULT 33

US-10-889-999-23

; Sequence 23, Application US/10889999

; Publication No. US20040247590A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/889,999

; CURRENT FILING DATE: 2004-07-13

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23



```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-889-999-23
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
    |||||:
DB 2 KLVFFAE 8
```

```
RESULT 34
US-10-889-999-24
; Sequence 24, Application US/10889999
; Publication No. US20040247590A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/889,999
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-889-999-24
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
    |||||:
DB 1 KLVFFAE 7
```

```
RESULT 35
US-10-890-070-21
; Sequence 21, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-070-21
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
    |||||:
DB 4 KLVFFAE 10
```

```
RESULT 36
US-10-890-070-22
; Sequence 22, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-070-22
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
    |||||:
DB 3 KLVFFAE 9
```

```
RESULT 37
US-10-890-070-23
; Sequence 23, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
```

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-10-890-070-23

Query Match 91.2%; Score 31; DB 5; Length 10;

Best Local Similarity 85.7%; Pred. No. 4.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 2 KLVFFAE 8

RESULT 38

US-10-890-070-24

; Sequence 24, Application US/10890070

; Publication No. US20040247591A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/890,070

; CURRENT FILING DATE: 2004-07-12

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-10-890-070-24

Query Match 91.2%; Score 31; DB 5; Length 10;

Best Local Similarity 85.7%; Pred. No. 4.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 1 KLVFFAE 7

RESULT 39

US-10-890-000-21

; Sequence 21, Application US/10890000

; Publication No. US20040265301A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/890,000

; CURRENT FILING DATE: 2004-07-12

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-10-890-000-21

Query Match 91.2%; Score 31; DB 5; Length 10;

Best Local Similarity 85.7%; Pred. No. 4.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 4 KLVFFAE 10

RESULT 40

US-10-890-000-22

; Sequence 22, Application US/10890000

; Publication No. US20040265301A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/890,000

; CURRENT FILING DATE: 2004-07-12

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-10-890-000-22

Query Match 91.2%; Score 31; DB 5; Length 10;

Best Local Similarity 85.7%; Pred. No. 4.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 3 KLVFFAE 9

RESULT 41

US-10-890-000-23

; Sequence 23, Application US/10890000

; Publication No. US20040265301A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/890,000

; CURRENT FILING DATE: 2004-07-12

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-000-23

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 2 KLVFFAE 8  
|||||:

## RESULT 42

US-10-890-000-24  
; Sequence 24, Application US/10890000  
; Publication No. US20040265301A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,000  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-000-24

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 1 KLVFFAE 7  
|||||:

## RESULT 43

US-10-823-463-21  
; Sequence 21, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015

; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-21

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 4 KLVFFAE 10  
|||||:

## RESULT 44

US-10-823-463-22  
; Sequence 22, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-22

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 3 KLVFFAE 9

## RESULT 45

US-10-823-463-23  
; Sequence 23, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-23

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 2 KLVFFAE 8

## RESULT 46

US-10-823-463-24  
; Sequence 24, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-24

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 1 KLVFFAE 7

## RESULT 47

US-10-822-968-21  
; Sequence 21, Application US/10822968  
; Publication No. US20050059591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/822,968  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-822-968-21

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 4 KLVFFAE 10

## RESULT 48

US-10-822-968-22  
; Sequence 22, Application US/10822968

```
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
US-10-822-968-22

Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 3 KLVFFAE 9

RESULT 49
US-10-822-968-23
; Sequence 23, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
US-10-822-968-23

Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 2 KLVFFAE 8

RESULT 50
US-10-822-968-24
; Sequence 24, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
US-10-822-968-24

Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 1 KLVFFAE 7

RESULT 51
US-10-777-792-21
; Sequence 21, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
```

; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-777-792-21

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||  
Db 4 KLVFFAE 10

RESULT 52  
US-10-777-792-22  
; Sequence 22, Application US/10777792  
; Publication No. US20050059802A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/777,792  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-777-792-22

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||  
Db 3 KLVFFAE 9

RESULT 53  
US-10-777-792-23  
; Sequence 23, Application US/10777792  
; Publication No. US20050059802A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/777,792  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-777-792-23

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||  
Db 2 KLVFFAE 8

RESULT 54  
US-10-777-792-24  
; Sequence 24, Application US/10777792  
; Publication No. US20050059802A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/777,792  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-777-792-24

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||  
Db 1 KLVFFAE 7

RESULT 55  
US-10-825-958-27  
; Sequence 27, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine

; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-10-825-958-27

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 4 KLVFFAE 10

RESULT 56  
US-10-890-071-21  
; Sequence 21, Application US/108900071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-21

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 4 KLVFFAE 10

RESULT 57  
US-10-890-071-22  
; Sequence 22, Application US/108900071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique

; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-22

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 3 KLVFFAE 9

RESULT 58  
US-10-890-071-23  
; Sequence 23, Application US/108900071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-23

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 2 KLVFFAE 8

RESULT 59  
US-10-890-071-24  
; Sequence 24, Application US/108900071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.

```
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-10-890-071-24
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
   |||||:
Db 1 KLVFFAE 7
```

## RESULT 60

```
US-10-890-024-21
; Sequence 21, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-10-890-024-21
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
   |||||:
Db 4 KLVFFAE 10
```

## RESULT 61

```
US-10-890-024-22
; Sequence 22, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-10-890-024-22
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
   |||||:
Db 3 KLVFFAE 9
```

## RESULT 62

```
US-10-890-024-23
; Sequence 23, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-10-890-024-23
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
   |||||:
Db 2 KLVFFAE 8
```

## RESULT 63

```
US-10-890-024-24
; Sequence 24, Application US/10890024
; Publication No. US20050158304A1
```



```
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-024-24
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFPAQ 7
Db      1 KLVFFFAE 7
```

```
RESULT 64
US-10-928-926-21
; Sequence 21, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-21
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
```

```
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
Db      4 KLVFFFAE 10
```

```
RESULT 65
US-10-928-926-22
; Sequence 22, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-22
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFPAQ 7
Db      3 KLVFFFAE 9
```

```
RESULT 66
US-10-928-926-23
; Sequence 23, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
```

; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-928-926-23

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
Db 2 KLVFFFAE 8  
|||||:

RESULT 67  
US-10-928-926-24  
; Sequence 24, Application US/10928926  
; Publication No. US20050196399A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/928,926  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US/09/724,961  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-928-926-24

Query Match 91.2%; Score 31; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
Db 1 KLVFFFAE 7  
|||||:

RESULT 68  
US-11-058-757-21  
; Sequence 21, Application US/11058757  
; Publication No. US20050142132A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/11/058,757  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-11-058-757-21

Query Match 91.2%; Score 31; DB 6; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
Db 4 KLVFFFAE 10  
|||||:

RESULT 69  
US-11-058-757-22  
; Sequence 22, Application US/11058757  
; Publication No. US20050142132A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/11/058,757  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-11-058-757-22

Query Match 91.2%; Score 31; DB 6; Length 10;  
Best Local Similarity 85.7%; Pred. No. 4.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 3 KLVFFAE 9

## RESULT 70

US-11-058-757-23  
; Sequence 23, Application US/11058757  
; Publication No. US20050142132A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/11/058,757  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-11-058-757-23

## Query Match

Best Local Similarity 91.2%; Score 31; DB 6; Length 10;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 2 KLVFFAE 8

## RESULT 71

US-11-058-757-24  
; Sequence 24, Application US/11058757  
; Publication No. US20050142132A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/11/058,757  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-11-058-757-24

## Query Match

Best Local Similarity 91.2%; Score 31; DB 6; Length 10;

Best Local Similarity 85.7%; Pred. No. 4.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 1 KLVFFAE 7

## RESULT 72

US-09-988-842-9  
; Sequence 9, Application US/09988842  
; Patent No. US20020143105A1  
; GENERAL INFORMATION:  
; APPLICANT: Johansson, Jan  
; TITLE OF INVENTION: OF AMYLOID FORMATION  
; FILE REFERENCE: 12125-002001  
; CURRENT APPLICATION NUMBER: US/09/988,842  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: US 60/251,662  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 60/253,695  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
US-09-988-842-9

## Query Match

Best Local Similarity 91.2%; Score 31; DB 3; Length 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 2 KLVFFAE 8

## RESULT 73

US-09-988-842-25  
; Sequence 25, Application US/09988842  
; Patent No. US20020143105A1  
; GENERAL INFORMATION:  
; APPLICANT: Johansson, Jan  
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION  
; FILE REFERENCE: 12125-002001  
; CURRENT APPLICATION NUMBER: US/09/988,842  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: US 60/251,662  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 60/253,695  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
US-09-988-842-25

## Query Match

Best Local Similarity 91.2%; Score 31; DB 3; Length 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 1 KLVFFAE 7

Db 2 KLVFFAE 8

## RESULT 74

US-10-235-483-14

; Sequence 14, Application US/10235483

; Publication No. US20030087407A1

; GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio

; BAUMANN, Marc

; FRANGIONE, Blas

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL

; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE

; DEPOSITS

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/235,483

; FILING DATE: 06-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/766,596

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-235-483-14

Query Match

Best Local Similarity 91.2%; Score 31; DB 4; Length 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 2 KLVFFAE 8

## RESULT 75

US-10-237-673-20

; Sequence 20, Application US/10237673

; Publication No. US20040121398A1

; GENERAL INFORMATION:

; APPLICANT: FUJITSU LIMITED

; APPLICANT: DAIICHI PHARMACEUTICAL CO., LTD.

; TITLE OF INVENTION: Method for predicting protein-protein interactions

; FILE REFERENCE: GP01-1001PCT

; CURRENT APPLICATION NUMBER: US/10/237,673

; CURRENT FILING DATE: 2002-09-10

; PRIOR APPLICATION NUMBER: JP P2000-72485

; PRIOR FILING DATE: 2000-03-10

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-237-673-20

Query Match

Best Local Similarity 91.2%; Score 31; DB 4; Length 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 1 KLVFFAE 7

Search completed: December 29, 2005, 18:49:49

Job time : 78.3387 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 23.371 Seconds  
(without alignments)  
24.763 Million cell updates/sec

Title: US-10-009-122-18  
Perfect score: 34  
Sequence: 1 KLVEFAA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: /cgm2\_6/ptodata/1/iaa/5\_COMB.pep.\*
- 2: /cgm2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgm2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgm2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 5: /cgm2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	2	US-09-747-408-18
2	34	100.0	7	2	US-09-747-408-19
3	34	100.0	28	2	US-09-388-890-12
4	34	100.0	28	2	US-09-660-954-12
5	34	100.0	35	2	US-09-623-548A-979
6	34	100.0	35	2	US-09-623-548A-1006
7	34	100.0	35	2	US-09-657-276-979
8	34	100.0	35	2	US-09-657-276-1006
9	34	100.0	40	1	US-08-304-585-8
10	34	100.0	43	2	US-09-573-789-1
11	34	100.0	43	2	US-09-859-261-1
12	34	100.0	63	1	US-08-462-859A-3
13	34	100.0	63	1	US-08-123-659A-3
14	34	100.0	63	1	US-08-464-247A-3
15	34	100.0	63	1	US-08-464-248A-3
16	34	100.0	99	2	US-08-339-708A-6
17	31	91.2	7	1	US-08-127-904-14
18	31	91.2	7	2	US-09-264-709A-13
19	31	91.2	7	4	PCT-US94-10475-14
20	31	91.2	8	1	US-08-630-645-1
21	31	91.2	8	2	US-08-766-596A-1
22	31	91.2	8	2	US-09-668-314C-73
23	31	91.2	8	4	PCT-US96-10220-1
24	31	91.2	9	2	US-08-766-596A-64
25	31	91.2	10	2	US-08-970-833-3
26	31	91.2	10	2	US-09-724-961-21
27	31	91.2	10	2	US-09-724-961-22

28	31	91.2	10	2	US-09-724-961-23	Sequence 23, Appl
29	31	91.2	10	2	US-09-724-961-24	Sequence 24, Appl
30	31	91.2	10	2	US-09-580-018-21	Sequence 21, Appl
31	31	91.2	10	2	US-09-580-018-22	Sequence 22, Appl
32	31	91.2	10	2	US-09-580-018-23	Sequence 23, Appl
33	31	91.2	10	2	US-09-580-018-24	Sequence 24, Appl
34	31	91.2	10	2	US-09-724-551-21	Sequence 21, Appl
35	31	91.2	10	2	US-09-724-551-22	Sequence 22, Appl
36	31	91.2	10	2	US-09-724-551-23	Sequence 23, Appl
37	31	91.2	10	2	US-09-724-551-24	Sequence 24, Appl
38	31	91.2	10	2	US-09-724-940-21	Sequence 21, Appl
39	31	91.2	10	2	US-09-724-940-22	Sequence 22, Appl
40	31	91.2	10	2	US-09-724-940-23	Sequence 23, Appl
41	31	91.2	10	2	US-09-724-940-24	Sequence 24, Appl
42	31	91.2	11	1	US-08-630-645-14	Sequence 14, Appl
43	31	91.2	11	2	US-08-766-596A-14	Sequence 14, Appl
44	31	91.2	11	2	US-09-988-842-9	Sequence 9, Appl
45	31	91.2	11	2	US-09-988-842-25	Sequence 25, Appl
46	31	91.2	11	4	PCT-US96-10220-14	Sequence 14, Appl
47	31	91.2	14	2	US-09-594-366-5	Sequence 5, Appl
48	31	91.2	14	2	US-09-992-800-5	Sequence 5, Appl
49	31	91.2	15	1	US-08-612-785B-14	Sequence 14, Appl
50	31	91.2	15	1	US-08-612-785B-37	Sequence 37, Appl
51	31	91.2	15	2	US-08-617-267C-14	Sequence 14, Appl
52	31	91.2	15	2	US-08-766-596A-56	Sequence 56, Appl
53	31	91.2	15	2	US-08-766-596A-57	Sequence 57, Appl
54	31	91.2	15	2	US-08-766-596A-58	Sequence 58, Appl
55	31	91.2	15	2	US-08-766-596A-61	Sequence 61, Appl
56	31	91.2	15	2	US-08-766-596A-63	Sequence 63, Appl
57	31	91.2	15	2	US-08-766-596A-65	Sequence 65, Appl
58	31	91.2	17	2	US-09-264-709A-2	Sequence 2, Appl
59	31	91.2	17	2	US-09-594-366-3	Sequence 3, Appl
60	31	91.2	17	2	US-09-623-548A-950	Sequence 950, App
61	31	91.2	17	2	US-09-623-548A-983	Sequence 983, App
62	31	91.2	17	2	US-09-992-800-3	Sequence 3, Appl
63	31	91.2	17	2	US-09-657-276-950	Sequence 950, App
64	31	91.2	17	2	US-09-657-276-983	Sequence 983, App
65	31	91.2	19	2	US-08-970-833-11	Sequence 11, Appl
66	31	91.2	19	2	US-09-723-384-5	Sequence 5, Appl
67	31	91.2	19	2	US-09-724-961-75	Sequence 75, Appl
68	31	91.2	19	2	US-09-724-552-5	Sequence 5, Appl
69	31	91.2	19	2	US-09-580-018-75	Sequence 75, Appl
70	31	91.2	19	2	US-09-723-927-5	Sequence 5, Appl
71	31	91.2	19	2	US-09-724-489-5	Sequence 5, Appl
72	31	91.2	19	2	US-09-724-477-5	Sequence 5, Appl
73	31	91.2	19	2	US-09-723-762-5	Sequence 5, Appl
74	31	91.2	19	2	US-09-201-430-5	Sequence 5, Appl
75	31	91.2	19	2	US-09-724-551-75	Sequence 75, Appl
76	31	91.2	19	2	US-10-815-353-5	Sequence 5, Appl
77	31	91.2	19	2	US-10-816-529-5	Sequence 5, Appl
78	31	91.2	19	2	US-10-815-391-5	Sequence 5, Appl
79	31	91.2	19	2	US-10-816-022-5	Sequence 5, Appl
80	31	91.2	19	2	US-09-724-940-75	Sequence 75, Appl
81	31	91.2	19	2	US-10-834-609-5	Sequence 5, Appl
82	31	91.2	19	2	US-10-884-892-5	Sequence 5, Appl
83	31	91.2	20	2	US-08-970-833-10	Sequence 10, Appl
84	31	91.2	20	2	US-09-724-953-33	Sequence 33, Appl
85	31	91.2	20	2	US-09-724-567-33	Sequence 33, Appl
86	31	91.2	20	2	US-09-979-952-33	Sequence 33, Appl
87	31	91.2	20	2	US-09-565-817-33	Sequence 33, Appl
88	31	91.2	26	1	US-08-304-585-7	Sequence 7, Appl
89	31	91.2	28	1	US-08-346-849-4	Sequence 4, Appl
90	31	91.2	28	1	US-08-302-808-7	Sequence 7, Appl
91	31	91.2	28	1	US-08-609-090-2	Sequence 2, Appl
92	31	91.2	28	1	US-08-986-948-7	Sequence 7, Appl
93	31	91.2	28	1	US-08-293-284A-4	Sequence 4, Appl
94	31	91.2	28	1	US-08-461-216-2	Sequence 2, Appl
95	31	91.2	28	2	US-09-388-890-2	Sequence 2, Appl
96	31	91.2	28	2	US-09-388-890-3	Sequence 3, Appl
97	31	91.2	28	2	US-09-388-890-4	Sequence 4, Appl
98	31	91.2	28	2	US-09-388-890-5	Sequence 5, Appl
99	31	91.2	28	2	US-09-388-890-6	Sequence 6, Appl
100	31	91.2	28	2	US-09-388-890-7	Sequence 7, Appl

101	31	91.2	28	2	US-09-388-890-8	Sequence 8, Appli	174	31	91.2	40	2	US-09-861-847A-8	Sequence 8, Appli
102	31	91.2	28	2	US-09-388-890-9	Sequence 9, Appli	175	31	91.2	40	2	US-09-988-842-3	Sequence 3, Appli
103	31	91.2	28	2	US-09-388-890-10	Sequence 10, Appli	176	31	91.2	40	2	US-10-455-218-1	Sequence 1, Appli
104	31	91.2	28	2	US-09-388-890-13	Sequence 13, Appli	177	31	91.2	40	2	US-10-151-614-1	Sequence 1, Appli
105	31	91.2	28	2	US-09-388-890-14	Sequence 14, Appli	178	31	91.2	40	2	US-09-623-548A-956	Sequence 956, App
106	31	91.2	28	2	US-09-264-709A-1	Sequence 1, Appli	179	31	91.2	40	2	US-09-623-548A-962	Sequence 962, App
107	31	91.2	28	2	US-08-723-661B-2	Sequence 2, Appli	180	31	91.2	40	2	US-09-623-548A-968	Sequence 968, App
108	31	91.2	28	2	US-09-660-954-2	Sequence 3, Appli	181	31	91.2	40	2	US-09-623-548A-978	Sequence 978, App
109	31	91.2	28	2	US-09-660-954-3	Sequence 4, Appli	182	31	91.2	40	2	US-09-623-548A-989	Sequence 989, App
110	31	91.2	28	2	US-09-660-954-4	Sequence 5, Appli	183	31	91.2	40	2	US-09-623-548A-995	Sequence 995, App
111	31	91.2	28	2	US-09-660-954-5	Sequence 6, Appli	184	31	91.2	40	2	US-09-623-548A-1005	Sequence 1005, Ap
112	31	91.2	28	2	US-09-660-954-6	Sequence 7, Appli	185	31	91.2	40	2	US-09-657-276-956	Sequence 956, App
113	31	91.2	28	2	US-09-660-954-7	Sequence 8, Appli	186	31	91.2	40	2	US-09-657-276-962	Sequence 962, App
114	31	91.2	28	2	US-09-660-954-8	Sequence 9, Appli	187	31	91.2	40	2	US-09-657-276-968	Sequence 968, App
115	31	91.2	28	2	US-09-660-954-9	Sequence 10, Appli	188	31	91.2	40	2	US-09-657-276-978	Sequence 978, App
116	31	91.2	28	2	US-09-660-954-10	Sequence 11, Appli	189	31	91.2	40	2	US-09-657-276-989	Sequence 989, App
117	31	91.2	28	2	US-09-660-954-13	Sequence 13, Appli	190	31	91.2	40	2	US-09-657-276-995	Sequence 995, App
118	31	91.2	28	2	US-09-660-954-14	Sequence 14, Appli	191	31	91.2	40	2	US-09-657-276-1005	Sequence 1005, Ap
119	31	91.2	28	2	US-08-898-300-4	Sequence 4, Appli	192	31	91.2	40	2	US-09-962-955D-36	Sequence 36, Appl
120	31	91.2	28	2	US-08-824-513-4	Sequence 4, Appli	193	31	91.2	40	4	PCT-US92-06700-1	Sequence 1, Appli
121	31	91.2	28	2	US-09-623-548A-959	Sequence 959, App	194	31	91.2	41	1	US-08-302-808-4	Sequence 4, Appli
122	31	91.2	28	2	US-09-623-548A-965	Sequence 965, App	195	31	91.2	41	1	US-08-682-245A-3	Sequence 3, Appli
123	31	91.2	28	2	US-09-623-548A-976	Sequence 976, App	196	31	91.2	41	1	US-08-986-948-4	Sequence 4, Appli
124	31	91.2	28	2	US-09-623-548A-992	Sequence 992, App	197	31	91.2	42	1	US-07-744-767A-2	Sequence 2, Appli
125	31	91.2	28	2	US-09-623-548A-1003	Sequence 1003, Ap	198	31	91.2	42	1	US-08-179-574-1	Sequence 1, Appli
126	31	91.2	28	2	US-09-657-276-959	Sequence 959, App	199	31	91.2	42	1	US-08-271-162-5	Sequence 5, Appli
127	31	91.2	28	2	US-09-657-276-965	Sequence 965, App	200	31	91.2	42	1	US-08-347-144-1	Sequence 1, Appli
128	31	91.2	28	2	US-09-657-276-976	Sequence 976, App	201	31	91.2	42	1	US-08-462-859A-19	Sequence 19, Appl
129	31	91.2	28	2	US-09-657-276-992	Sequence 992, App	202	31	91.2	42	1	US-08-123-659A-19	Sequence 19, Appl
130	31	91.2	28	2	US-09-657-276-1003	Sequence 1003, Ap	203	31	91.2	42	1	US-08-464-247A-19	Sequence 19, Appl
131	31	91.2	28	2	US-09-865-294A-66	Sequence 66, Appl	204	31	91.2	42	1	US-08-464-248A-19	Sequence 19, Appl
132	31	91.2	30	1	US-08-609-090-3	Sequence 3, Appli	205	31	91.2	42	1	US-08-476-464A-1	Sequence 1, Appli
133	31	91.2	30	1	US-09-861-847A-1	Sequence 1, Appli	206	31	91.2	42	1	US-08-304-585-2	Sequence 2, Appli
134	31	91.2	34	1	US-08-609-090-4	Sequence 4, Appli	207	31	91.2	42	1	US-08-302-808-5	Sequence 5, Appli
135	31	91.2	34	1	US-08-475-579A-4	Sequence 4, Appli	208	31	91.2	42	1	US-08-268-348A-1	Sequence 1, Appli
136	31	91.2	35	1	US-08-304-585-6	Sequence 6, Appli	209	31	91.2	42	1	US-08-268-348A-2	Sequence 2, Appli
137	31	91.2	35	1	US-08-612-785B-16	Sequence 16, Appl	210	31	91.2	42	1	US-08-268-348A-3	Sequence 3, Appli
138	31	91.2	35	1	US-08-612-785B-36	Sequence 36, Appl	211	31	91.2	42	1	US-08-268-348A-4	Sequence 4, Appli
139	31	91.2	35	1	US-08-612-785B-38	Sequence 38, Appl	212	31	91.2	42	1	US-08-268-348A-5	Sequence 5, Appli
140	31	91.2	35	1	US-08-612-785B-40	Sequence 40, Appl	213	31	91.2	42	1	US-08-268-348A-6	Sequence 6, Appli
141	31	91.2	35	1	US-08-617-267C-16	Sequence 16, Appl	214	31	91.2	42	1	US-08-433-734-2	Sequence 2, Appli
142	31	91.2	36	1	US-08-609-090-6	Sequence 6, Appli	215	31	91.2	42	1	US-08-609-090-9	Sequence 9, Appli
143	31	91.2	36	2	US-09-861-847A-6	Sequence 6, Appli	216	31	91.2	42	1	US-07-737-371E-72	Sequence 72, Appl
144	31	91.2	36	2	US-09-861-847A-11	Sequence 11, Appli	217	31	91.2	42	1	US-08-422-333-4	Sequence 4, Appli
145	31	91.2	38	1	US-08-302-808-1	Sequence 1, Appli	218	31	91.2	42	1	US-08-682-245A-4	Sequence 4, Appli
146	31	91.2	38	1	US-07-737-371B-68	Sequence 68, Appl	219	31	91.2	42	1	US-08-986-948-5	Sequence 5, Appli
147	31	91.2	38	1	US-08-986-948-1	Sequence 1, Appli	220	31	91.2	42	2	US-08-717-551A-2	Sequence 2, Appli
148	31	91.2	38	2	US-09-623-548A-975	Sequence 975, App	221	31	91.2	42	2	US-09-388-890-1	Sequence 20, Appl
149	31	91.2	38	2	US-09-623-548A-1002	Sequence 1002, Ap	222	31	91.2	42	2	US-09-005-215-20	Sequence 23, Appl
150	31	91.2	38	2	US-09-657-276-975	Sequence 975, App	223	31	91.2	42	2	US-09-242-724-23	Sequence 23, Appl
151	31	91.2	38	1	US-09-657-276-1002	Sequence 1002, Ap	224	31	91.2	42	2	US-08-923-930-2	Sequence 2, Appli
152	31	91.2	39	1	US-08-304-585-5	Sequence 5, Appli	225	31	91.2	42	2	US-09-660-954-1	Sequence 1, Appli
153	31	91.2	39	1	US-08-302-808-2	Sequence 2, Appli	226	31	91.2	42	2	US-08-923-055-2	Sequence 2, Appli
154	31	91.2	39	1	US-08-609-090-7	Sequence 7, Appli	227	31	91.2	42	2	US-08-922-889-2	Sequence 2, Appli
155	31	91.2	39	1	US-08-682-245A-1	Sequence 1, Appli	228	31	91.2	42	2	US-09-731-460-1	Sequence 1, Appli
156	31	91.2	39	1	US-08-986-948-2	Sequence 2, Appli	229	31	91.2	42	2	US-09-133-866-2	Sequence 2, Appli
157	31	91.2	40	1	US-07-744-767A-1	Sequence 1, Appli	230	31	91.2	42	2	US-09-723-384-1	Sequence 1, Appli
158	31	91.2	40	1	US-08-235-400-2	Sequence 2, Appli	231	31	91.2	42	2	US-09-724-961-42	Sequence 42, Appl
159	31	91.2	40	1	US-08-476-464A-2	Sequence 2, Appli	232	31	91.2	42	2	US-09-724-552-1	Sequence 1, Appli
160	31	91.2	40	1	US-08-304-585-1	Sequence 1, Appli	233	31	91.2	42	2	US-09-580-018-42	Sequence 42, Appl
161	31	91.2	40	1	US-08-433-734-1	Sequence 3, Appli	234	31	91.2	42	2	US-10-455-218-2	Sequence 2, Appli
162	31	91.2	40	1	US-08-609-090-8	Sequence 8, Appli	235	31	91.2	42	2	US-09-723-927-1	Sequence 1, Appli
163	31	91.2	40	1	US-07-737-371B-69	Sequence 69, Appl	236	31	91.2	42	2	US-09-724-489-1	Sequence 1, Appli
164	31	91.2	40	1	US-08-682-245A-2	Sequence 2, Appli	237	31	91.2	42	2	US-09-724-477-1	Sequence 1, Appli
165	31	91.2	40	1	US-08-986-948-3	Sequence 3, Appli	238	31	91.2	42	2	US-09-723-762-1	Sequence 1, Appli
166	31	91.2	40	1	US-08-461-216-1	Sequence 1, Appli	239	31	91.2	42	2	US-09-201-430-1	Sequence 1, Appli
167	31	91.2	40	2	US-08-959-148-1	Sequence 1, Appli	240	31	91.2	42	2	US-09-724-551-42	Sequence 42, Appl
168	31	91.2	40	2	US-09-242-724-22	Sequence 22, Appli	241	31	91.2	42	2	US-10-815-353-1	Sequence 1, Appli
169	31	91.2	40	2	US-08-723-661B-1	Sequence 1, Appli	242	31	91.2	42	2	US-10-278-181-1	Sequence 1, Appli
170	31	91.2	40	2	US-09-062-365-3	Sequence 3, Appli	243	31	91.2	42	2	US-10-816-529-1	Sequence 1, Appli
171	31	91.2	40	2	US-09-133-866-1	Sequence 1, Appli	244	31	91.2	42	2	US-09-623-548A-955	Sequence 955, App
172	31	91.2	40	2	US-09-861-847A-7	Sequence 7, Appli	245	31	91.2	42	2	US-09-623-548A-961	Sequence 961, App
173	31	91.2	40	2			246	31	91.2	42	2	US-09-623-548A-967	Sequence 967, App

247	31	91.2	42	2	US-09-623-548A-98A
248	31	91.2	42	2	US-09-623-548A-994
249	31	91.2	42	2	US-10-815-391-1
250	31	91.2	42	2	US-10-816-022-1
251	31	91.2	42	2	US-09-724-953-34
252	31	91.2	42	2	US-09-657-276-955
253	31	91.2	42	2	US-09-657-276-961
254	31	91.2	42	2	US-09-657-276-967
255	31	91.2	42	2	US-09-657-276-988
256	31	91.2	42	2	US-09-657-276-994
257	31	91.2	42	2	US-09-724-567-34
258	31	91.2	42	2	US-09-724-940-42
259	31	91.2	42	2	US-09-863-294A-65
260	31	91.2	42	2	US-09-979-953-34
261	31	91.2	42	2	US-09-585-817-34
262	31	91.2	42	2	US-09-963-955D-37
263	31	91.2	42	2	US-09-706-574A-20
264	31	91.2	42	2	US-10-934-609-1
265	31	91.2	42	2	US-10-884-892-1
266	31	91.2	42	4	PCT-US92-06700-2
267	31	91.2	42	4	PCT-US93-00325-1
268	31	91.2	42	4	PCT-US95-08302-5
269	31	91.2	42	6	5220013-12
270	31	91.2	42	6	5220013-14
271	31	91.2	42	6	52230482-12
272	31	91.2	43	1	US-08-235-400-1
273	31	91.2	43	1	US-08-437-067-1
274	31	91.2	43	1	US-08-302-808-6
275	31	91.2	43	1	US-08-079-511-1
276	31	91.2	43	1	US-08-467-607-1
277	31	91.2	43	1	US-08-404-831-1
278	31	91.2	43	1	US-08-602-264A-3
279	31	91.2	43	1	US-08-469-363-1
280	31	91.2	43	1	US-08-612-785B-1
281	31	91.2	43	1	US-08-475-579A-1
282	31	91.2	43	1	US-08-850-392-1
283	31	91.2	43	1	US-07-737-371B-70
284	31	91.2	43	1	US-08-986-948-6
285	31	91.2	43	1	US-08-975-977-1
286	31	91.2	43	1	US-08-817-423-1
287	31	91.2	43	2	US-08-920-162A-1
288	31	91.2	43	2	US-08-461-018A-3
289	31	91.2	43	2	US-08-976-191-1
290	31	91.2	43	2	US-08-976-179-1
291	31	91.2	43	2	US-09-216-958-3
292	31	91.2	43	2	US-09-356-931-1
293	31	91.2	43	2	US-08-733-202-1
294	31	91.2	43	2	US-08-703-675C-1
295	31	91.2	43	2	US-09-390-693-1
296	31	91.2	43	2	US-08-617-267C-1
297	31	91.2	43	2	US-09-303-655-1
298	31	91.2	43	2	US-08-294-819-1
299	31	91.2	43	2	US-09-408-283-1
300	31	91.2	43	2	US-09-280-966-1

## ALIGNMENTS

RESULT 1  
US-09-747-408-18  
; Sequence 18, Application US/09747408  
; Patent No. 6670399  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23

```

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match      100.0%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFPAQ 7
        |||||
Db      1 KLVFFPAQ 7

RESULT 2
US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: Cerebral Amyloid Angiopathy
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match      100.0%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFPAQ 7
        |||||
Db      1 KLVFFPAQ 7

RESULT 3
US-09-388-890-12
; Sequence 12, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: /09/388,890
; FILING DATE:
; CLASSIFICATION:

```



```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: E22Q B(1-28) peptide of amyloid B protein
US-09-388-890-12

Query Match 100.0%; Score 34; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.49; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAQ 22

RESULT 4
US-09-660-954-12
; Sequence 12, Application US/09660954
; Patent No. 6471960
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/660,954
; FILING DATE: 13-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/686,959
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: E22Q B(1-28) peptide of amyloid B protein
US-09-660-954-12

Query Match 100.0%; Score 34; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.49; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAQ 22

RESULT 5
US-09-623-548A-979
; Sequence 979, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 979
; LENGTH: 35
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-979

Query Match 100.0%; Score 34; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.62; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 KLVFFAQ 7
DB 11 KLVFFAQ 17

RESULT 6
US-09-623-548A-1006
; Sequence 1006, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
```

;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
;; FILE REFERENCE: 2110  
;; CURRENT APPLICATION NUMBER: US/09/623,548A  
;; PRIOR FILING DATE: 2000-09-05  
;; PRIOR APPLICATION NUMBER: 60/134,406  
;; PRIOR FILING DATE: 1999-05-17  
;; PRIOR APPLICATION NUMBER: 60/153,406  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: 60/159,783  
;; PRIOR FILING DATE: 1999-10-18  
;; NUMBER OF SEQ ID NOS: 1617  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 1006  
;; LENGTH: 35  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
US-09-623-548A-1006

Query Match 100.0%; Score 34; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||  
Db 11 KLVFFPAQ 17

RESULT 7  
US-09-657-276-979  
;; Sequence 979 Application US/09657276  
;; Patent No. 6887470  
;; GENERAL INFORMATION:  
;; APPLICANT: Conjuchem, Inc.  
;; APPLICANT: Bridon, Dominique  
;; APPLICANT: Ezrin, Alan  
;; APPLICANT: Milner, Peter  
;; APPLICANT: Holmes, Darren  
;; APPLICANT: Thibaudeau, Karen  
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
;; FILE REFERENCE: 2110  
;; CURRENT APPLICATION NUMBER: US/09/657,276  
;; CURRENT FILING DATE: 2000-09-07  
;; PRIOR APPLICATION NUMBER: 60/134,406  
;; PRIOR FILING DATE: 1999-05-17  
;; PRIOR APPLICATION NUMBER: 60/153,406  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: 60/159,783  
;; PRIOR FILING DATE: 1999-10-18  
;; NUMBER OF SEQ ID NOS: 1617  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 979  
;; LENGTH: 35  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
US-09-657-276-979

Query Match 100.0%; Score 34; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||  
Db 11 KLVFFPAQ 17

RESULT 8  
US-09-657-276-1006  
;; Sequence 1006 Application US/09657276  
;; Patent No. 6887470  
;; GENERAL INFORMATION:  
;; APPLICANT: Conjuchem, Inc.  
;; APPLICANT: Bridon, Dominique  
;; APPLICANT: Ezrin, Alan  
;; APPLICANT: Milner, Peter  
;; APPLICANT: Holmes, Darren  
;; APPLICANT: Thibaudeau, Karen  
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
;; FILE REFERENCE: 2110  
;; CURRENT APPLICATION NUMBER: US/09/657,276  
;; CURRENT FILING DATE: 2000-09-07  
;; PRIOR APPLICATION NUMBER: 60/134,406  
;; PRIOR FILING DATE: 1999-05-17  
;; PRIOR APPLICATION NUMBER: 60/153,406  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: 60/159,783  
;; PRIOR FILING DATE: 1999-10-18  
;; NUMBER OF SEQ ID NOS: 1617  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 1006  
;; LENGTH: 35  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
US-09-657-276-1006

Query Match 100.0%; Score 34; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||  
Db 11 KLVFFPAQ 17

RESULT 9  
US-08-304-585-8  
;; Sequence 8 Application US/08304585  
;; Patent No. 5721106  
;; GENERAL INFORMATION:  
;; APPLICANT: Maggio, John E.  
;; APPLICANT: Mantyh, Patrick W.  
;; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
;; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.  
;; STREET: P.O. Box 581415  
;; CITY: Minneapolis  
;; STATE: MN  
;; COUNTRY: USA  
;; ZIP: 55458-1415  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/304,585  
;; FILING DATE: 12-SEP-1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Muetting, Ann M.

REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110.00010120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-304-585-8

Query Match 100.0%; Score 34; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.71; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||  
DB 16 KLVFFPAQ 22

## RESULT 10

US-09-573-789-1  
Sequence 1, Application US/09573789  
Patent No. 6737038  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Pharma Company (formerly DuPont Pharmaceuticals  
APPLICANT: Company)  
APPLICANT: Zaczek, Robert  
APPLICANT: Olson, Richard E.  
APPLICANT: Seiffert, Dietmar A.  
APPLICANT: Thompson, Lorin A.

TITLE OF INVENTION: USE OF SMALL MOLECULE RADIOLOGANDS TO DISCOVER INHIBITORS OF AMY  
FILE REFERENCE: PH-7048-A  
CURRENT APPLICATION NUMBER: US/09/573,789  
CURRENT FILING DATE: 2000-05-17  
PRIOR APPLICATION NUMBER: US 09/438,901  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 60/108,147  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 60/131,284  
PRIOR FILING DATE: 1999-04-27  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 43  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-573-789-1

Query Match 100.0%; Score 34; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 0.76; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||  
DB 16 KLVFFPAQ 22

## RESULT 11

US-09-859-261-1  
Sequence 1, Application US/09859261  
Patent No. 6878363  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Pharma Company (formerly DuPont Pharmaceuticals  
APPLICANT: Company)  
APPLICANT: Zaczek, Robert  
APPLICANT: Olson, Richard E.  
APPLICANT: Seiffert, Dietmar A.  
APPLICANT: Thompson, Lorin A.

TITLE OF INVENTION: USE OF SMALL MOLECULE RADIOLOGANDS TO DISCOVER INHIBITORS OF AMY  
FILE REFERENCE: PH-7215  
CURRENT APPLICATION NUMBER: US/09/859,261  
CURRENT FILING DATE: 2001-05-17  
PRIOR APPLICATION NUMBER: US 60/204,685  
PRIOR FILING DATE: 2001-08-06  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 43  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-859-261-1

Query Match 100.0%; Score 34; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 0.76; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||  
DB 16 KLVFFPAQ 22

## RESULT 12

US-08-462-859A-3  
Sequence 3, Application US/08462859A  
Patent No. 5652092  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, J. S.  
APPLICANT: Vitek, M. P.

TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESS: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 07470-8426

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,859A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,844-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)831-3246  
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-859A-3

Query Match 100.0%; Score 34; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 1.1; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||

Db 25 KLVPFAQ 31

## RESULT 13

US-08-123-659A-3

; Sequence 3, Application US/08123659A

; Patent No. 5656477

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Anne Rosenblum

; STREET: 163 Delaware Avenue, Suite 212

; CITY: Delmar

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 12054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/123.659A

; FILING DATE: 20-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Rosenblum, Anne M.

; REGISTRATION NUMBER: 30,419

; REFERENCE/DOCKET NUMBER: 31,844-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (518)475-0611

; TELEFAX: (518)475-0619

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 63 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-123-659A-3

Query Match 100.0%; Score 34; DB 1; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7

Db 25 KLVPFAQ 31

## RESULT 14

US-08-464-247A-3

; Sequence 3, Application US/08464247A

; Patent No. 5693478

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,247A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2158

; TELEFAX: 201-683-4117

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 63 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-464-247A-3

Query Match 100.0%; Score 34; DB 1; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7

Db 25 KLVPFAQ 31

## RESULT 15

US-08-464-248A-3

; Sequence 3, Application US/08464248A

; Patent No. 5703209

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,248A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-02

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201)831-3246

; TELEFAX: (201)831-3305

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 63 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

```

; MOLECULE TYPE: protein
US-08-464-248A-3

Query Match      100.0%; Score 34; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 25 KLVFFPAQ 31

RESULT 16
US-08-339-708A-6
; Sequence 6, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Maehiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hihiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-708A-6

Query Match      100.0%; Score 34; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 16 KLVFFPAQ 22

RESULT 17
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Amnestic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,904
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
US-08-127-904-14

Query Match      91.2%; Score 31; DB 1; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 1 KLVFFPAE 7

RESULT 18
US-09-264-709A-13
; Sequence 13, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; TITLE OF INVENTION: Improve the Quality of Life
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-13

Query Match      91.2%; Score 31; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 KLVFFPAQ 7  
| | | | |  
DB 1 KLVFFFAE 7

RESULT 19  
PCT-US94-10475-14  
; Sequence 14, Application PC/TUS9410475  
; GENERAL INFORMATION:  
; APPLICANT: Eugene Roberts  
; TITLE OF INVENTION: Method For  
; TITLE OF INVENTION: Antagonizing Amyloid n  
; TITLE OF INVENTION: Effects of Amyloid n  
; TITLE OF INVENTION: Protein and Improving  
; TITLE OF INVENTION: the Quality of Life  
; TITLE OF INVENTION: in Individuals  
; TITLE OF INVENTION: With Alzheimer Disease  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: City of Hope  
; STREET: 1500 East Duarte Road  
; CITY: Duarte  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91010-0269  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3M Double Density 5 1/4"  
; MEDIUM TYPE: diskette  
; COMPUTER: Wang PC  
; OPERATING SYSTEM: MS DOS Version 3.20  
; SOFTWARE: Microsoft  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/10475  
; FILING DATE: 16 September 1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: U. S. Application  
; PRIOR APPLICATION DATA: Serial No.  
; PRIOR APPLICATION DATA: 08/127,904; filed  
; PRIOR APPLICATION DATA: 29 September 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Irons, Edward S.  
; REGISTRATION NUMBER: 16,541  
; REFERENCE/DOCKET NUMBER: None  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 626-3564 or 783-6030  
; TELEFAX: (202) 783-6031  
; TELEX: None  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7  
; TYPE: Amino Acid  
; STRANDEDNESS:  
; TOPOLOGY: Unknown  
; PCT-US94-10475-14

Query Match 91.2%; Score 31; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
| | | | |  
DB 1 KLVFFFAE 7

RESULT 20  
US-08-630-645-1  
; Sequence 1, Application US/08630645  
; Patent No. 5948763  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/766,596A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/630,645  
;; FILING DATE: 10-APR-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/478,326  
;; FILING DATE: 06-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: YUN, Allen C.  
;; REGISTRATION NUMBER: 37,971  
;; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-766-596A-1

Query Match 91.2%; Score 31; DB 2; Length 8;  
Best Local Similarity 85.7%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
DB 1 KLVFFAE 7

RESULT 22  
US-09-668-314C-73  
;; Sequence 73, Application US/09668314C  
;; Patent No. 6844148  
;; GENERAL INFORMATION:  
;; APPLICANT: Gurney, et al  
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREOF  
;; FILE REFERENCE: 28341/6280NCP  
;; CURRENT APPLICATION NUMBER: US/09/668,314C  
;; CURRENT FILING DATE: 2000-09-22  
;; PRIOR APPLICATION NUMBER: US 60/169,232  
;; PRIOR FILING DATE: 1999-12-06  
;; PRIOR APPLICATION NUMBER: US 09/416,901  
;; PRIOR FILING DATE: 1999-10-13  
;; PRIOR APPLICATION NUMBER: US 60/155,493  
;; PRIOR FILING DATE: 1999-09-23  
;; PRIOR APPLICATION NUMBER: US 09/404,133  
;; PRIOR FILING DATE: 1999-09-23  
;; PRIOR APPLICATION NUMBER: PCT/US99/20881  
;; PRIOR FILING DATE: 1999-09-23  
;; PRIOR APPLICATION NUMBER: US 60/101,594  
;; PRIOR FILING DATE: 1998-09-24  
;; NUMBER OF SEQ ID NOS: 84  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 73  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic peptide  
US-09-668-314C-73

Query Match 91.2%; Score 31; DB 2; Length 8;  
Best Local Similarity 85.7%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

DB 1 KLVFFAE 7  
RESULT 23  
PCT-US96-10220-1  
;; Sequence 1, Application PC/TUS9610220  
;; GENERAL INFORMATION:  
;; APPLICANT:  
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
;; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
;; NUMBER OF SEQUENCES: 26  
;; CORRESPONDENCE ADDRESS:  
;; STREET: 419 Seventh Street, N.W., Suite 400  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US96/10220  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/478,326  
;; FILING DATE: 06-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/630,645  
;; FILING DATE: 10-APR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BROWDY, Roger L.  
;; REGISTRATION NUMBER: 25,618  
;; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
PCT-US96-10220-1

Query Match 91.2%; Score 31; DB 4; Length 8;  
Best Local Similarity 85.7%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
DB 1 KLVFFAE 7

RESULT 24  
US-08-766-596A-64  
;; Sequence 64, Application US/08766596A  
;; Patent No. 6462171  
;; GENERAL INFORMATION:  
;; APPLICANT: SOTO-JARA, Claudio  
;; APPLICANT: BRAUNMANN, Marc  
;; APPLICANT: FRANGIONE, Blas  
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
;; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
;; NUMBER OF SEQUENCES: 69  
;; CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-64

Query Match 91.2%; Score 31; DB 2; Length 9;  
Best Local Similarity 85.7%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
DB 2 KLVFFAE 8

RESULT 25  
US-08-970-833-3  
Sequence 3, Application US/08970833  
Patent No. 6022859  
GENERAL INFORMATION:  
APPLICANT: Kieselring, Laura L.  
APPLICANT: Murphy, Regina M.  
TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 411 East Wisconsin Avenue  
CITY: Milwaukee  
STATE: Wisconsin  
COUNTRY: U.S.A.  
ZIP: 53202-4497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,833  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Baker, Jean C.

REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 960296.94291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5709  
TELEFAX: (414) 271-3552  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-970-833-3

Query Match 91.2%; Score 31; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
DB 1 KLVFFAS 7

RESULT 26  
US-09-724-961-21  
Sequence 21, Application US/09724961  
Patent No. 6743427  
GENERAL INFORMATION:  
APPLICANT: Schenk, Dale B.  
APPLICANT: Bard, Frederique  
APPLICANT: Vasquez, Nicki  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
FILE REFERENCE: 15270J-004750UC  
CURRENT APPLICATION NUMBER: US/09/724,961  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 09/580,015  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/322,289  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: US 09/201,430  
PRIOR FILING DATE: 1998-11-30  
PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
PRIOR FILING DATE: 1998-11-30  
PRIOR APPLICATION NUMBER: US 60/080,970  
PRIOR FILING DATE: 1998-04-07  
PRIOR APPLICATION NUMBER: US 60/067,740  
PRIOR FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 21  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: 10-mer peptide  
OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
OTHER INFORMATION: peptide)  
US-09-724-961-21

Query Match 91.2%; Score 31; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
DB 4 KLVFFAE 10

RESULT 27  
US-09-724-961-22  
Sequence 22, Application US/09724961  
Patent No. 6743427



```
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
;
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 3 KLVFFAE 9

RESULT 28
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-23

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 2 KLVFFAE 8

RESULT 29
US-09-724-961-24
; Sequence 24, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
;
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-24

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 1 KLVFFAE 7

RESULT 30
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
```

; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-21

Query Match 91.2%; Score 31; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
DB 4 KLVFFAE 10

RESULT 31  
US-09-580-018-22  
; Sequence 22, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-22

Query Match 91.2%; Score 31; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
DB 3 KLVFFAE 9

RESULT 32  
US-09-580-018-23  
; Sequence 23, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-23

Query Match 91.2%; Score 31; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
DB 2 KLVFFAE 8

RESULT 33  
US-09-580-018-24  
; Sequence 24, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-24

Query Match 91.2%; Score 31; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
DB 1 KLVFFAE 7

RESULT 34  
US-09-724-551-21  
; Sequence 21, Application US/09724551  
; Patent No. 6787637  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/724,551  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1

```
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-21
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
    |||||:
Db 4 KLVFFPAE 10
```

## RESULT 35

```
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
    |||||:
Db 3 KLVFFPAE 9
```

## RESULT 36

```
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
```

```
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
    |||||:
Db 2 KLVFFPAE 8
```

## RESULT 37

```
US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
    |||||:
Db 1 KLVFFPAE 7
```

## RESULT 38

```
US-09-724-940-21
; Sequence 21, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
```

```
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-21

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
   |||||:
Db 4 KLVFFPAE 10

RESULT 39
US-09-724-940-22
; Sequence 22, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/724,940
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-22

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
   |||||:
Db 4 KLVFFPAE 10

US-09-724-940-22
; Sequence 22, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/724,940
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-22

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
   |||||:
Db 4 KLVFFPAE 10
```

```
Db 3 KLVFFPAE 9

RESULT 40
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/724,940
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
   |||||:
Db 2 KLVFFPAE 8

RESULT 41
US-09-724-940-24
; Sequence 24, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/724,940
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
```

; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-24

Query Match 91.2%; Score 31; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
Db 1 KLVFFAE 7

RESULT 42  
US-08-630-645-14  
; Sequence 14, Application US/08630645  
; Patent No. 5948763  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,645  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-630-645-14

Query Match 91.2%; Score 31; DB 1; Length 11;  
Best Local Similarity 85.7%; Pred. No. 0.9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
Db 2 KLVFFAE 8

RESULT 43  
US-08-766-596A-14  
; Sequence 14, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-14

Query Match 91.2%; Score 31; DB 2; Length 11;  
Best Local Similarity 85.7%; Pred. No. 0.9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
| | | | |  
Db 2 KLVFFAE 8

RESULT 44  
US-09-988-842-9  
; Sequence 9, Application US/09988842  
; Patent No. 6716589  
; GENERAL INFORMATION:  
; APPLICANT: Johansson, Jan  
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION  
; TITLE OF INVENTION: OF AMYLOID FORMATION

```
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match          91.2%; Score 31; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 0.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 2 KLVFFAE 8

RESULT 45
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match          91.2%; Score 31; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 0.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 2 KLVFFAE 8

RESULT 46
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEROF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
```

```
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-10220-14

Query Match          91.2%; Score 31; DB 4; Length 11;
Best Local Similarity 85.7%; Pred. No. 0.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 2 KLVFFAE 8

RESULT 47
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-5

Query Match          91.2%; Score 31; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 4 KLVFFAE 10

RESULT 48
US-09-992-800-5
```

```
; Sequence 5, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-5

Query Match          91.2%; Score 31; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
DB      4 KLVFFPAE 10

RESULT 49
US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match          91.2%; Score 31; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
DB      6 KLVFFPAE 12

RESULT 50
US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match          91.2%; Score 31; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
DB      6 KLVFFPAE 12
```

RESULT 51  
US-08-617-267C-14  
; Sequence 14, Application US/08617267C  
; Patent No. 6319498  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/617,267C  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PFI-002CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-617-267C-14

Query Match 91.2%; Score 31; DB 2; Length 15;  
Best Local Similarity 85.7%; Pred. No. 1.2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 1 KLVFFAE 7

RESULT 52  
US-08-766-596A-56  
; Sequence 56, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:

STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 08-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-56

Query Match 91.2%; Score 31; DB 2; Length 15;  
Best Local Similarity 85.7%; Pred. No. 1.2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 5 KLVFFAE 11

RESULT 53  
US-08-766-596A-57  
; Sequence 57, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:



```
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/630,645
/ FILING DATE: 10-APR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/478,326
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: YUN, Allen C.
/ REGISTRATION NUMBER: 37,971
/ REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-766-596A-57

Query Match          91.2%; Score 31; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      5 KLVFFAE 11
|||||:

RESULT 54
US-08-766-596A-58
; Sequence 58, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
```

```
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 58:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-766-596A-58

Query Match          91.2%; Score 31; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      5 KLVFFAE 11
|||||:

RESULT 55
US-08-766-596A-61
; Sequence 61, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 61:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-766-596A-61

Query Match          91.2%; Score 31; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 KLVFFAQ 7  
Db 5 KLVFFAE 11

## RESULT 56

US-08-766-596A-63  
; Sequence 63, Application US/08766596A  
; Patent No. 6462171

## GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc

; APPLICANT: FRANGIONE, Blas

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL

; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/766,596A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 63:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-766-596A-63

Query Match 91.2%; Score 31; DB 2; Length 15;

Best Local Similarity 85.7%; Pred. No. 1.2;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 5 KLVFFAE 11

## RESULT 57

US-08-766-596A-65

; Sequence 65, Application US/08766596A

; Patent No. 6462171

## GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio

; APPLICANT: BAUMANN, Marc

; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/766,596A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 65:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-766-596A-65

Query Match 91.2%; Score 31; DB 2; Length 15;

Best Local Similarity 85.7%; Pred. No. 1.2;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 5 KLVFFAE 11

## RESULT 58

US-09-264-709A-2

; Sequence 2, Application US/09264709A

; Patent No. 6320024

## GENERAL INFORMATION:

; APPLICANT: Roberts, Eugene

; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and

; FILE REFERENCE: 2124-310

; CURRENT APPLICATION NUMBER: US/09/264,709A

; CURRENT FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 08/797,782

; PRIOR FILING DATE: 1997-02-07

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-264-709A-2

Query Match 91.2%; Score 31; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 5 KLVFFAE 11

RESULT 59  
US-09-594-366-3  
; Sequence 3, Application US/09594366  
; Patent No. 6582945  
; GENERAL INFORMATION:  
; APPLICANT: Raso, Victor  
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO  
; FILE REFERENCE: BBRI-2004  
; CURRENT APPLICATION NUMBER: US/09/594,366  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/139,408  
; PRIOR FILING DATE: 1999-06-16  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-594-366-3

Query Match 91.2%; Score 31; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 8 KLVFFAE 14

RESULT 60  
US-09-623-548A-950  
; Sequence 950, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 950  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-950

Query Match 91.2%; Score 31; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 5 KLVFFAE 11

RESULT 61  
US-09-623-548A-983  
; Sequence 983, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 983  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-983

Query Match 91.2%; Score 31; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db 5 KLVFFAE 11

RESULT 62  
US-09-992-800-3  
; Sequence 3, Application US/09992800  
; Patent No. 6872554  
; GENERAL INFORMATION:  
; APPLICANT: Raso, Victor  
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO  
; FILE REFERENCE: BBRI-2006  
; CURRENT APPLICATION NUMBER: US/09/992,800  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: 09/594,366  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/139,408  
; PRIOR FILING DATE: 1999-06-16  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-992-800-3

Query Match 91.2%; Score 31; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 8 KLVFFAE 14

## RESULT 63

US-09-657-276-950  
; Sequence 950, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 950  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide

## US-09-657-276-950

Query Match 91.2%; Score 31; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 5 KLVFFAE 11

## RESULT 64

US-09-657-276-983  
; Sequence 983, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406

; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 983  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-983

Query Match 91.2%; Score 31; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 5 KLVFFAE 11

## RESULT 65

US-08-970-833-11  
; Sequence 11, Application US/08970833  
; Patent No. 6022859  
; GENERAL INFORMATION:  
; APPLICANT: Kiesel, Laura L.  
; APPLICANT: Murphy, Regina M.  
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 411 East Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53202-4497  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/970,833  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baker, Jean C.  
; REGISTRATION NUMBER: 35,433  
; REFERENCE/DOCKET NUMBER: 960296.94291  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 277-5709  
; TELEFAX: (414) 271-3552  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-970-833-11

Query Match 91.2%; Score 31; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 1.6;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 10 KLVFFAE 16

```
RESULT 66
US-09-723-384-5
; Sequence 5, Application US/09723384
; Patent No. 6710226
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/09/723,384
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-384-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      4 KLVFFAE 10

RESULT 67
US-09-724-961-75
; Sequence 75, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; OTHER INFORMATION: Cys residue
; NAME/KEY: MOD_RES
```

```
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-724-961-75

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      4 KLVFFAE 10

RESULT 68
US-09-724-552-5
; Sequence 5, Application US/09724552
; Patent No. 6750324
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/09/724,552
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,019A
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-552-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      4 KLVFFAE 10

RESULT 69
US-09-580-018-75
; Sequence 75, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Abeta 13-28  
; OTHER INFORMATION: peptide with two Gly residues added and inserted  
; OTHER INFORMATION: Cys residue  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = N-acetyl His  
US-09-580-018-75

Query Match 91.2%; Score 31; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 1.6;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 4 KLVFFAE 10

## RESULT 70

US-09-723-927-5  
; Sequence 5, Application US/09723927  
; Patent No. 6787138  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-004720US  
; CURRENT APPLICATION NUMBER: US/09/723,927  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-09-723-927-5

Query Match 91.2%; Score 31; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 1.6;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 4 KLVFFAE 10

## RESULT 71

US-09-724-489-5  
; Sequence 5, Application US/09724489  
; Patent No. 6787140  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-004720US  
; CURRENT APPLICATION NUMBER: US/09/724,489  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/201,430  
; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-09-724-489-5

Query Match 91.2%; Score 31; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 1.6;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 4 KLVFFAE 10

## RESULT 72

US-09-724-477-5  
; Sequence 5, Application US/09724477  
; Patent No. 6787143  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-004720US  
; CURRENT APPLICATION NUMBER: US/09/724,477  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-09-724-477-5

Query Match 91.2%; Score 31; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 1.6;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 4 KLVFFAE 10

## RESULT 73

US-09-723-762-5  
; Sequence 5, Application US/09723762

```
; Patent No. 6787144
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/723,762
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-762-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      4 KLVFFAE 10
|||||:

RESULT 74
US-09-201-430-5
; Sequence 5, Application US/09201430
; Patent No. 6787523
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/201,430
; CURRENT FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-201-430-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KLVFFAQ 7
Db      4 KLVFFAE 10
|||||:

RESULT 75
US-09-724-551-75
; Sequence 75, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; OTHER INFORMATION: Cys residue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-724-551-75

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      4 KLVFFAE 10
|||||:

Search completed: December 29, 2005, 17:52:40
Job time : 24.471 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 95.4032 Seconds  
(without alignments)  
32.238 Million cell updates/sec

Title: US-10-009-122-18  
Perfect score: 34  
Sequence: 1 KLVFFAQ 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	7	4	AAB48492
2	34	100.0	7	4	AAB48491
3	34	100.0	7	4	AAB82640
4	34	100.0	7	4	AAB82639
5	34	100.0	7	5	AAB96827
6	34	100.0	7	5	AAB96828
7	34	100.0	7	5	AAU11665
8	34	100.0	7	5	AAU11666
9	34	100.0	7	8	ADQ37330
10	34	100.0	7	8	ADQ37331
11	34	100.0	7	9	ADY37938
12	34	100.0	7	9	ADY37937
13	34	100.0	9	2	AAR45239
14	34	100.0	10	4	AAB82641
15	34	100.0	10	5	AAU96829
16	34	100.0	10	9	ADY37939
17	34	100.0	15	7	ADK82697
18	34	100.0	28	2	AAW01414
19	34	100.0	28	6	AAB35600
20	34	100.0	28	6	ABG72244
21	34	100.0	35	4	AAB91830
22	34	100.0	35	4	AAB91803
23	34	100.0	40	2	AAW47232
24	34	100.0	42	6	ABP97887

25	34	100.0	42	9	ADV42360	Human amy
26	34	100.0	42	9	ADZ88256	Human amy
27	34	100.0	42	9	AEA37375	Human amy
28	34	100.0	53	2	AAR55697	Sequence
29	34	100.0	63	2	AAW26391	Human amy
30	34	100.0	63	2	AAW26511	Human amy
31	34	100.0	63	2	AAW42975	Beta-amy1
32	34	100.0	63	2	AAW44746	APP-RAP 7
33	34	100.0	99	2	AAR74695	Beta-amy1
34	34	100.0	100	5	AAE14377	Human amy
35	34	100.0	108	5	AAE14385	Gamma-sec
36	31	91.2	7	2	AAR88300	Non-amnes
37	31	91.2	7	2	AAR87921	Test pept
38	31	91.2	7	4	AAB67281	Residues
39	31	91.2	7	5	ABB04920	Human amy
40	31	91.2	7	6	ABB82630	Abeta fib
41	31	91.2	7	6	AAE35454	Abeta pep
42	31	91.2	7	6	AAE35453	Abeta pep
43	31	91.2	7	7	ADP20746	Human bet
44	31	91.2	7	7	ADP50855	Human cal
45	31	91.2	7	8	ADP64922	Beta-amy1
46	31	91.2	7	8	ADQ37278	Vaccine a
47	31	91.2	8	2	AAW32551	Human amy
48	31	91.2	8	4	AAE10663	Human amy
49	31	91.2	8	4	AAE02615	Human amy
50	31	91.2	8	5	ABU78624	Human alp
51	31	91.2	8	6	ABU09765	Human amy
52	31	91.2	8	6	ABR61959	Human amy
53	31	91.2	8	7	ABW00134	Beta-amy1
54	31	91.2	8	8	ADQ37385	Antifibri
55	31	91.2	8	8	ADZ08900	Human bet
56	31	91.2	8	9	AEA51423	C-Abeta 1
57	31	91.2	8	9	AEA51420	A 16-22-C
58	31	91.2	8	9	AEA62831	Immuocon
59	31	91.2	8	9	AEA62834	Immuocon
60	31	91.2	8	9	ABU79063	Aggregati
61	31	91.2	9	7	ABW00197	Peptide #
62	31	91.2	9	8	AD136003	Human amy
63	31	91.2	9	8	AD135849	Human amy
64	31	91.2	9	8	AD135871	Human amy
65	31	91.2	9	8	AD135903	Human amy
66	31	91.2	9	9	AEA51414	A 16-23-C
67	31	91.2	9	9	AEA51417	C-A 16-23
68	31	91.2	9	9	AEA62825	Immuocon
69	31	91.2	10	3	AAU79938	Beta-amy1
70	31	91.2	10	3	AAU79938	Human APP
71	31	91.2	10	4	AAB46226	Human APP
72	31	91.2	10	4	AAB46225	Human APP
73	31	91.2	10	4	AAB46227	Human APP
74	31	91.2	10	4	AAB46227	Human APP
75	31	91.2	10	6	AAE35455	Abeta pep
76	31	91.2	10	6	ADQ37280	Vaccine a
77	31	91.2	10	8	ADQ37371	Human amy
78	31	91.2	11	2	AAW32560	Anti-amy1
79	31	91.2	11	2	AAU52586	Peptide #
80	31	91.2	11	5	AAU99431	Human amy
81	31	91.2	11	5	AAE29504	Human amy
82	31	91.2	11	5	ABU79013	Human amy
83	31	91.2	11	6	ABW00147	Human amy
84	31	91.2	12	6	AAE35466	Abeta pep
85	31	91.2	12	8	ADQ37289	Vaccine a
86	31	91.2	12	8	ADZ08892	Human bet
87	31	91.2	12	9	AAE35465	Abeta pep
88	31	91.2	13	6	AAE35467	Abeta pep
89	31	91.2	13	6	ADZ37467	Human amy
90	31	91.2	13	8	ADJ71477	N-termina
91	31	91.2	13	8	ADQ37408	Human amy
92	31	91.2	13	8	ADQ37290	Vaccine a
93	31	91.2	14	6	ADZ08887	Beta-A4 s
94	31	91.2	14	6	ADJ71465	N-termina
95	31	91.2	14	8	ADJ71478	N-termina
96	31	91.2	14	8	ADZ08889	Human bet
97	31	91.2	14	9	ADZ08889	Human bet



98	31	91.2	15	2	AAW02334	Aaw02334 Beta-amyl	171	31	91.2	28	4	AA355594	Aa355594 Human c1o
99	31	91.2	15	2	AAW89358	Aaw89358 Beta-amyl	172	31	91.2	28	4	AA355592	Aa355592 Human c1o
100	31	91.2	15	2	AAW89354	Aaw89354 Beta-amyl	173	31	91.2	28	4	AA355593	Aa355593 Human c1o
101	31	91.2	15	5	ABG71014	Abg71014 Long form	174	31	91.2	28	4	AA355597	Aa355597 Human c1o
102	31	91.2	15	5	AB505162	Ab505162 Beta amyl	175	31	91.2	28	4	AA355596	Aa355596 Human c1o
103	31	91.2	15	5	AAE26271	Aae26271 Human bet	176	31	91.2	28	4	AA355598	Aa355598 Human c1o
104	31	91.2	15	6	ABU79057	Abu79057 Aggregati	177	31	91.2	28	4	AA355592	Aa355592 Human c1o
105	31	91.2	15	6	ABU79064	Abu79064 Aggregati	178	31	91.2	28	4	AA355590	Aa355590 Human c1o
106	31	91.2	15	6	ABU79060	Abu79060 Aggregati	179	31	91.2	28	4	AA355590	Aa355590 Human c1o
107	31	91.2	15	6	ABU79055	Abu79055 Aggregati	180	31	91.2	28	4	AA355590	Aa355590 Human c1o
108	31	91.2	15	6	ABU79056	Abu79056 Aggregati	181	31	91.2	28	4	AA355590	Aa355590 Human c1o
109	31	91.2	15	6	ABU79062	Abu79062 Aggregati	182	31	91.2	28	4	AA355590	Aa355590 Human c1o
110	31	91.2	15	7	ABW00190	Abw00190 Peptide #	183	31	91.2	28	4	AA355590	Aa355590 Human c1o
111	31	91.2	15	7	ABW00198	Abw00198 Peptide #	184	31	91.2	28	4	AA355590	Aa355590 Human c1o
112	31	91.2	15	7	ABW00189	Abw00189 Peptide #	185	31	91.2	28	4	AA355590	Aa355590 Human c1o
113	31	91.2	15	7	ABW00191	Abw00191 Peptide #	186	31	91.2	28	4	AA355590	Aa355590 Human c1o
114	31	91.2	15	7	ABW00196	Abw00196 Peptide #	187	31	91.2	28	4	AA355590	Aa355590 Human c1o
115	31	91.2	15	7	ABW00194	Abw00194 Peptide #	188	31	91.2	28	4	AA355590	Aa355590 Human c1o
116	31	91.2	15	7	ADK82695	Adk82695 Beta-amyl	189	31	91.2	28	4	AA355590	Aa355590 Human c1o
117	31	91.2	15	7	ADK82700	Adk82700 Beta-amyl	190	31	91.2	28	4	AA355590	Aa355590 Human c1o
118	31	91.2	15	8	ADJ71466	Adj71466 N-termina	191	31	91.2	28	5	AAE26081	Aae26081 Beta amyl
119	31	91.2	15	8	ADJ71453	Adj71453 N-termina	192	31	91.2	28	5	AAE26081	Aae26081 Beta amyl
120	31	91.2	15	8	ADJ71479	Adj71479 N-termina	193	31	91.2	28	5	AAE26081	Aae26081 Beta amyl
121	31	91.2	15	8	ADJ71467	Adj71467 N-termina	194	31	91.2	28	5	AAE26081	Aae26081 Beta amyl
122	31	91.2	15	8	ADJ71454	Adj71454 N-termina	195	31	91.2	28	5	AAE26081	Aae26081 Beta amyl
123	31	91.2	16	8	ADJ71480	Adj71480 N-termina	196	31	91.2	28	5	AAE26081	Aae26081 Beta amyl
124	31	91.2	16	8	ADJ71441	Adj71441 N-termina	197	31	91.2	28	5	AAE26081	Aae26081 Beta amyl
125	31	91.2	16	8	ADJ71467	Adj71467 N-termina	198	31	91.2	28	5	AAE26081	Aae26081 Beta amyl
126	31	91.2	16	8	ADJ71467	Adj71467 N-termina	199	31	91.2	28	5	AAE26081	Aae26081 Beta amyl
127	31	91.2	17	2	AAE54703	Aae54703 Beta-amyl	200	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
128	31	91.2	17	2	AAW18880	Aaw18880 Beta-amyl	201	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
129	31	91.2	17	4	AAE911774	Aae911774 Amyloid b	202	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
130	31	91.2	17	4	AAE911807	Aae911807 Amyloid b	203	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
131	31	91.2	17	4	AAE911807	Aae911807 Amyloid b	204	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
132	31	91.2	17	5	AAE911807	Aae911807 Amyloid b	205	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
133	31	91.2	17	5	AAE911807	Aae911807 Amyloid b	206	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
134	31	91.2	17	6	AAE911807	Aae911807 Amyloid b	207	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
135	31	91.2	17	8	ADJ65843	Adj65843 Amyloid B	208	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
136	31	91.2	17	8	ADN02827	Adn02827 Mammalian	209	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
137	31	91.2	17	8	ADN02827	Adn02827 Mammalian	210	31	91.2	28	6	ABG72236	Abg72236 Mutant D1
138	31	91.2	18	3	AAE10963	Aae10963 Beta-amyl	211	31	91.2	28	7	AAE10963	Aae10963 Beta-amyl
139	31	91.2	18	3	AAE10963	Aae10963 Beta-amyl	212	31	91.2	28	7	AAE10963	Aae10963 Beta-amyl
140	31	91.2	19	2	AAW18882	Aaw18882 Trp-Beta-	213	31	91.2	28	8	ADQ37255	Adq37255 Vaccine a
141	31	91.2	19	3	AAE79935	Aae79935 Beta-amyl	214	31	91.2	28	8	ADQ37255	Adq37255 Vaccine a
142	31	91.2	19	4	AAE49097	Aae49097 Human amyl	215	31	91.2	28	8	ADQ37255	Adq37255 Vaccine a
143	31	91.2	19	4	AAE49097	Aae49097 Human amyl	216	31	91.2	28	8	ADQ37255	Adq37255 Vaccine a
144	31	91.2	20	3	AAE46201	Aae46201 Human APP	217	31	91.2	28	9	AAE46201	Aae46201 Human APP
145	31	91.2	20	3	AAE46201	Aae46201 Human APP	218	31	91.2	28	9	AAE46201	Aae46201 Human APP
146	31	91.2	20	5	AAE06431	Aae06431 Beta-amyl	219	31	91.2	28	9	AAE06431	Aae06431 Beta-amyl
147	31	91.2	21	2	AAE30941	Aae30941 Beta-secr	220	31	91.2	28	9	AAE30941	Aae30941 Beta-secr
148	31	91.2	22	8	ADK83670	Adk83670 Amyloidog	221	31	91.2	28	9	AAE30941	Aae30941 Beta-secr
149	31	91.2	24	2	AAE52569	Aae52569 Alzheimer	222	31	91.2	28	9	AAE52569	Aae52569 Alzheimer
150	31	91.2	24	9	AAE809195	Aae809195 Human bet	223	31	91.2	28	9	AAE809195	Aae809195 Human bet
151	31	91.2	24	9	AAE809194	Aae809194 Human bet	224	31	91.2	28	9	AAE809194	Aae809194 Human bet
152	31	91.2	26	2	AAW47229	Aaw47229 Beta-amyl	225	31	91.2	28	9	AAW47229	Aaw47229 Beta-amyl
153	31	91.2	26	6	ABU63718	Abu63718 Rat amyl	226	31	91.2	28	9	AAW47229	Aaw47229 Beta-amyl
154	31	91.2	26	7	ADP55647	Adp55647 Human A b	227	31	91.2	28	9	AAW47229	Aaw47229 Beta-amyl
155	31	91.2	26	7	ADP55647	Adp55647 Human A b	228	31	91.2	28	9	AAW47229	Aaw47229 Beta-amyl
156	31	91.2	26	7	ADP55647	Adp55647 Human A b	229	31	91.2	28	9	AAW47229	Aaw47229 Beta-amyl
157	31	91.2	27	2	AAE33409	Aae33409 Human amyl	230	31	91.2	28	9	AAE33409	Aae33409 Human amyl
158	31	91.2	28	1	AAE70594	Aae70594 Sequence	231	31	91.2	28	9	AAE70594	Aae70594 Sequence
159	31	91.2	28	1	AAE90381	Aae90381 Synthetic	232	31	91.2	28	9	AAE90381	Aae90381 Synthetic
160	31	91.2	28	2	AAE60368	Aae60368 Beta-amyl	233	31	91.2	28	9	AAE60368	Aae60368 Beta-amyl
161	31	91.2	28	2	AAE54702	Aae54702 Beta-amyl	234	31	91.2	28	9	AAE54702	Aae54702 Beta-amyl
162	31	91.2	28	2	AAE64171	Aae64171 A4-P(1)-28	235	31	91.2	28	9	AAE64171	Aae64171 A4-P(1)-28
163	31	91.2	28	2	AAE64164	Aae64164 Generic b	236	31	91.2	28	9	AAE64164	Aae64164 Generic b
164	31	91.2	28	2	AAE64172	Aae64172 A4-B(1)-28	237	31	91.2	28	9	AAE64172	Aae64172 A4-B(1)-28
165	31	91.2	28	2	AAE64170	Aae64170 A4-O(1)-28	238	31	91.2	28	9	AAE64170	Aae64170 A4-O(1)-28
166	31	91.2	28	2	AAW01413	Aaw01413 Beta/A4-a	239	31	91.2	28	9	AAW01413	Aaw01413 Beta/A4-a
167	31	91.2	28	2	AAE39805	Aae39805 Beta-amyl	240	31	91.2	28	9	AAE39805	Aae39805 Beta-amyl
168	31	91.2	28	2	AAW81467	Aaw81467 Synthetic	241	31	91.2	28	9	AAW81467	Aaw81467 Synthetic
169	31	91.2	28	4	AAE35591	Aae35591 Human c1o	242	31	91.2	28	9	AAE35591	Aae35591 Human c1o
170	31	91.2	28	4	AAE35595	Aae35595 Human c1o	243	31	91.2	28	9	AAE35595	Aae35595 Human c1o

Abg71016 Long form  
Abb05164 BEVVHHHQ  
Aae35430 Abeta pep  
Adj64067 Human bet  
Adq37254 Vaccine a  
Aw81471 Synthetic  
Aau11776 Synthetic  
Aau11771 Synthetic  
Adu42779 Amyloid b  
Adu42774 Amyloid b  
Adm97743 Amyloid b  
Adp73823 Loop inse  
Adm97744 Amyloid b  
Aar60362 Beta-amyl  
Aaw92722 Human tac  
Aab91826 Amyloid b  
Aab91799 Amyloid b  
Adu24436 Novel glu  
Adu24441 Novel glu  
Adu46715 Gln3 amyl  
Adu46710 Amyloid b  
Ady81762 Human bet  
Adz71362 Human bet  
Adz71367 Human bet  
Aea35400 Novel QC  
Aea3395 Novel QC  
Aeb92568 Glutamin  
Aeb92573 Glutamin  
Aar60363 Beta-amyl  
Aaw81472 Synthetic  
Aay25134 Human am  
Aay52132 Human am  
Adu08509 Human am  
Aap96148 Human am  
Adu81763 Human bet  
Aar33191 Beta-amyl  
Aar60364 Beta-amyl  
Add11651 Human bet  
Aaw23335 Amyloid b  
Aaw37507 Amyloid b  
Aaw47226 Beta-amyl  
Aay14099 Human bet  
Aay39804 Beta-amyl  
Aaw9584 Wild type  
Aaw81473 Synthetic  
Aay39339 Beta-amyl  
Aay25135 Human am  
Aaw92723 Human tac  
Aab84426 Partial s  
Aab84429 Partial s  
Aab91786 Amyloid b  
Aab91813 Amyloid b  
Aab91819 Amyloid b  
Aab91780 Amyloid b  
Aab91792 Amyloid b  
Aab91829 Amyloid b  
Aab91802 Amyloid b

ALIGNMENTS

RESULT 1  
ID AAB48492 standard; peptide; 7 AA.  
XX  
AC AAB48492;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Antifibrillogenic peptide #19.  
XX  
KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
KW Alzheimer's disease.  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT Modified-site 7 /note= "C-terminal amide"  
XX  
XX WO200068263-A2.  
PN 16-NOV-2000.  
PD  
XX  
XX 04-MAY-2000; 2000WO-CA000515.  
PP  
XX  
XX 05-MAY-1999; 99US-0132592P.  
PR  
XX  
XX (NEUR-) NEUROCHEM INC.  
PA  
XX  
XX Chalifour R, Gervais F, Gupta A;  
PI  
XX  
XX WPI; 2001-031852/04.  
DR  
XX  
XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
PT its isomer or peptidomimetic.  
PT  
XX  
XX Claim 7; Page 25; 46pp; English.  
PS  
XX  
XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
CC binding region and the prot-prot interaction region of the human amyloid  
CC protein  
XX  
XX Sequence 7 AA;  
SQ  
Query Match 100.0%; Score 34; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVFFPAQ 7  
DB 1 KLVFFPAQ 7  
RESULT 2  
ID AAB48491 standard; peptide; 7 AA.  
XX  
XX AAB48491;  
XX  
XX 02-MAR-2001 (first entry)  
DT  
XX  
XX Antifibrillogenic peptide #18.  
DE  
XX  
XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
KW Alzheimer's disease.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200068263-A2.  
PN  
XX  
XX 16-NOV-2000.  
PD  
XX  
XX 04-MAY-2000; 2000WO-CA000515.  
PP  
XX  
XX 05-MAY-1999; 99US-0132592P.  
PR  
XX  
XX (NEUR-) NEUROCHEM INC.  
PA

XX Chalifour R, Gervais F, Gupta A;  
 XX WPI; 2001-031852/04.  
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.  
 XX Claim 7; Page 25; 46pp; English.  
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein  
 XX Sequence 7 AA;  
 Query Match 100.0%; Score 34; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 Db 1 KLVFFAQ 7  
 RESULT 3  
 AAB82640  
 ID AAB82640 standard; peptide; 7 AA.  
 XX AAB82640;  
 AC AAB82640;  
 XX 02-OCT-2001 (first entry)  
 XX All-D peptide used in Alzheimer's disease vaccine.  
 DE Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.  
 KW Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..7 /note= "all D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"  
 FT  
 XX WO200139796-A2.  
 PN  
 XX 07-JUN-2001.  
 XX 29-NOV-2000; 2000WO-CA001413.  
 XX 29-NOV-1999; 99US-0168594P.  
 PR 28-NOV-2000; 2000US-00724842.  
 XX (NEUR-) NEUROCHEM INC.  
 PA  
 XX Chalifour R, Hebert L, Kong X, Gervais F;  
 PI WPI; 2001-441458/47.  
 DR Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT which elicits production of antibodies to prevent fibrillogenesis and  
 PT associated cellular toxicity.  
 XX Disclosure; Page 11; 31pp; English.

CC The present sequence is that of an all-D peptide suitable for use in  
 CC preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients  
 XX Sequence 7 AA;  
 Query Match 100.0%; Score 34; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 Db 1 KLVFFAQ 7  
 RESULT 4  
 AAB82639  
 ID AAB82639 standard; peptide; 7 AA.  
 XX AAB82639;  
 AC AAB82639;  
 XX 02-OCT-2001 (first entry)  
 XX All-D peptide used in Alzheimer's disease vaccine.  
 DE Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.  
 KW Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..7 /note= "all D-form residues"  
 FT  
 XX WO200139796-A2.  
 PN  
 XX 07-JUN-2001.  
 XX 29-NOV-2000; 2000WO-CA001413.  
 XX 29-NOV-1999; 99US-0168594P.  
 PR 28-NOV-2000; 2000US-00724842.  
 XX (NEUR-) NEUROCHEM INC.  
 PA  
 XX Chalifour R, Hebert L, Kong X, Gervais F;  
 PI WPI; 2001-441458/47.  
 DR Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT

PT which elicits production of antibodies to prevent fibrillogenesis and  
 PT associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in  
 CC preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see A882622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in A882623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 |||||  
 Db 1 KLVFFPAQ 7

RESULT 5  
 AAU96827  
 ID AAU96827 standard; peptide; 7 AA.

XX AAU96827;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #17.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..7 /note= "Preferably D-form residue"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.  
 XX (NEUR-) NEUROCHEM INC.  
 XX Gervais P, Kong X, Chalifour R, Migneault D;  
 XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 22; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A-t-(A-l)n-k-z-A-l-a-b (I) where z = 0-1;  
 CC A-t = an amyloid targeting moiety; A-l-n-k = a linker moiety; and A-l-a-b  
 CC = a labelling moiety. Also included are imaging amyloid deposition or  
 CC diagnosing an amyloid-related condition in a patient involving  
 CC administering (I) to the patient, and ultrasound imaging (I) in the  
 CC patient to determine the presence of amyloid or amyloid-related condition  
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and  
 CC instructions for the preparation and use of the radiopharmaceutical in  
 CC the imaging of amyloid or an amyloid-related condition. The agents are  
 CC used for imaging amyloid deposition and for diagnosing an amyloid related  
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible  
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 |||||

Db 1 KLVFFPAQ 7

RESULT 6  
 AAU96828  
 ID AAU96828 standard; peptide; 7 AA.

XX AAU96828;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #18.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..7



XX PA (NEUR-) NEUROCHEM INC.  
 XX PI Green AM, Gervais F;  
 XX DR WPI; 2002-075222/10.  
 XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40  
 PT inhibitor.  
 XX XX  
 XX PS Disclosure; Page 10; 68pp; English.  
 XX CC The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting a  
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
 CC The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)  
 XX SQ Sequence 7 AA;  
 Query Match 100.0%; Score 34; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVPFAQ 7  
 |||||  
 Db 1 KLVPFAQ 7  
 RESULT 9  
 ADQ37330  
 ID ADQ37330 standard; peptide; 7 AA.  
 XX AC ADQ37330;  
 XX DT 07-OCT-2004 (first entry)  
 XX DE Antifibrillogenic amyloidosis inhibiting peptide.  
 XX KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiac; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX OS Synthetic.  
 XX XX  
 XX PN WO2004058239-A1.  
 XX XX  
 XX PD 15-JUL-2004.  
 XX XX  
 XX PF 24-DEC-2003; 2003WO-CA002021.  
 XX XX  
 XX PR 24-DEC-2002; 2002US-0436379P.  
 XX PR 23-JUN-2003; 2003US-0482214P.  
 XX XX

PA (NEUR-) NEUROCHEM INT LTD.  
 XX Gervais F, Bellini F;  
 XX WPI; 2004-543342/52.  
 XX DR  
 XX PT Composition for treating e.g. Alzheimer's disease comprises first agent  
 PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.  
 XX XX  
 XX PS Disclosure; Page 70; 143pp; English.  
 XX CC The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.  
 XX SQ Sequence 7 AA;  
 Query Match 100.0%; Score 34; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVPFAQ 7  
 |||||  
 Db 1 KLVPFAQ 7  
 RESULT 10  
 ADQ37331  
 ID ADQ37331 standard; peptide; 7 AA.  
 XX AC ADQ37331;  
 XX XX  
 XX DT 07-OCT-2004 (first entry)  
 XX DE Antifibrillogenic amyloidosis inhibiting peptide.  
 XX KW amyloid-beta; amyloid-beta related disease;

amyloid-beta fibril formation; immune response; nootropic; neuroprotective; cerebroprotective; haemostatic; ophthalmological; antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic; anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic; cardiant; antidepressant; endocrine; hypnotic; amyloid-beta fibril formation modulator; immune system modulator; Alzheimer's disease; mild cognitive impairment; mild-to-moderate cognitive impairment; vascular dementia; cerebral amyloid angiopathy; hereditary cerebral haemorrhage; senile dementia; Down's syndrome; inclusion body myositis; age-related macular degeneration; hypothyroidism; cerebrovascular disease; cardiovascular disease; memory loss; anxiety; behavioural dysfunction; neurological condition; psychological condition; vaccine antigen.

XX Synthetic.

XX OS

XX FH Key Location/Qualifiers

XX FT Modified-site 7 /note= "amidated"

XX PN WO2004058239-A1.

XX PD 15-JUL-2004.

XX PF 24-DEC-2003; 2003WO-CA002021.

XX PR 24-DEC-2002; 2002US-0436379P.

XX PR 23-JUN-2003; 2003US-0482214P.

XX XX

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Bellini F;

XX PI WPI; 2004-543342/52.

XX PT Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.

XX PS Disclosure; Page 70; 143pp; English.

XX CC The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

CC CC nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep

CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; CC having amyloid-beta deposits. The present sequence represents a peptide CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide CC in the exemplification of the present invention.

XX SQ Sequence 7 AA;

XX Query Match 100.0%; Score 34; DB 8; Length 7;

XX Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 KLVFFPAQ 7

XX DB 1 KLVFFPAQ 7

XX RESULT 11

XX ADV37938

XX ID ADV37938 standard; peptide; 7 AA.

XX AC ADV37938;

XX XX

XX DT 19-MAY-2005 (first entry)

XX XX

XX DE Amyloid-targeting peptide, SEQ ID NO:18, for use in imaging agent.

XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru; transmissible spongiform encephalopathy; scrapie; BSE;

XX KW Alzheimers disease; neurological disease; amyloidosis;

XX KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 7 /note= "C-terminal amide"

XX XX

XX PN US2005048000-A1.

XX XX

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX XX (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Kong X, Chalifour R, Migneault D;

XX XX WPI; 2005-212201/22.

XX XX

XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform encephalopathy, primary amyloidosis or Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 18, 34pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent. The imaging agent comprises an amyloid targeting moiety (such as a peptide) joined to a labeling moiety via a linking moiety, and is preferably able to cross the blood-brain barrier. The invention also relates to a kit for preparing a radiopharmaceutical preparation from the imaging agent of the invention, a method for imaging amyloid deposition in a patient and a method for diagnosing an amyloid-related condition in a patient. The amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-related conditions such as Creutzfeld-Jakob disease (CJD), Kuru, transmissible cerebral amyloidosis (also known as transmissible virus dementias), familial CJD, scrapie, transmissible mink encephalopathy,



CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 CC mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 |||||  
 Db 1 KLVFFPAQ 7

# RESULT 12

ADY37937  
 ID ADY37937 standard; peptide; 7 AA.

XX AC ADY37937;

XX DT 19-MAY-2005 (first entry)

XX DE Amyloid-targeting peptide, SEQ ID NO:17, for use in imaging agent.

XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 KW transmissible spongiform encephalopathy; scrapie; BSE;  
 KW Alzheimers disease; neurological disease; amyloidosis;  
 KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX PN US2005048000-A1.

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Kong X, Chalifour R, Migneault D;

XX DR WPI; 2005-212201/22.

XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform  
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 17; 34pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent. The imaging  
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 CC a labeling moiety via a linking moiety, and is preferably able to cross  
 CC the blood-brain barrier. The invention also relates to a kit for  
 CC preparing a radiopharmaceutical preparation from the imaging agent of the  
 CC invention, a method for imaging amyloid deposition in a patient and a  
 CC method for diagnosing an amyloid-related condition in a patient. The  
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,  
 CC transmissible cerebral amyloidosis (also known as transmissible virus  
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,

CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 CC mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 |||||  
 Db 1 KLVFFPAQ 7

# RESULT 13

AAR45239  
 ID AAR45239 standard; peptide; 9 AA.

XX AC AAR45239;

XX DT 20-JUN-1994 (first entry)

XX DE Mutant amyloid precursor protein fragment.

XX KW Amyloid precursor protein; APP; beta amyloid protein; BAP; detection;  
 KW Alzheimer's disease; Down's syndrome.

XX OS Homo sapiens.

XX PN AU9338358-A.

XX PD 04-NOV-1993.

XX PF 03-MAY-1993; 93AU-00038358.

XX PR 01-MAY-1992; 92US-00877675.

XX PA (AMCY ) AMERICAN CYANAMID CO.

XX PI Vitek MP, Jacobsen JS;

XX DR WPI; 1993-406194/51.

XX DR N-PSDB; AAQ54267.

XX PT New mutant forms of amyloid precursor protein - for detecting cpds. that  
 PT modify activity of enzymes involved in precursor cleavage, also new  
 PT nucleic acid encoding them.

XX PS Disclosure; Page 35; 66pp; English.

XX CC Recombinant polypeptides produced using the coding sequences of mutant  
 CC forms of amyloid precursor proteins comprising from the 5' to the 3' end  
 CC a sequence encoding a marker and either (1) a sequence encoding the N-  
 CC terminus of an amyloid precursor protein (APP) up to, but not including,  
 CC the nucleotides encoding the beta amyloid protein (BAP) domain or (2) the  
 CC BAP domain; or the two ligated together, can be used to detect drugs or  
 CC compounds that inhibit/augment the activity of proteolytic enzymes which  
 CC cleave APP to generate BAP fragments (deposition of which occurs in  
 CC patients with Alzheimers disease and Down's syndrome). This is a fragment  
 CC of amyloid precursor protein containing a mutation which is associated  
 CC with diseases involving BAP deposition

XX Sequence 9 AA;



Query Match 100.0%; Score 34; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. NO. 2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
Db 2 KLVFFPAQ 8

RESULT 14  
AAB82641  
ID AAB82641 standard; peptide; 10 AA.  
XX AAB82641;  
XX  
XX  
XX 02-OCT-2001 (first entry)  
XX  
XX All-D peptide used in Alzheimer's disease vaccine.  
XX  
XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
KW therapy; antigen.  
XX  
XX Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 1. .10 /note= "all D-form residues"  
FT  
XX  
XX WO2001139796-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX  
XX 29-NOV-2000; 2000WO-CA001413.  
XX  
XX 29-NOV-1999; 99US-0168594P.  
XX 28-NOV-2000; 2000US-00724842.  
XX  
XX (NEUR-) NEUROCHEM INC.  
XX  
XX Chalifour R, Hebert L, Kong X, Gervais F;  
XX WPI; 2001-441458/47.  
XX  
XX Preventing/treating amyloid-related disease, especially Alzheimer's  
FT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
FT which elicits production of antibodies to prevent fibrillogenesis and  
PT associated cellular toxicity.  
PT  
XX  
XX Disclosure; Page 11; 31pp; English.

CC The present sequence is that of an all-D peptide suitable for use in  
CC preparing vaccines for preventing or treating Alzheimer's disease and  
CC other amyloid related disorders in humans. It is based on a portion of  
CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
CC inserting 1 or more amino acid residues, or by substituting 1 or more  
CC amino acid residues with other amino acid residues or non-amino acid  
CC fragments. Vaccines of the invention are produced using 'non-self'  
CC peptides synthesised from the unnatural D-configuration amino acids to  
CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
CC aggregated to be operative or immunogenic. They preferably interact with  
CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
CC fragments, protein conjugates, immunogenic derivative peptides and  
CC immunogenic peptidomimetics. Examples include all-D peptides  
CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
CC prion protein related disorders, or systemic amyloidosis associated with  
CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.

CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
CC amyloidosis found in long-term haemodialysis patients  
XX  
SQ Sequence 10 AA;  
Query Match 100.0%; Score 34; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. NO. 0.65;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
Db 4 KLVFFPAQ 10

RESULT 15  
AAU96829  
ID AAU96829 standard; peptide; 10 AA.  
XX  
XX AAU96829;  
XX  
XX 30-JUL-2002 (first entry)  
XX  
XX Amyloid targeting peptide #19.  
XX  
XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
KW transmissible cerebral amyloidosis; transmissible virus dementia;  
KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
KW bovine spongiform encephalopathy; inflammation associated amyloid;  
KW primary amyloidosis; feline spongiform encephalopathy;  
KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
KW dialysis-related amyloidosis; light chain-related amyloidosis;  
KW cerebral amyloid angiopathy.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 1. .10 /note= "Preferably D-form residue"  
FT  
XX  
XX WO200207781-A2.  
XX  
XX 31-JAN-2002.  
XX  
XX 25-JUL-2001; 2001WO-CA001071.  
XX  
XX 25-JUL-2000; 2000US-0220808P.  
XX 24-JUL-2001; 2001US-00915092.  
XX  
XX (NEUR-) NEUROCHEM INC.  
XX  
XX Gervais F, Kong X, Chalifour R, Migneault D;  
XX WPI; 2002-371447/40.  
XX  
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
PT plaques and/or for the treatment of amyloidosis disorders.  
PT  
XX  
XX Claim 49; Page 22; 57pp; English.

CC The invention relates to an amyloid-targeting imaging agent comprising an  
CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
CC agent is of general formula A\_t-(A\_l)\_n\_k-z-A\_l\_a\_b (1) where z = 0 - 1;  
CC A\_t = an amyloid targeting moiety; A\_l\_n\_k = a linker moiety; and A\_l\_a\_b  
CC = a labelling moiety. Also included are imaging amyloid deposition or  
CC diagnosing an amyloid-related condition in a patient involving  
CC administering (1) to the patient, and ultrasound imaging (1) in the  
CC patient to determine the presence of amyloid or amyloid-related condition  
CC ; and a kit for preparing a radiopharmaceutical preparation comprising  
CC (1), a reducing agent, a buffering agent, a transchelating agent, and  
CC instructions for the preparation and use of the radiopharmaceutical in  
CC the imaging of amyloid or an amyloid-related condition. The agents are  
CC used for imaging amyloid deposition and for diagnosing an amyloid related  
CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible

CC cerebral amyloidoses (transmissible virus dementias), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiotomy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 34; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.65;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
 |||||  
 Db 4 KLVFFAQ 10

RESULT 16  
 ADY37939  
 ID ADY37939 standard; peptide; 10 AA.  
 XX  
 AC ADY37939;  
 XX  
 DT 19-MAY-2005 (first entry)  
 XX  
 DE Amyloid-targeting peptide, SEQ ID NO:19, for use in imaging agent.

XX  
 KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 KW transmissible spongiform encephalopathy; scrapie; BSE;  
 KW Alzheimer's disease; neurological disease; amyloidosis;  
 KW non-insulin dependent diabetes; metabolic disorder.

XX Synthetic.

XX US2005048000-A1.

XX 03-MAR-2005.

XX 03-DEC-2003; 2003US-00728028.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX 29-JAN-2003; 2003US-0443231P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2005-212201/22.

XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform  
 encephalopathy, primary amyloidosis or Alzheimer's disease.

XX Disclosure; SEQ ID NO 19; 34pp; English.

XX The invention relates to an amyloid-targeting imaging agent. The imaging  
 agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 a labeling moiety via a linking moiety, and is preferably able to cross  
 the blood-brain barrier. The invention also relates to a kit for  
 preparing a radiopharmaceutical preparation from the imaging agent of the  
 invention, a method for imaging amyloid deposition in a patient and a  
 method for diagnosing an amyloid-related condition in a patient. The  
 amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,  
 transmissible cerebral amyloidosis (also known as transmissible virus  
 dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
 bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,

CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiotomy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 34; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.65;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
 |||||  
 Db 4 KLVFFAQ 10

RESULT 17  
 ADX82697  
 ID ADX82697 standard; peptide; 15 AA.  
 XX  
 AC ADX82697;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Beta-amyloid peptide #3 recognised by antibody to treat senile dementia.

XX fusion antibody; senile dementia; beta-amyloid peptide; fibre;  
 KW immunocell.

XX Homo sapiens.

XX CN1396183-A.

XX 12-FEB-2003.

XX 13-JUL-2001; 2001CN-00120278.

XX 13-JUL-2001; 2001CN-00120278.

XX (ZHAN/) ZHANG X.

XX Zhang X, Zhang J;

XX WPI; 2003-442233/42.

XX Human fusion antibody for reducing cerebral amyloid fibers associated  
 with senile dementia.

XX Claim 1; Page 2; 26pp; Chinese.

XX The invention relates to a human fusion antibody for preventing and  
 treating senile dementia. The antibody recognises and binds the beta-  
 amyloid peptide and the fibres generated by it. The human antibody Pc  
 segment recognized by human immunocells are sequentially contained by its  
 terminals from N to C. The fusion gene coding for the antibody is also  
 CC disclosed. This sequence represents a beta-amyloid peptide recognised by  
 the antibody.

XX Sequence 15 AA;

Query Match 100.0%; Score 34; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.97;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
 |||||  
 Db 1 KLVFFAQ 7

```

RESULT 18
AAW01414
ID AAW01414 standard; protein; 28 AA.
AC AAW01414;
XX
XX 20-JAN-1997 (first entry)
XX
XX Beta/A4-amyloid peptide residues 1-28 Dutch.
XX
XX Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;
KW Alzheimer's disease; stimulation; investigation; pathogenesis;
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type; control;
KW cerebral amyloid angiopathy; cerebral; haemorrhage; haemorrhage.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 22
FT /note= "wild type Glu substd. with Gln"
XX
XX W09615799-Al.
XX
XX 30-MAY-1996.
XX
XX 22-NOV-1995; 95WO-US015007.
XX
XX 22-NOV-1994; 94US-00347144.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Anderson S;
XX
XX WPI; 1996-268332/27.
XX
XX Use of agents which bind beta-amyloid peptide - for diagnosis, prevention
PT and treatment of vascular damage caused by amyloid deposits, partic. in
PT haemorrhaging and Alzheimer's disease.
XX
XX Example 1; Fig 1; 52pp; English.
XX
XX To investigate the effects of beta-amyloid peptide (BAP) on tissue
CC plasminogen activator (t-PA) 3 synthetic peptides were used. One peptide
CC contained 42 amino acids and corresp. to the full length BAP (AAR95248).
CC The other 2 peptides (AAR95249 and 50) contained the 28 N-terminal
CC residues of the BAP found in Alzheimer's disease and hereditary cerebral
CC haemorrhage with amyloidosis-Dutch type (HCHWA-D), respectively. In an
CC assay to determine the effect of the peptides on t-PA activation, each
CC peptide (AAR95248, 49 and 50) gave 1st order rate constant of activation
CC (k(app)) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and
CC 7.8 for null and fibrinogen controls. The results demonstrate that the
CC BAP are able to stimulate t-PA activity in vitro, which is significant in
CC that it provides a means for investigating and controlling the
CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
CC angiopathy related cerebral haemorrhage
XX
XX Sequence 28 AA;
XX
XX Query Match 100.0%; Score 34; DB 2; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 1.8;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KLVFFPAQ 7
XX |||||
XX Db 16 KLVFFPAQ 22
XX
XX RESULT 19
XX AAB35600
XX ID AAB35600 standard; peptide; 28 AA.
XX

```

```

AC AAB35600;
XX
XX 15-FEB-2001 (first entry)
XX
XX Human clone E22Q B(1-28) amyloid B peptide.
XX
XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW acute cardiovascular disease; therapy.
XX
XX Homo sapiens.
XX
XX US6136548-A.
XX
XX 24-OCT-2000.
XX
XX 02-SEP-1999; 99US-00388890.
XX
XX 22-NOV-1994; 94US-00347144.
XX 22-NOV-1995; 95WO-US015007.
XX 26-JUL-1996; 96US-00686959.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Anderson S;
XX
XX WPI; 2001-030939/04.
XX
XX Identifying mutant tissue-type plasminogen activator (t-PA) for improving
PT thrombolytic therapy or treating vascular hemorrhaging, by determining
PT whether t-PA binds to fibrin but not to a beta amyloid peptide.
XX
XX Example 3; Col 26; 23pp; English.
XX
XX The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischaemia and pulmonary embolism
XX
XX Sequence 28 AA;
XX
XX Query Match 100.0%; Score 34; DB 4; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 1.8;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KLVFFPAQ 7
XX |||||
XX Db 16 KLVFFPAQ 22
XX
XX RESULT 20
XX ABG72244
XX ID ABG72244 standard; peptide; 28 AA.
XX
XX AC ABG72244;
XX
XX 27-FEB-2003 (first entry)
XX
XX Mutant E22Q of human beta(1-28) peptide of amyloid beta peptide.
XX
XX Plasmin-mediated proteolysis; beta-amyloid peptide; brain cell;
KW brain tissue; tissue plasminogen activator; t-PA; Alzheimer's disease;
KW vascular haemorrhaging; thrombolytic therapy; neurological disorder;
KW nerve cell; neuroprotective; nootropic; beta(1-28) peptide;
KW amyloid beta peptide; mutant; mutein.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 22
FT

```





Query Match 100.0%; Score 34; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
DB 16 KLVFFAQ 22

RESULT 25  
ADV42360  
ID ADV42360 standard; peptide; 42 AA.  
XX  
AC ADV42360;  
XX  
DT 24-FEB-2005 (first entry)  
XX  
DE Human amyloid-beta peptide 42 (Dutch mutation), seq id 1.  
XX  
KW Neuroprotective; gene therapy; transgenic animal; beta-amyloid;  
KW amyloid-beta 42 Dutch; neurodegenerative disease.  
XX  
OS Homo sapiens.  
OS Synthetic.

Key Location/Qualifiers  
FH Key  
FT Misc-difference 22  
FT /note= "wild-type Glu replaced by Gln"  
XX  
XX US2004250302-A1.  
XX  
XX 09-DEC-2004.  
XX  
XX 25-MAY-2004; 2004US-00853593.  
XX  
XX 21-OCT-2003; 2003US-0512972P.  
XX  
XX (ENVI-) ENVIVO PHARM INC.  
XX  
XX Lowe DA, Koenig G, Cummings CJ;  
XX  
XX WPI; 2005-020614/02.  
XX  
XX N-PSDB; ADV42361.  
XX  
XX New transgenic fly expressing the Dutch mutation of the amyloid-beta  
XX peptide 42, useful in identifying an agent for treating neurodegenerative  
XX disease, e.g. Alzheimer's disease.  
XX  
XX Claim 1; SEQ ID NO 1; 25pp; English.  
XX  
XX The invention relates to a transgenic fly having a genome comprising a  
XX DNA sequence encoding a polypeptide having the amyloid-beta peptide 42  
XX containing the Dutch mutation of the 42-amino acid sequence. Further  
XX disclosed is a method for identifying an agent active in  
XX neurodegenerative disease. The transgenic fly is a transgenic Drosophila.  
XX The transgenic fly comprises embryonic, larval, pupal or adult stage. The  
XX DNA sequence is operatively linked to a tissue specific expression  
XX control sequence or is fused to a sequence encoding a signal peptide,  
XX which is the wingless (wg) signal peptide or the Argos (aos) signal  
XX peptide. The method also comprises providing a transgenic fly and a  
XX control wild-type fly, contacting the first transgenic fly and the  
XX control wild-type fly with a candidate agent, and observing a difference  
XX in phenotype between the first transgenic fly and the control fly, where  
XX a difference in phenotype of the first transgenic fly relative to the  
XX control fly indicates an agent active in neurodegenerative disease. The  
XX transgenic fly is useful in identifying an agent active in  
XX neurodegenerative disease for preparing a composition for treating  
XX neurodegenerative disease, e.g. Alzheimer's disease. The current sequence  
XX represents the human amyloid-beta peptide 42 containing the E22Q (Dutch  
XX mutation).

Sequence 42 AA;

Query Match 100.0%; Score 34; DB 9; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
DB 16 KLVFFAQ 22

RESULT 26  
ADZ88256  
ID ADZ88256 standard; protein; 42 AA.  
XX  
AC ADZ88256;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE Amyloid beta 42 (Dutch).  
XX  
KW mutant; amyloid-beta 42; Abeta42; transgenic; Iowa; Dutch; Flemish;  
KW Italian; Arctic; Tau; neurodegenerative disorder; Alzheimers disease;  
KW Drosophila; wingless; wg; signal peptide; Argos; aos.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
FH Key  
FT Misc-difference 22  
FT /label= Glu22Gln  
XX  
XX WO2005041650-A1.  
XX  
XX 12-MAY-2005.  
XX  
XX 21-OCT-2004; 2004WO-US034838.  
XX  
XX 21-OCT-2003; 2003US-0512913P.  
XX  
XX 21-OCT-2003; 2003US-0512970P.  
XX  
XX 21-OCT-2003; 2003US-0512972P.  
XX  
XX 21-OCT-2003; 2003US-0513149P.  
XX  
XX 21-OCT-2003; 2003US-0513152P.  
XX  
XX 25-MAY-2004; 2004US-00852892.  
XX  
XX 25-MAY-2004; 2004US-00852951.  
XX  
XX 25-MAY-2004; 2004US-00852973.  
XX  
XX 25-MAY-2004; 2004US-00852974.  
XX  
XX 25-MAY-2004; 2004US-00853593.  
XX  
XX (ENVI-) ENVIVO PHARM INC.  
XX  
XX Lowe DA, Cummings CJ, Koenig G;  
XX  
XX WPI; 2005-366469/37.  
XX  
XX N-PSDB; ADZ88261.  
XX  
XX New transgenic flies that express the human amyloid-beta 42 peptide  
XX containing a pathogenic (e.g. Iowa, Dutch, Flemish, Italian or Arctic)  
XX mutation, and optionally, a Tau protein, useful as models of  
XX neurodegenerative disorders.  
XX  
XX Claim 1; SEQ ID NO 2; 85pp; English.  
XX  
XX This sequence represents a mutant amyloid-beta 42 (Abeta42) protein. This  
XX sequence specifically represents Abeta42(Dutch). In this mutant protein  
XX Glu22 is mutated to Gln. The mutant coding sequence is used in the  
XX generation of a transgenic fly expressing a mutant Abeta42. The  
XX transgenic fly comprises a genome comprising: a DNA sequence encoding a  
XX polypeptide comprising the Abeta42 peptide containing the Iowa, Dutch,  
XX Flemish or Italian mutation; or a first DNA sequence that encodes a human  
XX Abeta42 peptide containing the Arctic mutation, and a second DNA sequence  
XX that encodes a Tau. The transgenic fly is useful as a model of  
XX neurodegenerative disorders, such as Alzheimer's disease. It may be used  
XX for identifying genetic modifiers or for identifying therapeutic  
XX compounds that may treat neurodegenerative disorders. The transgenic fly  
XX is a Drosophila. The DNA sequence(s) is/are operatively linked to an

expression control sequence. The expression control sequence is a tissue specific expression control sequence. The DNA sequence is fused to a sequence encoding a signal peptide. Identifying an agent active in neurodegenerative disease comprises providing a first transgenic fly with an observable phenotype; contacting it with a candidate agent; and observing a phenotype of the first transgenic fly relative to the phenotype of a control fly, where an observable fly difference in the phenotype of the first transgenic fly relative to the control fly is indicative of an agent active in neurodegenerative disease. The transgenic fly is an adult fly or is in its larval stage. The expression control sequence is a tissue specific expression control sequence or comprises a UAS control element. The first DNA sequence is fused to a sequence encoding a signal peptide. The signal peptide is the wingless (wg) signal peptide or the Argos (aos) signal peptide. The observable phenotype is selected from rough eye, concave wing, a behavioral phenotype, and locomotor dysfunction. Alternatively, identifying an agent active in neurodegenerative disease comprises providing the above transgenic fly and a control wild-type fly; contacting the first transgenic fly and the control wild-type fly with a candidate agent; and observing a difference in phenotype between the transgenic fly and the control fly, where a difference in phenotype is indicative of an agent active in neurodegenerative disease.

SQ Sequence 42 AA;

Query Match 100.0%; Score 34; DB 9; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||  
16 KLVFFPAQ 22

RESULT 27

AEA37375  
ID AEA37375 standard; peptide; 42 AA.

AC AEA37375;

DT 25-AUG-2005 (first entry)

DE Human amyloid-beta peptide 42 comprising Dutch mutation, SEQ ID 1.

XX Nootropic; Neuroprotective; CNS-Gen.; Antiinflammatory; Dermatological;  
KW Immunosuppressive; Cytostatic; Antiparkinsonian; Cerebroprotective;  
KW Muscular-Gen.; transgenic insect; Alzheimers disease;  
KW neurodegenerative disease; motor neurone disease; dementia;  
KW Guillain Barre syndrome; lupus; brain tumor; spinal cord tumor;  
KW Down syndrome; parkinsons disease; Pick's disease;  
KW restless legs syndrome; Sydenham's chorea; beta-amyloid.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Misc-difference 22

FT /note= "Wild-type Glu substituted with Gln"

XX US2005132424-A1.

XX 16-JUN-2005.

PD 21-OCT-2004; 2004US-00969898.

XX 21-OCT-2003; 2003US-0512972P.

PR 25-MAY-2004; 2004US-00853593.

XX (ENVI-) ENVIVO PHARM INC.

XX Lowe DA, Koenig G, Cummings CJ;

XX WPI; 2005-424631/43.

DR N-PSDB; AEA37376.

XX New transgenic fly comprising a human amyloid-beta peptide 42 containing  
PT a Dutch mutation and a Tau protein, useful for identifying agents to  
PT treat neurodegenerative disorders.

XX Claim 1; SEQ ID NO 1; 26pp; English.

XX The present invention relates to a transgenic fly whose genome comprises  
CC a first DNA sequence that encodes a human amyloid-beta (Abeta) peptide 42  
CC of amyloid precursor protein (APP) containing the Dutch mutation  
CC (AEA37375), and a second DNA sequence that encodes a human Tau protein.  
CC The Dutch mutation, Glu22Gln, is associated with Alzheimer's disease. The  
CC DNA sequence is also fused to a signal sequence. Also claimed is a method  
CC of identifying an agent active in neurodegenerative disease. The  
CC transgenic flies of the invention are useful for identifying genetic  
CC modifiers and therapeutic compounds for treating neurodegenerative  
CC disorders such as Alzheimer's disease, amyotrophic lateral sclerosis,  
CC dementia, Guillain-Barre syndrome, lupus, brain and spinal tumors, Down's  
CC syndrome, Parkinson's disease, Pick's disease, restless leg syndrome and  
CC Sydenham's chorea.

SQ Sequence 42 AA;

Query Match 100.0%; Score 34; DB 9; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||  
16 KLVFFPAQ 22

RESULT 28

AAE55697

ID AAE55697 standard; protein; 53 AA.

XX AC AAE55697;

XX 25-MAR-2003 (revised)

DT 29-DEC-1994 (first entry)

XX Sequence of unidentified protein sequence ID number 22.

XX Amyloid precursor protein; APP; plaque; beta/A4; Alzheimers; transgene;  
KW ss.

XX Synthetic.

XX WO9412627-A1.

XX 09-JUN-1994.

XX 24-NOV-1993; 93WO-US011480.

XX 25-NOV-1992; 92US-00989850.

PR 09-NOV-1993; 93US-00149222.

XX (CEPH-) CEPHALON INC.

XX Scott RW, Howland DS;

XX WPI; 1994-200256/24.

XX Transgenic animal model for Alzheimer's disease - contains transgene  
PT encoding amyloid protein under transcriptional control of synapsin gene  
PT promoter.

XX Example; Page 55; 94pp; English.

XX There was no apparent reference to sequence ID numbers 20, 21 or 22 in  
CC the specification. The specification describes a transgenic animal model  
CC for Alzheimer's disease. A transgenic animal harbouring a transgene  
CC coding for an amyloid protein under the control of a promoter is claimed.

CC The amyloid protein can be APP695, APP751 or APP770. The coding sequence  
 CC may contain a mutation, including the hereditary cerebral haemorrhage  
 CC with amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's disease  
 CC (FAD). Perhaps SQ IDs 20-22 corresp. to wt, HCHWA-DT and FAD? (Updated on  
 CC 25-MAR-2003 to correct PN field.)  
 XX Sequence 53 AA;

Query Match 100.0%; Score 34; DB 2; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7  
 Db 20 KLVFFFAQ 26

RESULT 29  
 AAW26391  
 ID AAW26391 standard; peptide; 63 AA.  
 XX AC AAW26391;

XX 25-MAR-2003 (revised)  
 DT 15-DEC-1997 (first entry)  
 XX Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;  
 KW mutin; secretase; Alzheimer's disease;  
 KW hereditary cerebral haemorrhage with amyloidosis; human.  
 XX Homo sapiens.

Key	Location/Qualifiers
Peptide	10..51
	/label= BAP(E22Q)
	/notes= "beta-amyloid protein E22Q mutant"
Cleavage-site	25..26
	/notes= "secretase cleavage site"
Domain	38..61
	/label= Transmembrane

US5652092-A.  
 29-JUL-1997.  
 05-JUN-1995; 95US-00462859.  
 01-MAY-1992; 92US-00877675.  
 20-SEP-1993; 93US-00123659.

(AMCY ) AMERICAN CYANAMID CO.

Jacobsen JS, Vitek MP;

WPI; 1997-392937/36.

Screening for compounds which reduce beta-amyloid protein formation -  
 using cells which express a construct encoding a marker and an amyloid  
 precursor mutin derived from APP isoforms.

Disclosure; Fig 5A; 84pp; English.

CC This peptide sequence shows the region of amyloid precursor protein (APP)  
 CC that includes a beta-amyloid protein (BAP) carrying a point mutation (BAP  
 CC E22Q) found in patients with hereditary cerebral haemorrhage with  
 CC amyloidosis of Dutch origin (HCHWA-D). In an attempt to engineer an APP  
 CC non-cleavable substrate for secretase, an APP-reporter (APP-REP) protein  
 CC that carries the E22Q mutation has been expressed in recombinant host  
 CC cells. This resulted in the secretion of an N-terminal fragment  
 CC indistinguishable from that of APP-REP 751 (see AAW26393-94). Non-  
 CC cleavable APP substrates can be used to detect other putative abnormal

CC APP processing events. They can also be used to investigate cellular post  
 CC -translational modifications to APP in order to determine the potential  
 CC influence on normal secretase and abnormal BAP 'clipping' activities.  
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 63 AA;

Query Match 100.0%; Score 34; DB 2; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 4.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7  
 Db 25 KLVFFFAQ 31

RESULT 30  
 AAW26511  
 ID AAW26511 standard; peptide; 63 AA.  
 XX AC AAW26511;

XX 25-MAR-2003 (revised)  
 DT 06-JAN-1998 (first entry)  
 XX Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;  
 KW mutin; secretase; Alzheimer's disease;  
 KW hereditary cerebral haemorrhage with amyloidosis; human.  
 XX Homo sapiens.

Key	Location/Qualifiers
Peptide	10..51
	/label= BAP(E22Q)
	/notes= "beta-amyloid protein E22Q mutant"
Cleavage-site	25..26
	/notes= "secretase cleavage site"
Domain	38..61
	/label= Transmembrane

US5656477-A.  
 12-AUG-1997.  
 20-SEP-1993; 93US-00123659.  
 01-MAY-1992; 92US-00877675.

(AMCY ) AMERICAN CYANAMID CO.

Jacobsen JS, Vitek MP;

WPI; 1997-414594/38.

Nucleic acid encoding amyloid precursor mutin(s) - comprising reporter  
 gene and coding sequence, for identifying compounds which modify the  
 activity of proteolytic enzymes which cleave APP.

Disclosure; Fig 5A; 84pp; English.

CC This peptide sequence shows the region of amyloid precursor protein (APP)  
 CC that includes a beta-amyloid protein (BAP) carrying a point mutation (BAP  
 CC E22Q) found in patients with hereditary cerebral haemorrhage with  
 CC amyloidosis of Dutch origin (HCHWA-D). In an attempt to engineer an APP  
 CC non-cleavable substrate for secretase, an APP-reporter (APP-REP) protein  
 CC that carries the E22Q mutation has been expressed in recombinant host  
 CC cells. This resulted in the secretion of an N-terminal fragment  
 CC indistinguishable from that of APP-REP 751 (see AAW26393-94). Non-  
 CC cleavable APP substrates can be used to detect other putative abnormal  
 CC APP processing events. They can also be used to investigate cellular post  
 CC -translational modifications to APP in order to determine the potential



CC	also to screen for drugs that will inhibit such cleavage
CC	Revised record issued on 09-SEP-2004 : Correction to feature table key
XX	Sequence 63 AA;
SQ	
	Query Match 100.0%; Score 34; DB 2; Length 63;
CC	Best Local Similarity 100.0%; Pred. NO. 4.1;
CC	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLVFFAQ 7
DB	25 KLVFFAQ 31
RESULT 32	
AAW44746	
ID	AAW44746 standard; protein; 63 AA.
XX	
XX	AAW44746;
XX	
DT	01-JUN-1998 (first entry)
XX	
DE	APP-REP 751 [BAP E22Q] peptide.
XX	
XX	Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
KW	epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
KW	Alzheimer's disease; cleavage.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PH	Key Location/Qualifiers
FT	Cleavage-site 25..26
FT	/note= "secretase cleavage site"
FT	Misc-difference 31
FT	/note= "Glu to Gln change from wild type sequence"
XX	
XX	US5693478-A.
PN	
XX	
PD	02-DEC-1997.
XX	
XX	05-JUN-1995; 95US-00464247.
XX	
XX	01-MAY-1992; 92US-00877675.
PR	
PR	20-SEP-1993; 93US-00123659.
XX	
XX	(AMCY ) AMERICAN CYANAMID CO.
PA	
XX	
XX	Jacobson JS, Vitek MP;
PI	
XX	WPI; 1998-031744/03.
DR	
XX	
PT	Amyloid precursor mutin reporter molecule assay containing antibody
PT	recognised marker - used to study pathways associated with Alzheimer's
PT	disease.
XX	
XX	Disclosure; Fig 5A; 84pp; English.
PS	
XX	
CC	This sequence represent the beta-amyloid protein sequence from the
CC	construct APP-REP751 [BAP E22Q]. The mutant sequence can be used in a
CC	method to study secretase and beta-amyloid protein (BAP)-generating
CC	pathways associated with Alzheimer's disease by studying proteolytic
CC	Cleavage of the reporter polypeptides (e.g. AAW44744 and AAW44745)
CC	
SQ	Sequence 63 AA;
	Query Match 100.0%; Score 34; DB 2; Length 63;
CC	Best Local Similarity 100.0%; Pred. NO. 4.1;
CC	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLVFFAQ 7

Db 25 KLVFFAQ 31

RESULT 33  
AAR74695  
ID AAR74695 standard; peptide; 99 AA.  
XX  
AC AAR74695;  
XX  
XX 25-MAR-2003 (revised)  
DT 11-NOV-1995 (first entry)  
XX  
XX Beta-amyloid precursor protein mutant C-terminal peptide.  
DE  
XX Human; beta-amyloid precursor protein mutant; C-terminal peptide;  
KW gene transfer; transgenic animal; Alzheimer disease model; gene therapy.  
KW  
XX Homo sapiens.  
OS  
XX EP653154-A2.  
PN  
XX 17-MAY-1995.  
PD  
XX 07-NOV-1994; 94EP-00117512.  
PP  
XX 12-NOV-1993; 93JP-00306026.  
PR  
XX (PARH ) HOECHST JAPAN LTD.  
PA  
XX Sato M, Kobayashi T, Tada N, Shoji M, Kawarabayashi T;  
PI WPI; 1995-180492/24.  
DR N-PSDB; AAQ88697.  
XX  
XX Transgenic animal model for Alzheimer's disease - contains DNA encoding  
PT part of beta-amyloid precursor protein in a gene construct designed for  
FT over-expression in various cell types.  
PT  
XX Claim 2; Page 13; 32pp; English.  
PS  
XX The sequence represents a human brain beta-amyloid precursor protein  
CC (APP) C-terminal peptide. The peptide is a Gln-22 mutant of AAR74694. DNA  
CC encoding the peptide may be transferred, along with a signal peptide  
CC (e.g. AAR74693) gene into somatic and germ cells of a non-human mammal,  
CC and the resulting transgenic animal may be used as a model for Alzheimer  
CC disease (AD). The animal model exhibits symptoms similar to AD, producing  
CC large quantities of APP C-terminal peptide, death of neuron cells in  
CC pyramidal cells at cerebral amyloid regions, increases in glial cells and  
CC deposition of abnormally phosphorylated tau protein. The animal model may  
CC be used to develop new therapies for AD, including gene therapy  
CC strategies. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 34; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
DB 16 KLVFFAQ 22

RESULT 34  
AAE14377  
ID AAE14377 standard; peptide; 100 AA.  
XX  
AC AAE14377;  
XX  
XX 12-MAR-2002 (first entry)  
DT  
XX Amyloid precursor protein beta-CTF domain #7.  
DE  
XX

Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;  
APP; beta-secretase; Alzheimer's disease.  
Unidentified.  
WO200183811-A1.  
XX  
XX 08-NOV-2001.  
PD  
XX  
XX 25-APR-2001; 2001WO-US013332.  
PF  
XX  
XX 01-MAY-2000; 2000US-0201053P.  
PR  
XX (MERI ) MERCK & CO INC.  
PA  
XX Li Y, Xu M, Huang Q, Gardell S;  
PI WPI; 2002-066536/09.  
XX  
XX Novel gamma secretase substrate for assaying gamma secretase activity and  
FT identifying compounds that regulate gamma secretase activity, e.g.  
FT inhibitors of gamma secretase useful for treating Alzheimer's disease.  
XX  
XX Claim 3; Page 6; 36pp; English.  
PS  
XX The invention relates to gamma-secretase substrates containing a  
CC hydrophilic polypeptide moiety covalently joined to the carboxyl terminus  
CC of a beta-CTF domain. A beta-CTF domain is a polypeptide that can be  
CC cleaved by gamma-secretase, and that approximates the C-terminal fragment  
CC (amino acids 596-695) of amyloid precursor protein (APP) produced after  
CC cleavage of APP by beta-secretase. The hydrophilic polypeptide moiety  
CC increases the solubility of the substrate in a zwitterionic detergent.  
CC The gamma-secretase substrate is used in in vitro assays employing  
CC zwitterionic detergent for measuring and characterising the enzyme. The assay  
CC methods are useful for purifying and characterising the enzyme, to screen  
CC for compounds that modulate gamma-secretase activity, and to test the  
CC ability of a particular compound that affect gamma-secretase activity.  
CC The compounds that modulate gamma-secretase activity include gamma-  
CC secretase inhibitors which are useful in the treatment of Alzheimer's  
CC disease, and in the characterisation of the biological importance of  
CC gamma-secretase. The present sequence is a beta-CTF domain used in the  
CC invention  
XX  
SQ Sequence 100 AA;

Query Match 100.0%; Score 34; DB 5; Length 100;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
DB 17 KLVFFAQ 23

RESULT 35  
AAE14385  
ID AAE14385 standard; protein; 108 AA.  
XX  
AC AAE14385;  
XX  
XX 12-MAR-2002 (first entry)  
DT  
XX Gamma-secretase substrate #7.  
DE  
XX Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;  
KW APP; beta-secretase; Alzheimer's disease; fusion protein.  
KW  
XX Unidentified.  
OS  
XX Key Location/Qualifiers  
FH 1..100  
FT Region /label= Beta-CTF\_domain  
FT Region 101..108

```

FT XX /note= "Hydrophilic moiety"
PN PN WO200183811-A1.
XX XX
PD PD 08-NOV-2001.
XX XX
PF PF 25-APR-2001; 2001WO-US013332.
XX XX
PR PR 01-MAY-2000; 2000US-0201053P.
XX XX
PA (MERI ) MERCK & CO INC.
XX XX
PI Li Y, Xu M, Huang Q, Gardell S;
XX XX
DR WPI; 2002-066536/09.
XX XX
PT Novel gamma secretase substrate for assaying gamma secretase activity and
PT identifying compounds that regulate gamma secretase activity, e.g.
PT inhibitors of gamma secretase useful for treating Alzheimer's disease.
XX XX
PS Claim 8; Page 9; 36pp; English.
XX XX
CC The invention relates to gamma-secretase substrates containing a
CC hydrophilic polypeptide moiety covalently joined to the carboxyl terminus
CC of a beta-CTF domain. A beta-CTF domain is a polypeptide that can be
CC cleaved by gamma-secretase, and that approximates the C-terminal fragment
CC (amino acids 596-695) of amyloid precursor protein (APP) produced after
CC cleavage of APP by beta-secretase. The hydrophilic polypeptide moiety
CC increases the solubility of the substrate in a zwitterionic detergent.
CC The gamma-secretase substrate is used in in vitro assays employing
CC zwitterionic detergent for measuring gamma-secretase activity. The assay
CC methods are useful for purifying and characterising the enzyme, to screen
CC for compounds that modulate gamma-secretase activity, and to test the
CC ability of a particular compound that affect gamma-secretase activity.
CC The compounds that modulate gamma-secretase activity include gamma-
CC secretase inhibitors which are useful in the treatment of Alzheimer's
CC disease, and in the characterisation of the biological importance of
CC gamma-secretase. The present sequence is an example of gamma-secretase
CC substrate of the invention. The substrate is a fusion protein containing
CC APP beta-CTF domain and a hydrophilic moiety
XX XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 34; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 17 KLVFFAQ 23

RESULT 36
AAR8300
ID AAR8300 standard; peptide; 7 AA.
XX XX
AC AAR8300;
XX XX
DT 23-FEB-1996 (first entry)
XX XX
DE Non-amnestic peptide Beta-A4 (16-22).
XX XX
KW memory; enhancer; topographic model; amnestic peptide binding site;
KW beta-A4.
XX XX
OS Synthetic.
XX XX
PN WO9507093-A1.
XX XX
PD 16-MAR-1995.
XX XX
PF 08-SEP-1994; 94WO-US010083.
XX XX

PR 08-SEP-1993; 93US-00117927.
XX XX
PA (CITY ) CITY OF HOPE.
XX XX
PI Roberts E;
XX XX
DR WPI; 1995-123235/16.
XX XX
PT Topographic model for amnestic peptide binding - used to design cpds.
PT which enhance memory; and new peptide(s) so designed.
XX XX
PS Disclosure; Page 28; 51pp; English.
XX XX
CC The peptide AAR8300 corresponds to residues 16-22 of beta-A4 was
CC designed as a potential memory enhancing peptide but was found not to be
CC amnestic. (Amnestic peptides are memory-enhancing at lower concentrations
CC than those at which they cause amnesia)
XX XX
SQ Sequence 7 AA;

Query Match 91.2%; Score 31; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 37
AAR87921
ID AAR87921 standard; peptide; 7 AA.
XX XX
AC AAR87921;
XX XX
DT 01-MAR-1996 (first entry)
XX XX
DE Test peptide used in study of antagonism of amyloid beta protein.
XX XX
KW amnesia; amyloid beta; Alzheimer's disease.
XX XX
OS Synthetic.
XX XX
PN WO9508999-A1.
XX XX
PD 06-APR-1995.
XX XX
PF 16-SEP-1994; 94WO-US010475.
XX XX
PR 29-SEP-1993; 93US-00127904.
XX XX
PA (CITY ) CITY OF HOPE.
XX XX
PI Roberts E;
XX XX
DR WPI; 1995-147244/19.
XX XX
PT New peptide(s) which block binding of amyloid beta protein - used for
PT antagonising the amnestic effects of amyloid beta protein, partic. in
PT Alzheimer's disease.
XX XX
PS Disclosure; Page 9; 27pp; English.
XX XX
CC The invention relates to three new peptides which block the amnestic
CC effects of amyloid beta protein and which can be used to ameliorate
CC amnesia and other neurotoxicity in Alzheimer's disease caused by
CC deposition of this protein. The peptides themselves are not amnestic or
CC memory-enhancing. The new peptides are described in AAR87912, AAR87913
CC and AAR87914. The present sequence is an additional peptide tested in the
CC process but found not to be active
XX XX
SQ Sequence 7 AA;

```

Query Match 91.2%; Score 31; DB 2; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
 Db 1 KLVFFAE 7

## RESULT 38

AAB67281  
 ID AAB67281 standard; peptide; 7 AA.

AC AAB67281;  
 XX

DT 20-APR-2001 (first entry)

DE Residues 16-22 of Alzheimer's Abeta peptide.

XX Alzheimer's; Abeta; beta-strand.

XX Homo sapiens.

PN WO200107473-A1.

XX 01-FEB-2001.

XX 28-JUL-2000; 2000WO-GB002901.

XX 28-JUL-1999; 99GB-00017724.

XX (STOTT/) STOTT K.

XX Stott K;

XX WPI; 2001-182777/18.

XX Novel chemical compound or composition useful for preventing beta-strand  
 association, comprises peptides containing N-alpha substituted L-amino  
 acids.

XX Claim 17; Page 46; 77pp; English.

XX The present invention relates to a chemical compound or composition  
 comprising a peptide with a beta strand forming section and associates  
 with a target beta-strand formed by a separate peptide-containing  
 molecule. The invention is useful for inhibiting or reversing the  
 association of target beta-strand, formed by Alzheimer's Abeta peptide  
 into a beta-sheet or beta-fibre and the aggregation of proteins or  
 peptides

XX Sequence 7 AA;

Query Match 91.2%; Score 31; DB 4; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
 Db 1 KLVFFAE 7

## RESULT 39

ABB04920  
 ID ABB04920 standard; peptide; 7 AA.

XX ABB04920;  
 XX

DT 14-MAR-2002 (first entry)

XX Human amyloid beta protein (beta-A4) peptide 16-22 SEQ ID NO:13.

XX Human; amyloid beta protein; beta-A4; memory enhancement; learning.

XX Homo sapiens.  
 XX US6320024-B1.  
 XX 20-NOV-2001.  
 XX 09-MAR-1999; 99US-00264709.  
 XX 07-FEB-1997; 97US-00797782.  
 XX (ROBE/) ROBERTS E.  
 XX Roberts E;  
 XX WPI; 2002-096566/13.  
 XX New peptide compound useful for design of substances that enhance memory.  
 XX Disclosure; Col 6; 30pp; English.

XX The present invention describes a novel peptide compound comprising Lys-  
 His-Tyr-beta-alanine, which has a memory modulating effect. The peptide  
 has nootropic activity. The peptide can be used for the development of  
 topographic models useful to design and synthesise memory-enhancing and  
 life-quality improving substances. The peptide compound restores the  
 balance between excitatory and inhibitory systems in the brain, which is  
 required for optimal acquisition and retention of learning and helps to  
 correct defects in the balance that arise as a result of aging.  
 XX infections and injury. The substances exert reyebernatizing effects on  
 nervous system function and has more prolonged desired effects at lower  
 doses than the peptide structures. The substances mimic the action of  
 active peptides without having a peptide structure and do not subject to  
 degradation of peptide-splitting enzymes in the gut or other tissues. The  
 present sequence represents a human amyloid beta protein (beta-A4)  
 peptide which is not amnesiac, and is used in the exemplification of the  
 present invention

XX Sequence 7 AA;

Query Match 91.2%; Score 31; DB 5; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
 Db 1 KLVFFAE 7

## RESULT 40

ABB82630  
 ID ABB82630 standard; peptide; 7 AA.

XX ABB82630;  
 AC

DT 04-FEB-2003 (first entry)

DE Abeta fibrillogenesis inhibitor peptide Abeta16-22.

XX Abeta; beta-amyloid; fibrillogenesis; fibril; nootropic; neuroprotective;  
 KW cerebroprotective; haemostatic; antipyrretic; nephrotropic; vasotropic;  
 KW dermatological; auditory; antidiabetic; cytostatic; antiinflammatory;  
 KW antimicrobial; anticonvulsant; antidiabetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 3..6

XX /note= "can be methylated; both the methylated and non-  
 methylated versions of this peptide are poor  
 fibrillogenesis inhibitor"

XX Modified-site 7

XX /note= "C-terminal CONH2"

XX WO200274931-A2.  
 XX 26-SEP-2002.  
 XX 20-MAR-2002; 2002WO-US008803.  
 XX 20-MAR-2001; 2001US-0277477P.  
 XX (UYCH-) UNIV CHICAGO.  
 XX Gordon DJ, Meredith SC;  
 XX WPI; 2003-040553/03.  
 XX Novel peptide for inhibiting fibrillogenesis, and for screening  
 PT fibrillogenesis inhibitors, has beta-strand with one face having hydrogen  
 PT bonds and other face blocking propagation of hydrogen bonding between  
 PT beta-strands.  
 XX Disclosure; Page 7; 151pp; English.  
 XX The invention relates to a peptide (I) inhibiting fibrillogenesis, that  
 CC comprises a beta-strand with two faces, where the first face has hydrogen  
 CC bonds, and the second face blocks or disrupts propagation of hydrogen  
 CC bonding between beta-strands needed to form fibrils. (I) is useful for  
 CC inhibiting fibrillogenesis, for detecting fibrils in a subject and for  
 CC screening candidate fibrillogenesis inhibitors. A pharmaceutical  
 CC composition comprising (I) is useful for inhibiting or disassembling  
 CC fibrils associated with pathological states such as Alzheimer's disease,  
 CC Down's syndrome, Dutch-type hereditary cerebral haemorrhage amyloidosis,  
 CC reactive amyloidosis, familial Mediterranean fever, familial amyloid  
 CC nephropathy with utricaria and deafness, Muckle-Wells syndrome,  
 CC idiopathic myeloma, macroglobulinemia-associated myeloma, familial  
 CC amyloid polynuropathy, familial amyloid cardiomyopathy, isolated cardiac  
 CC amyloid, systemic senile amyloidosis, adult onset diabetes, insulinoma,  
 CC isolated atrial amyloid, medullary carcinoma of the thyroid, familial  
 CC amyloidosis, hereditary cerebral haemorrhage with amyloidosis, familial  
 CC amyloidotic polynuropathy, scrapie, Creutzfeldt-Jakob disease, Gerstmann  
 CC -Straussler-Scheinker syndrome, bovine spongiform encephalitis, prion-  
 CC mediated diseases, or Huntington's disease. (I) is useful for treating  
 CC disease associated with fibrillogenesis or for creating and/or diagnosing  
 CC a subject which is a mammal, preferably human, having protein aggregation  
 CC disease or protein misfolding disease. The composition is useful in both  
 CC preventive and curative therapies of fibril based pathologies mentioned  
 CC above. The present sequence represents a peptide which can comprise  
 CC consecutive N-methylation, but is a weak inhibitor of Abeta  
 CC fibrillogenesis  
 XX Sequence 7 AA;  
 SQ

Query Match 91.2%; Score 31; DB 6; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 |||||:  
 Db 1 KLVFFAE 7

RESULT 41  
 AAE35454  
 ID AAE35454 standard; peptide; 7 AA.  
 XX AAE35454;  
 AC AAE35454;  
 XX 17-JUN-2003 (first entry)  
 DT Abeta peptide #25.  
 DE All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;

KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.  
 XX Unidentified.  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..7  
 FT /note= "D-form residues"  
 FT Modified-site 7  
 FT /note= "C-terminal amide"  
 XX WO200296937-A2.  
 XX 05-DEC-2002.  
 XX 29-MAY-2002; 2002WO-CA000763.  
 XX 29-MAY-2001; 2001US-00857847.  
 XX (NEUR-) NEUROCHEM INC.  
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;  
 XX WPI; 2003-201269/19.  
 XX Prevention and/or treatment of an amyloid-related disease e.g.  
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 XX Claim 1; Page 59; 44pp; English.  
 CC The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention  
 XX Sequence 7 AA;  
 SQ

Query Match 91.2%; Score 31; DB 6; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 |||||:  
 Db 1 KLVFFAE 7

RESULT 42  
 AAE35453  
 ID AAE35453 standard; peptide; 7 AA.  
 XX AAE35453;  
 AC AAE35453;  
 XX 17-JUN-2003 (first entry)  
 DT Abeta peptide #24.  
 DE Abeta peptide #24.  
 XX

KW	All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
KW	cerebral amyloid angiopathy; amyloid disease; amylosing spondylitis;
KW	psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
KW	Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
KW	chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
KW	Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
KW	ulcer; antiinflammatory; cystostatic; uropathic; therapy.
XX	Unidentified.
OS	
OS	
OS	
FT	Key Location/Qualifiers
FT	Misc-difference 1..7 /note= "D-form residues"
XX	
XX	WO200296937-A2.
PN	
PN	
PD	05-DEC-2002.
XX	
PF	29-MAY-2002; 2002WO-CA000763.
XX	
XX	29-MAY-2001; 2001US-00867847.
PR	
PR	(NEUR-) NEUROCHEM INC.
PA	
PI	Gervais F, Hebert L, Chalifour RJ, Kong X;
XX	WPI; 2003-201269/19.
XX	
XX	Prevention and/or treatment of an amyloid-related disease e.g.
PT	Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
XX	
XX	Claim 1; Page 59; 44pp; English.
XX	
CC	The invention relates to a method for prevention and/or treatment of an
CC	amyloid-related disease which comprises administration of an all-D-
CC	amyloid-beta peptide. The method is used for preventing and/or treating
CC	Alzheimer's and other amyloid related disease e.g. cerebral amyloid
CC	angiopathy; for altering serum levels of amyloid-beta in a mammal and
CC	favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
CC	the mammal; and reducing or inhibiting the formation of plaques. It is
CC	also used for treating AA (reactive) amyloid diseases including
CC	inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
CC	arthritis, amylosing spondylitis, psoriasis, psoriatic arthropathy,
CC	Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
CC	disease. AA deposits are also produced as a result of chronic microbial
CC	infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
CC	ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
CC	Certain malignant neoplasms can also result in AA fibril amyloid deposits
CC	including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
CC	and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
CC	present sequence is an Abeta peptide used to illustrate the method of the
CC	invention
XX	
XX	Sequence 7 AA;
XX	
Qy	Query Match 91.2%; Score 31; DB 6; Length 7;
Db	Best Local Similarity 85.7%; Pred. No. 2e+06;
Db	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0
Qy	1 KLVFFPAQ 7
Db	1 KLVFFPAE 7
XX	
XX	RESULT 43
XX	ADD20746
XX	ID ADD20746 standard; peptide; 7 AA.
XX	AC ADD20746;
XX	
XX	15-JAN-2004 (first entry)
XX	Human beta-amyloid 16-22 amino acid sequence.

XX human; calcitonin; multiple myeloma; medullary carcinoma;  
 KW aortic medical carcinoma; antidiabetic; nootropic; neuroprotective;  
 KW antiparkinsonian; fibril; type-II diabetes mellitus; amyloidosis;  
 KW self-aggregating peptide; amyloid-associated disease;  
 KW Alzheimer's disease; SAA amyloidosis; hereditary Icelandic syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003063760-A2.  
 XX  
 XX 07-AUG-2003.  
 XX  
 XX 30-JAN-2003; 2003WO-IL000079.  
 XX  
 XX 31-JAN-2002; 2002US-0352578P.  
 XX 01-JUL-2002; 2002US-0392266P.  
 XX 06-SEP-2002; 2002US-00235852.  
 XX 27-DEC-2002; 2002US-0436453P.  
 XX  
 XX (UYRA-) UNIV RAMOT AT TEL AVIV LTD.  
 XX  
 XX Gazit E;  
 XX  
 XX WPI; 2003-689501/65.  
 XX  
 XX New self-aggregating peptide useful for treating amyloid-associated  
 PT diseases e.g., Alzheimer's disease, Parkinson's disease, hereditary  
 PT Icelandic syndrome, multiple myeloma, medullary carcinoma.  
 XX  
 XX Example 21; Fig 1; 138pp; English.  
 XX  
 XX This invention relates to novel self-aggregating peptides that can be  
 CC used for the diagnosis and treatment of amyloid-associated diseases.  
 CC Specifically, it refers to peptides, and antibodies directed  
 CC thereagainst, which can prevent or reduce fibril formation and  
 CC disaggregate formed aggregates by competitive destabilisation.  
 CC Accordingly, these compositions can be used directly to inhibit the  
 CC production of islet amyloid polypeptides (IAPPs) and for the inhibition  
 CC of amyloidosis. As such they are useful for treating a variety of  
 CC unrelated pathological conditions including type-II diabetes mellitus,  
 CC Alzheimer's disease, SAA amyloidosis, hereditary Icelandic syndrome,  
 CC multiple myeloma, medullary carcinoma, aortic medical carcinoma.  
 CC Additionally, they can be described as exhibiting activities such as  
 CC antidiabetic, nootropic, neuroprotective and antiparkinsonian. This  
 CC peptide sequence is a human medin peptide fragment (also known as milk  
 CC fat globule-EGF factor 8 protein, which is the main constituent of aortic  
 CC medial amyloid deposits). This peptide sequence is a human calcitonin-  
 CC derived peptide fragment 2 used to show self-assembly and hydrophobicity  
 CC of amyloid proteins in an exemplification of the invention.  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 91.2%; Score 31; DB 7; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFPAQ 7  
 Db 1 KLVFFPAE 7  
 RESULT 45  
 ADP64922  
 ID ADP64922 standard; protein; 7 AA.  
 XX  
 AC ADP64922;  
 XX  
 XX 09-SEP-2004 (first entry)  
 DT  
 XX Beta-amyloid central core structure amino acid sequence.  
 DE  
 XX spherical nanostructure; tubular nanostructure; field emitter device;  
 KW

KW nanoscale environment; electron emission lithography; memory cell;  
 KW mechanical transmission device; electronic inverter;  
 KW heat transfer device; electron emission; beta-amyloid;  
 KW central aromatic core structure; nanotube self-assembly;  
 KW Alzheimer's disease; beta-amyloid core recognition element.  
 XX  
 XX Synthetic.  
 XX  
 XX WO2004052773-A2.  
 XX  
 XX 24-JUN-2004.  
 XX  
 XX 09-DEC-2003; 2003WO-IL001045.  
 XX  
 XX 09-DEC-2002; 2002US-0431709P.  
 XX 31-MAR-2003; 2003US-0458378P.  
 XX  
 XX (UYRA-) UNIV RAMOT AT TEL AVIV LTD.  
 XX  
 XX Reches M, Gazit E;  
 XX  
 XX WPI; 2004-480855/45.  
 XX  
 XX Tubular of spherical nanostructure for e.g. use in obtaining information  
 PT from nanoscale environment, is composed of peptides including aromatic or  
 PT polyaromatic amino acids.  
 XX  
 XX Example 1; Fig 9a; 94pp; English.  
 XX  
 XX The present invention describes a tubular of spherical nanostructure  
 CC composed of peptides including no more than 4 aromatic or polyaromatic  
 CC amino acids. Also described: (1) a method of generating a tubular or  
 CC spherical nanostructure; (2) a field emitter device; (3) a device for  
 CC obtaining information from a nanoscale environment; (4) an apparatus for  
 CC electron emission lithography; (5) a memory cell; (6) a mechanical  
 CC transmission device; (7) an electronic inverter having a first switching  
 CC device and a second switching device; (8) a composition; (9) a heat  
 CC transfer device; (10) a method of emitting electrons; and (11) a method  
 CC of obtaining information from a nanoscale environment. The nanostructure  
 CC can be used in a field emitter device, a device for obtaining information  
 CC from a nanoscale environment, an apparatus for electron emission  
 CC lithography, a memory cell, a mechanical transmission device, an  
 CC electronic inverter, and a matrix-containing composition. It is used in  
 CC emitting electrons, in obtaining information from a nanoscale  
 CC environment, in recording binary information, in transmitting mechanical  
 CC motion, grabbing and/or in manipulating nanoscale objects, and  
 CC transferring heat. The nanostructure is highly robust under extreme pH  
 CC and temperatures. It enhances electromagnetic fields near ultra small  
 CC metal objects. The use of nanostructure as gates in electronic device  
 CC allows operation at low gate voltage and enables the switching of several  
 CC individual devices on the same substrates. The present sequence  
 CC represents a beta-amyloid central aromatic core structure amino acid  
 CC sequence, which is used in an example from the present invention for the  
 CC nanotube self-assembly of Alzheimer's beta-amyloid core recognition  
 CC element.  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 91.2%; Score 31; DB 8; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFPAQ 7  
 Db 1 KLVFFPAE 7  
 RESULT 46  
 ADQ37278  
 ID ADQ37278 standard; peptide; 7 AA.  
 XX  
 AC ADQ37278;  
 XX

DT 07-OCT-2004 (first entry)  
 DE Vaccine antigen amyloid-beta related amino acid sequence.  
 XX  
 XX amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX  
 OS Synthetic.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..7 /note= "D-form residues"  
 FT  
 XX WO2004058239-A1.  
 XX  
 XX 15-JUL-2004.  
 XX  
 XX 24-DEC-2003; 2003WO-CA002021.  
 XX  
 XX 24-DEC-2002; 2002US-0436379P.  
 XX 23-JUN-2003; 2003US-0482214P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX  
 XX Gervais F, Bellini F;  
 XX WPI; 2004-543342/52.  
 XX  
 XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.  
 XX  
 PS Disclosure; Page 67; 143pp; English.  
 XX  
 CC The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C): (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic

CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as a vaccine antigen in the exemplification of the  
 XX present invention.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 91.2%; Score 31; DB 8; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 DB 1 KLVFFPAE 7

# RESULT 47

ADQ37279

XX ADQ37279 standard; peptide; 7 AA.

XX AC ADQ37279;

XX DT 07-OCT-2004 (first entry)

XX DE Vaccine antigen amyloid-beta related amino acid sequence.

XX KW amyloid-beta; amyloid-beta related disease;

XX KW amyloid-beta fibril formation; immune response; neurotropic;

XX KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

XX KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;

XX KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

XX KW cardiant; antidepressant; endocrine; hypnotic;

XX KW amyloid-beta fibril formation modulator; immune system modulator;

XX KW Alzheimer's disease; mild cognitive impairment;

XX KW mild-to-moderate cognitive impairment; vascular dementia;

XX KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

XX KW senile dementia; Down's syndrome; inclusion body myositis;

XX KW age-related macular degeneration; hypothyroidism;

XX KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;

XX KW behavioural dysfunction; neurological condition; psychological condition;

XX KW vaccine antigen.  
 XX  
 XX Synthetic.

XX Key Location/Qualifiers  
 XX Misc-difference 1..7 /note= "D-form residues"  
 XX Modified-site 7 /note= "amidated"

XX FT WO2004058239-A1.

XX FT 15-JUL-2004.

XX PD 24-DEC-2003; 2003WO-CA002021.

XX PF 24-DEC-2002; 2002US-0436379P.

XX PR 23-JUN-2003; 2003US-0482214P.

XX PR (NEUR-) NEUROCHEM INT LTD.

XX PA Gervais F, Bellini F;

XX PI WPI; 2004-543342/52.

XX DR  
 XX



PT Composition for treating e.g. Alzheimer's disease comprises first agent  
PT that prevents or treats amyloid-beta related disease and second agent  
PT that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 67; 14pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
CC modulates amyloid-beta fibril formation or induces a prophylactic or  
CC therapeutic immune response against amyloid-beta fibril formation; or  
CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
CC fibril formation. Also described is a kit comprising (C). (C) have  
CC nootropic, neuroprotective, cerebroprotective, haemostatic,  
CC ophthalmologic, antithyroid, vasotropic, cardiovascular, tranquiliser,  
CC uteratic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
CC and can be used as amyloid-beta fibril formation modulators, and as  
CC immune system modulators. (C) can be used for preventing or treating an  
CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
CC Down's syndrome, inclusion body myositis, age-related macular  
CC degeneration, or a condition associated with Alzheimer's disease  
CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
CC field deficits, incoordination, gait disturbance, transient ischaemic  
CC attack or stroke, transient alertness, attention deficit, frequent falls,  
CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
CC damage), or a psychological condition (e.g. depression, delusions,  
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
CC having amyloid-beta deposits. The present sequence represents a peptide  
CC that can be used as a vaccine antigen in the exemplification of the  
CC present invention.

XX Sequence 7 AA;

Query Match 91.2%; Score 31; DB 8; Length 7;  
Best Local Similarity 85.7%; Pred. NO. 2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||  
Db 1 KLVFFAE 7

RESULT 48

AAW32551  
ID AAW32551 standard; peptide; 8 AA.

XX AAW32551;

XX 21-JAN-1998 (first entry)

XX Amyloidogenic sequence amyloid beta-peptide.

XX Anti-amyloid peptide; iBeta; abnormal protein folding inhibitor;  
KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;  
KW human prion disease; Kuru; Creutzfeldt-Jakob disease;  
KW Gerstmann-Strausler-Scheinker Syndrome; animal prion disease;  
KW prion associated human neurodegenerative disease; scrapie;  
KW spongiform encephalopathy; transmissible mink encephalopathy;  
KW Chronic wasting disease; mule; deer; elk; human.

XX Homo sapiens.  
OS Synthetic.

XX WO9639834-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US010220.

XX 07-JUN-1995; 95US-00478326.

XX 10-APR-1996; 96US-00630645.

XX (UWNY ) UNIV NEW YORK STATE.

XX Soto-Jara C, Baumann MH, Frangione B;

XX WPI; 1997-051637/05.

XX New inhibitors of fibrillogenesis proteins or peptides - used for  
PT preventing, treating or detecting amyloidosis disorders such as  
PT Alzheimer's disease.

XX Disclosure; Fig 1A; 63pp; English.

XX A method has been developed for the prevention or treatment of a disorder  
CC or disease associated with the formation of amyloid or amyloid-like  
CC deposits, involving the abnormal folding of a protein or peptide. The  
CC method involves administering an inhibitory peptide which prevents the  
CC abnormal folding or which dissolves existing amyloid or amyloid-like  
CC deposits, where the peptide comprises a sequence of 3-15 amino acid  
CC residues and has a hydrophobic cluster of at least 3 amino acids, where  
CC at least one of the 3 amino acids is a beta-sheet blocking amino acid  
CC residue selected from Pro, Gly, Asn and His. The present sequence  
CC represents an amyloidogenic sequence, amyloid beta-peptide, which is  
CC involved in the formation of several amyloid deposits. The inhibitory  
CC peptide is capable of associating with a structural determinant on the  
CC protein or peptide to structurally block and inhibit the abnormal folding  
CC into amyloid or amyloid-like deposits. The method can be used for  
CC preventing, treating or detecting e.g. Alzheimer's dementia or disease,  
CC Down's syndrome, other amyloidosis disorders, human prion diseases such  
CC as Kuru, Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker  
CC Syndrome, prion associated human neurodegenerative diseases or animal  
CC prion diseases such as scrapie, spongiform encephalopathy, transmissible  
CC mink encephalopathy and chronic wasting disease of mule deer and elk

XX Sequence 8 AA;

Query Match 91.2%; Score 31; DB 2; Length 8;  
Best Local Similarity 85.7%; Pred. NO. 2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||  
Db 1 KLVFFAE 7

RESULT 49

AAE10663

ID AAE10663 standard; peptide; 8 AA.

XX AAE10663;

XX 10-DEC-2001 (first entry)

XX Human amyloid precursor protein substrate alpha-secretase peptide #2.  
XX Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;  
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;  
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;  
KW alpha-secretase.  
XX Homo sapiens.

```

XX FH Key Key Location/Qualifiers
XX FT Cleavage-site 4. .5
XX FN GB2357767-A.
XX PD 04-JUL-2001.
XX XX
XX PF 22-SEP-2000; 2000GB-00023315.
XX PR 23-SEP-1999; 99US-00404133.
XX PR 23-SEP-1999; 99US-0155493P.
XX PR 23-SEP-1999; 99WO-US020881.
XX PR 13-OCT-1999; 99US-00416901.
XX PR 06-DEC-1999; 99US-0169232P.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX PI Bienkowski MJ, Gurney M;
XX DR WPI; 2001-444208/48.
XX PT
XX FT Polypeptide comprising fragments of human aspartyl protease with amyloid
XX PT precursor protein processing activity and alpha-secretase activity, for
XX PT identifying modulators useful in treating Alzheimer's disease.
XX PS Claim 10; Page 163; 187pp; English.
XX CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
XX CC proteins which lack transmembrane domain or amino terminal domain or
XX CC cytoplasmic domain and retains alpha-secretase activity and amyloid
XX CC protein precursor (APP) processing activity. The proteins of the
XX CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
XX CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
XX CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
XX CC are useful for treating Alzheimer's disease (AD) which causes progressive
XX CC dementia with consequent formation of amyloid plaques, neurofibrillary
XX CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
XX CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
XX CC with the substrate under acidic conditions and determining the level of
XX CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
XX CC precursor protein (APP) substrate alpha-secretase peptide which is used
XX CC for determining the enzymatic activity of Asp-1 protein lacking
XX CC transmembrane domain (TM) and containing a (His)6 tag
XX SQ Sequence 8 AA;

Query Match 91.2%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

Qy 1 KLVFFPAQ 7
Db |||||:
1 KLVFFPAE 7

RESULT 50
AAE02615
ID AAE02615 standard; peptide; 8 AA.
XX AC AAE02615;
XX XX
XX DT 10-AUG-2001 (first entry)
XX DE Human amyloid precursor protein substrate alpha-secretase peptide #2.
XX KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
XX KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;
XX KW beta-secretase.
XX OS Homo sapiens.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX FH Key Key Location/Qualifiers

```

```

PT Cleavage-site 4. .5
XX WO200123533-A2.
XX PD 05-APR-2001.
XX XX
XX PF 22-SEP-2000; 2000WO-US026080.
XX PR 23-SEP-1999; 99US-0155493P.
XX PR 23-SEP-1999; 99WO-US020881.
XX PR 13-OCT-1999; 99US-00416901.
XX PR 06-DEC-1999; 99US-0169232P.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX PI Gurney M, Bienkowski MJ;
XX DR WPI; 2001-290516/30.
XX PT
XX FT Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX PT protein, useful for the treatment of Alzheimer's disease.
XX PS Claim 10; Page 98; 189pp; English.
XX CC The present invention relates to enzymes for cleaving the alpha-
XX CC secretase site of the amyloid precursor protein (APP) and methods of
XX CC identifying those enzymes. The methods may be used to identify enzymes
XX CC that may be used to cleave the alpha-secretase cleavage site of the APP
XX CC protein. The enzymes may be used to treat or modulate the progress of
XX CC Alzheimer's disease. The present sequence is human amyloid precursor
XX CC protein (APP) substrate alpha-secretase peptide which is used for
XX CC determining the enzymatic activity of Asp-1 deltam (His)6 protein
XX SQ Sequence 8 AA;

Query Match 91.2%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

Qy 1 KLVFFPAQ 7
Db |||||:
1 KLVFFPAE 7

RESULT 51
ABB78624
ID ABB78624 standard; peptide; 8 AA.
XX AC ABB78624;
XX XX
XX DT 16-JUL-2002 (first entry)
XX DE Human alpha secretase (Abeta12-28) peptide SEQ ID NO:73.
XX KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic.
XX OS Homo sapiens.
XX PN GB2367060-A.
XX XX
XX PD 27-MAR-2002.
XX PF 29-OCT-2001; 2001GB-00025934.
XX PR 23-SEP-1999; 99US-00404133.
XX PR 23-SEP-1999; 99US-0155493P.
XX PR 23-SEP-1999; 99WO-US020881.
XX PR 13-OCT-1999; 99US-00416901.
XX PR 06-DEC-1999; 99US-0169232P.
XX PR 22-SEP-2000; 2000GB-00023315.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX FH

```

PI Blenkowski MJ, Gurney M;  
XX  
XX WPI; 2002-397167/43.  
XX  
XX Human aspartyl protease 1 substrates useful in assays to detect aspartyl  
XX PT protease activity, e.g. for the diagnosis of Alzheimer's disease.  
XX PS  
XX Example 15; Page 92; 182pp; English.

The present invention describes a human aspartyl protease 1 (hu-Asp1) substrate (I) which comprises a peptide of no more than 50 amino acids, and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1 proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with (I) under acidic conditions; and (b) determining the level of hu-Asp1 proteolytic activity; (2) a purified polynucleotide (III) comprising a nucleotide sequence that hybridises under stringent conditions to the non coding strand complementary to a defined 1804 nucleotide sequence (see ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane domain; (3) a purified polynucleotide (III') comprising a sequence that hybridises under stringent conditions to (III) (the nucleotide sequence encodes a polypeptide further lacking a pro-peptide domain corresponding to amino acids 23-62 of hu-Asp1 (see ABB7589)); (4) a vector (IV) comprising (III) or (III'); and (5) a host cell (V) transformed or transfected with (III), (III') and/or (IV). The hu-Asp1 protease substrate (I) may be used as an enzyme substrate in assays to detect aspartyl protease activity, (II) and therefore diagnose diseases associated with aberrant hu-Asp1 expression and activity such as Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present sequence represents a human alpha secretase peptide, which is used in an example from the present invention

Sequence 8 AA;

Query Match 91.2%; Score 31; DB 5; Length 8;  
Best Local Similarity 85.7%; Pred. No. 2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
Db |||||:  
1 KLVFFAE 7

RESULT 52  
ABU09765  
ID ABU09765 standard; peptide; 8 AA.  
XX  
XX AC ABU09765;  
XX DT 17-JUN-2003 (first entry)  
XX DS Amyloidogenic Amyloid beta-peptide #1.  
XX KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;  
KW pathological beta-sheet-rich conformation; Down's syndrome;  
KW amyloidosis disorder; human prion disease; kuru; CJD;  
KW Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker syndrome; GSS;  
KW prion associated human neurodegenerative disease; animal prion disease;  
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;  
KW chronic wasting disease.  
OS Homo sapiens.  
XX  
XX PN US6462171-B1.  
XX PD 08-OCT-2002.  
XX PF 12-DEC-1996; 96US-00766596.  
XX XX 07-JUN-1995; 95US-00478326.  
PR 10-APR-1996; 96US-00630645.



CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents an  
 CC antifibrillogenic peptide which is used in the exemplification of the  
 CC present invention.

XX Sequence 8 AA;

Query Match 91.2%; Score 31; DB 8; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVPFAQ 7

Db 1 KLVPFAE 7

RESULT 56

AD208900  
 ID AD208900 standard; peptide; 8 AA.

AC AD208900;

DT 16-JUN-2005 (first entry)

DE Human beta-amyloid peptide (SEQ ID No:125) probed with anti-amyloid IgG.

XX amyloid; antibody engineering; antibody production;  
 KW amyloid-associated disorder; Alzheimers disease; cancer; allergy;  
 KW autoimmune disease; Parkinsons disease;  
 KW acquired immune deficiency syndrome; multiple sclerosis; migraine;  
 KW dementia; infection; neurotropic; neuroprotective; cytostatic;  
 KW antiallergic; immunosuppressive; antiparkinsonian; antimigraine;  
 KW antimicrobial; anti-HIV; beta-amyloid.

OS Homo sapiens.

XX WO2005028511-A2.

XX 31-MAR-2005.

XX 26-MAR-2004; 2004WO-US009522.

XX 28-MAR-2003; 2003US-0458469P.

PR 28-MAR-2003; 2003US-0458474P.  
 PR 28-MAR-2003; 2003US-0458509P.  
 PR 28-MAR-2003; 2003US-0458510P.  
 XX (CENZ ) CENTOCOR INC.  
 PA (MERC/) MERCKEN M.  
 PA (BENS/) BENSON J M.  
 XX Mercken M, Benson JM;  
 XX WPI; 2005-242565/25.  
 XX New isolated mammalian anti-amyloid antibodies useful for treating  
 PT amyloid-associated disorders, such as Alzheimer's disease, cancer,  
 PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,  
 PT migraine and dementia.  
 XX Example 4; SEQ ID NO 125; 306pp; English.

XX The invention relates to at least one isolated mammalian amyloid antibody  
 CC comprising at least one variable region comprising at least one heavy  
 CC chain and at least one light chain. Of a fully defined sequence of SEQ ID  
 CC NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:  
 CC (i) at least one isolated mammalian amyloid antibody that binds to the  
 CC same region of an amyloid polypeptide as an antibody comprising at least  
 CC one heavy chain or light chain complementarity determining region (CDR)  
 CC having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)  
 CC at least one isolated mammalian amyloid antibody, comprising at least one  
 CC human CDR, where the antibody specifically binds at least one epitope  
 CC selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined  
 CC sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic  
 CC acid encoding at least one of any of the isolated mammalian amyloid  
 CC antibodies mentioned and having at least one human CDR of a fully defined  
 CC sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an  
 CC isolated nucleic acid vector comprising an isolated nucleic acid encoding  
 CC an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising  
 CC an isolated nucleic acid encoding an amyloid antibody, (vi) a method of  
 CC producing at least one amyloid antibody, (vii) a composition comprising  
 CC at least one of any of the isolated mammalian amyloid antibodies  
 CC mentioned, and at least one pharmaceutical carrier or diluent, (viii) an  
 CC anti-idiotypic antibody or fragment that specifically binds at least one  
 CC of the amyloid antibodies mentioned, (ix) a method of diagnosing or  
 CC treating an amyloid related condition in a cell, tissue, organ or animal,  
 CC comprising contacting or administering a composition comprising at least  
 CC one of the antibodies mentioned, with, or to, the cell, tissue, organ or  
 CC animal, (x) a medical device comprising at least one amyloid antibody  
 CC mentioned, where the device is suitable for contacting or administering  
 CC at least one amyloid antibody, (xi) an article of manufacture for human  
 CC pharmaceutical or diagnostic use, comprising packaging material and a  
 CC container comprising a solution or a lyophilized form of at least one of  
 CC the amyloid antibodies mentioned, and (xii) a method of producing at  
 CC least one of the isolated mammalian amyloid antibodies, comprising  
 CC providing a host cell or transgenic animal or transgenic plant or plant  
 CC cell capable of expressing the antibody in recoverable amounts. The  
 CC methods and compositions of the present invention are useful for  
 CC producing therapeutic compositions and devices for treating amyloid-  
 CC associated disorders, such as Alzheimer's disease, cancer, allergies,  
 CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,  
 CC migraine, dementia and infections. This sequence represents a peptide  
 CC from human beta-amyloid probed with anti-beta-amyloid IgG antibodies.

Sequence 8 AA;

Query Match 91.2%; Score 31; DB 9; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVPFAQ 7

Db 1 KLVPFAE 7

RESULT 57

```

AEA51423
ID AEA51423 standard; peptide; 8 AA.
XX AC AEA51423;
XX DT 08-SEP-2005 (first entry)
XX DE C-Abeta 16-22 peptide immunogen, SEQ ID NO: 54.
XX KW immunoconjugate; immunostimulant; neuroprotective; nontropic; virucide;
XX KW cytostatic; amyloidosis; Alzheimers disease; Down's syndrome;
XX KW viral infection; cancer.
XX OS Unidentified.
XX PN WO2005058941-A2.
XX PD 30-JUN-2005.
XX PF 17-DEC-2004; 2004WO-US044093.
XX PR 17-DEC-2003; 2003US-0530481P.
XX PA (ELAN-) ELAN PHARM INC.
XX PA (AMHP ) WYETH.
XX PI Arumugham RG, Prasad AK;
XX DR WPI; 2005-467099/47.
XX PT Conjugating peptide immunogen by reacting derivatized protein/polypeptide
XX PT carrier with a reactive group of an amino acid of the peptide immunogen
XX PT so that the peptide immunogen is conjugated to derivatized
XX PT protein/polypeptide carrier.
XX PS Example 10; SEQ ID NO 54; 150pp; English.
XX CC The present invention relates to methods of producing an immunogenic
XX CC conjugate of a peptide immunogen comprising Abeta peptide or fragments of
XX CC Abeta or analogs with a protein/polypeptide carrier. Given is a method of
XX CC conjugating a peptide immunogen, Abeta peptide, via a reactive group of a
XX CC residue to a protein/polypeptide carrier. The method comprises reacting a
XX CC derivatized protein/polypeptide carrier with a reactive group of an amino
XX CC acid of the Abeta peptide. In conjugating a peptide immunogen, the
XX CC keyhole limpet hemocyanin (KLH), immunoglobulin molecules, thyroglobulin,
XX CC and growth factors or hormones and preferably contains a T-cell epitope,
XX CC or is a bacterial toxoid. The growth factor or hormone is selected from
XX CC IL-1, IL-2, gamma-interferon, IL-10, GM-CSF, MIP-1alpha, MIP-1beta, or
XX CC RANTES. Described is a method of inducing an immune response in a
XX CC mammalian subject by administering an amount of the immunogenic
XX CC composition to the subject. The conjugate is useful in the manufacture of
XX CC a medicament for use in the treatment, prophylaxis, or amelioration of an
XX CC amyloidogenic disease. The disease is Alzheimer's disease or Down's
XX CC syndrome. It is also useful for treating viral infection or cancers. The
XX CC present sequence is the C-Abeta 16-22 peptide immunogen, SEQ ID NO: 54.
XX SQ Sequence 8 AA;
XX Query Match 91.2%; Score 31; DB 9; Length 8;
XX Best Local Similarity 85.7%; Pred. No. 2e+06;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KLVFFPAQ 7
XX DB |||||:
XX 2 KLVFFPAE 8
XX RESULT 58
XX AEA51420
XX ID AEA51420 standard; peptide; 8 AA.
XX AC AEA51420;
XX DT 08-SEP-2005 (first entry)
XX DE C-Abeta 16-22 peptide immunogen, SEQ ID NO: 54.
XX KW immunoconjugate; immunostimulant; neuroprotective; nontropic; virucide;
XX KW cytostatic; amyloidosis; Alzheimers disease; Down's syndrome;
XX KW viral infection; cancer.
XX OS Unidentified.
XX PN WO2005058941-A2.
XX PD 30-JUN-2005.
XX PF 17-DEC-2004; 2004WO-US044093.
XX PR 17-DEC-2003; 2003US-0530481P.
XX PA (ELAN-) ELAN PHARM INC.
XX PA (AMHP ) WYETH.
XX PI Arumugham RG, Prasad AK;
XX DR WPI; 2005-467099/47.
XX PT Conjugating peptide immunogen by reacting derivatized protein/polypeptide
XX PT carrier with a reactive group of an amino acid of the peptide immunogen
XX PT so that the peptide immunogen is conjugated to derivatized
XX PT protein/polypeptide carrier.
XX PS Example 10; SEQ ID NO 54; 150pp; English.
XX CC The present invention relates to methods of producing an immunogenic
XX CC conjugate of a peptide immunogen comprising Abeta peptide or fragments of
XX CC Abeta or analogs with a protein/polypeptide carrier. Given is a method of
XX CC conjugating a peptide immunogen, Abeta peptide, via a reactive group of a
XX CC residue to a protein/polypeptide carrier. The method comprises reacting a
XX CC derivatized protein/polypeptide carrier with a reactive group of an amino
XX CC acid of the Abeta peptide. In conjugating a peptide immunogen, the
XX CC keyhole limpet hemocyanin (KLH), immunoglobulin molecules, thyroglobulin,
XX CC and growth factors or hormones and preferably contains a T-cell epitope,
XX CC or is a bacterial toxoid. The growth factor or hormone is selected from
XX CC IL-1, IL-2, gamma-interferon, IL-10, GM-CSF, MIP-1alpha, MIP-1beta, or
XX CC RANTES. Described is a method of inducing an immune response in a
XX CC mammalian subject by administering an amount of the immunogenic
XX CC composition to the subject. The conjugate is useful in the manufacture of
XX CC a medicament for use in the treatment, prophylaxis, or amelioration of an
XX CC amyloidogenic disease. The disease is Alzheimer's disease or Down's
XX CC syndrome. It is also useful for treating viral infection or cancers. The
XX CC present sequence is the C-Abeta 16-22 peptide immunogen, SEQ ID NO: 54.
XX SQ Sequence 8 AA;
XX Query Match 91.2%; Score 31; DB 9; Length 8;
XX Best Local Similarity 85.7%; Pred. No. 2e+06;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KLVFFPAQ 7
XX DB |||||:
XX 2 KLVFFPAE 8
XX RESULT 58
XX AEA51420
XX ID AEA51420 standard; peptide; 8 AA.
XX AC AEA51420;
XX DT 08-SEP-2005 (first entry)
XX DE Immunoconjugate Abeta peptide, SEQ ID NO 51.

```

XX Immunoconjugate; immunotherapy; immunotoxin; tumor-associated antigen;  
 KW antigen; antibacterial; virucide; fungicide; antiparasitic;  
 KW neuroprotective; nootropic; cytostatic; immunotherapy; immunostimulant;  
 KW Alzheimer's disease; cancer.  
 OS Homo sapiens.  
 XX WO2005058940-A2.  
 XX 30-JUN-2005.  
 XX 17-DEC-2004; 2004WO-US042701.  
 XX 17-DEC-2003; 2003US-0530480P.  
 XX (AMHP ) WYETH.  
 XX Arumugham RG, Prasad AK;  
 PI WPI; 2005-488538/49.  
 DR Conjugating peptide immunogen, by derivatizing functional groups of  
 XX protein or polypeptide carrier, reacting reactive group of amino acid  
 PT residue of peptide immunogen with carrier having functional groups, to  
 PT produce conjugate.  
 XX Example 10; SEQ ID NO 51; 155pp; English.  
 XX The present invention relates to producing an immunogenic conjugate of a  
 CC peptide immunogen with a protein or polypeptide carrier. Specifically,  
 CC conjugating (M1) the peptide immunogen through a reactive group of an  
 CC amino acid residue to a protein/polypeptide carrier (PC) having  
 CC functional groups, by derivatizing functional groups of PC, reacting  
 CC derivatized PC with a peptide immunogen to produce the conjugate,  
 CC unreacted functional groups, so that the conjugate elicits immune  
 CC responses against peptide immunogen. In (M1), the carrier is chosen from  
 CC for example, human serum albumin, keyhole limpet hemocyanin (KLH), and  
 CC immunoglobulin molecules, hepatitis B surface antigen (HBsAg19.23), and  
 CC cholera toxin. The carrier contains a T-cell epitope. The carrier is a  
 CC bacterial or viral protein such as influenza hemagglutinin, and malaria  
 CC circumsporozoite (CS) protein. Preferably, the carrier is C.pneumoniae ORF  
 CC T858. The peptide immunogen can also be an antigen from a malignant  
 CC tumor. Antibacterial; Virucide; Fungicide; Antiparasitic; Neuroprotective  
 CC ; Nootropic; Cytostatic; Immunotherapy. The method is useful for inducing  
 CC an immune response against pathogens, in a mammalian subject, and  
 CC Alzheimer's disease and cancer. The present sequence is a Abeta16-22-C  
 CC peptide.

XX Sequence 8 AA;  
 SQ Query Match 91.2%; Score 31; DB 9; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVFFAQ 7  
 |||||:  
 Db 1 KLVFFAE 7

RESULT 60  
 AEA62834  
 ID AEA62834 standard; peptide; 8 AA.

XX AEA62834;

XX 08-SEP-2005 (first entry)

XX Immunoconjugate Abeta peptide, SEQ ID NO 54.

XX Immunoconjugate; immunotherapy; immunotoxin; tumor-associated antigen;  
 KW antigen; antibacterial; virucide; fungicide; antiparasitic;

KW neuroprotective; nootropic; cytostatic; immunotherapy; immunostimulant;  
 KW Alzheimer's disease; cancer.  
 OS Homo sapiens.  
 XX WO2005058940-A2.  
 XX 30-JUN-2005.  
 XX 17-DEC-2004; 2004WO-US042701.  
 XX 17-DEC-2003; 2003US-0530480P.  
 XX (AMHP ) WYETH.  
 XX Arumugham RG, Prasad AK;  
 PI WPI; 2005-488538/49.  
 DR Conjugating peptide immunogen, by derivatizing functional groups of  
 XX protein or polypeptide carrier, reacting reactive group of amino acid  
 PT residue of peptide immunogen with carrier having functional groups, to  
 PT produce conjugate.  
 XX Example 10; SEQ ID NO 54; 155pp; English.  
 XX The present invention relates to producing an immunogenic conjugate of a  
 CC peptide immunogen with a protein or polypeptide carrier. Specifically,  
 CC conjugating (M1) the peptide immunogen through a reactive group of an  
 CC amino acid residue to a protein/polypeptide carrier (PC) having  
 CC functional groups, by derivatizing functional groups of PC, reacting  
 CC derivatized PC with a peptide immunogen to produce the conjugate,  
 CC unreacted functional groups, so that the conjugate elicits immune  
 CC responses against peptide immunogen. In (M1), the carrier is chosen from  
 CC for example, human serum albumin, keyhole limpet hemocyanin (KLH), and  
 CC immunoglobulin molecules, hepatitis B surface antigen (HBsAg19.23), and  
 CC cholera toxin. The carrier contains a T-cell epitope. The carrier is a  
 CC bacterial or viral protein such as influenza hemagglutinin, and malaria  
 CC circumsporozoite (CS) protein. Preferably, the carrier is C.pneumoniae ORF  
 CC T858. The peptide immunogen can also be an antigen from a malignant  
 CC tumor. Antibacterial; Virucide; Fungicide; Antiparasitic; Neuroprotective  
 CC ; Nootropic; Cytostatic; Immunotherapy. The method is useful for inducing  
 CC an immune response against pathogens, in a mammalian subject, and  
 CC Alzheimer's disease and cancer. The present sequence is a C-Abeta16-22-C  
 CC peptide.

XX Sequence 8 AA;

Query Match 91.2%; Score 31; DB 9; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVFFAQ 7  
 |||||:  
 Db 2 KLVFFAE 8

RESULT 61  
 ABU79063  
 ID ABU79063 standard; peptide; 9 AA.

XX ABU79063;

XX 17-JUN-2003 (first entry)

XX Aggregation blocking peptide #15.

XX Amyloid formation; amyloid-like deposit; Alzheimer's disease;  
 KW pathological beta-sheet-rich conformation; Down's syndrome;  
 KW amyloidosis disorder; human prion disease; kuru, CJD;  
 KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;  
 KW prion associated human neurodegenerative disease; animal prion disease;



KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;  
 KW chronic wasting disease.  
 XX Unidentified.  
 XX US6462171-B1.  
 XX  
 XX 08-OCT-2002.  
 PD  
 XX  
 XX 12-DEC-1996; 96US-00766596.  
 XX  
 XX 07-JUN-1995; 95US-00478326.  
 PR 10-APR-1996; 96US-00630645.  
 XX  
 XX (UYNV ) UNIV NEW YORK STATE.  
 PA  
 XX Soto-Jara C, Baumann MH, Frangione B;  
 PI WPI; 2003-379012/36.  
 XX  
 XX Novel inhibitory peptides which inhibit and structurally block abnormal  
 PT folding of protein into amyloid or amyloid-like deposit and into  
 PT pathological beta-sheet rich conformation, useful for treating  
 PT Alzheimer's disease.  
 XX  
 XX Disclosure; Col 51-52; 51pp; English.  
 PS  
 XX The invention describes an isolated inhibitory peptide (I) which  
 CC interacts with a hydrophobic beta-sheet forming cluster of amino acid  
 CC residues on a protein or peptide for amyloid or amyloid-like deposit  
 CC formation, and inhibits or structurally blocks the abnormal folding of  
 CC proteins and peptides into amyloid or amyloid-like deposits and into  
 CC pathological beta-sheet rich conformation. (I) is useful for disorders or  
 CC diseases associated with abnormal protein folding into amyloid or amyloid  
 CC -like deposits or into pathological beta-sheet-rich precursors of such  
 CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis  
 CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease  
 CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated  
 CC human neurodegenerative diseases as well as animal prion diseases such as  
 CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and  
 CC chronic wasting disease of mule deer and elk. (I) is also useful for  
 CC detecting and diagnosing the presence or absence of amyloid or amyloid-  
 CC like deposits in vivo and its precursors. This is the amino acid sequence  
 CC of peptide associated with the inhibition of amyloid or amyloid like  
 XX deposits  
 XX  
 SQ Sequence 9 AA;  
 Query Match 91.2%; Score 31; DB 6; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 Db 2 KLVFFAE 8  
 |||||:  
 |||||:  
 RESULT 62  
 ABW00197  
 ID ABW00197 standard; peptide; 9 AA.  
 XX  
 AC ABW00197;  
 XX  
 XX 15-JAN-2004 (first entry)  
 DT  
 XX Peptide #15 used in the invention.  
 DE  
 XX Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;  
 KW Alzheimer's disease.  
 XX  
 XX Unidentified.  
 OS  
 XX US2003087407-A1.  
 PN

XX 08-MAY-2003.  
 XX  
 XX 06-SEP-2002; 2002US-00235483.  
 XX  
 XX 07-JUN-1995; 95US-00478326.  
 PR 10-APR-1996; 96US-00630645.  
 PR 12-DEC-1996; 96US-00766596.  
 XX  
 XX (UYNV ) UNIV NEW YORK STATE.  
 PA  
 XX Soto-Jara C, Baumann MH, Frangione B;  
 PI WPI; 2003-616149/58.  
 DR  
 XX New inhibitory peptide, useful for preparing a composition for  
 PT diagnosing, preventing or treating disorders associated with amyloid-like  
 PT fibril deposits, e.g. Alzheimer's disease, or prion related  
 PT encephalopathies.  
 XX  
 XX Claim 1; Page 28; 52pp; English.  
 PS  
 XX The invention relates to inhibitory peptide comprising a portion of at  
 CC least three amino acid residues and a sequence predicted not to adopt a  
 CC beta-sheet structure that associates with a hydrophobic beta-sheet  
 CC cluster on a protein or peptide involved in the abnormal folding into a  
 CC beta-sheet structure, to structurally block the abnormal folding of the  
 CC protein or peptide. The inhibitory peptide is useful for preparing a  
 CC composition for preventing, treating or detecting disorders or diseases  
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and  
 CC prion related encephalopathies. The invention is also useful in gene  
 CC therapy. The present sequence is a peptide used in the invention  
 XX  
 SQ Sequence 9 AA;  
 Query Match 91.2%; Score 31; DB 7; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 Db 2 KLVFFAE 8  
 |||||:  
 |||||:  
 RESULT 63  
 ADI36003  
 ID ADI36003 standard; peptide; 9 AA.  
 XX  
 AC ADI36003;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Amyloid beta peptide SEQ ID NO:157.  
 DE  
 XX amyloid beta peptide; vaccine; immunisation; neuroprotective;  
 KW Alzheimer's disease.  
 XX  
 XX Synthetic.  
 OS  
 XX WO2004006861-A2.  
 PN  
 XX 22-JAN-2004.  
 PD  
 XX 16-JUL-2003; 2003WO-US022280.  
 PF  
 XX 17-JUL-2002; 2002US-0396245P.  
 PR  
 XX (MIND-) MINDSET BIOPHARMACEUTICALS INC.  
 PA Chain DG, Fitzer-Attas C;  
 XX WPI; 2004-122759/12.  
 DR  
 XX



PT New amyloid beta peptide, useful for preparing a composition for  
 PT preventing the formation or progression of amyloid plaques for preventing  
 XX or treating Alzheimer's disease.

PS Example 6; SEQ ID NO 157; 69pp; English.

XX The present invention describes an isolated amyloid beta peptide or its  
 CC homologue which is selected by a method comprising: (a) determining the  
 CC binding value of each amino acid of a subsequence of amyloid beta peptide  
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)  
 CC determining the resulting score of all amino acids of the subsequence,  
 CC based on the binding value of each amino acid obtained in step (1); and  
 CC (c) comparing the resulting score to a preselected value. Also described:  
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier  
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;  
 CC (3) predicting the reaction of an individual to a vaccine; (4) matching a  
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,  
 CC for immunisation of an individual based on the HLA haplotype of the  
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta  
 CC peptide to an individual based on the HLA haplotype of the individual;  
 CC and (6) preventing the formation or progression of amyloid plaques. The  
 CC amyloid beta peptide has neuroprotective activity, and can be used in  
 CC vaccines. The amyloid beta peptide is useful for preparing a composition  
 CC for preventing the formation or progression of amyloid plaques for  
 CC preventing or treating Alzheimer's disease. The present sequence  
 CC represents an amyloid beta (Abeta) peptide, which is used in an example  
 CC from the present invention.

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 8; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
 DB 1 KLVFFAE 7

RESULT 64

AD135849  
 ID AD135849 standard; peptide; 9 AA.

XX AC AD135849;

XX DT 22-APR-2004 (first entry)

XX DE Amyloid beta peptide SEQ ID NO:3.

XX KW amyloid beta peptide; vaccine; immunisation; neuroprotective;  
 XX KW Alzheimer's disease.

XX OS Synthetic.

XX PN WO2004006861-A2.

XX PD 22-JAN-2004.

XX PF 16-JUL-2003; 2003WO-US022280.

XX PR 17-JUL-2002; 2002US-0396245P.

XX PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.

XX PI Chain DG, Fitzer-Attas C;

XX DR WPI; 2004-122759/12.

XX New amyloid beta peptide, useful for preparing a composition for  
 PT preventing the formation or progression of amyloid plaques for preventing  
 XX or treating Alzheimer's disease.

XX Example 1; SEQ ID NO 3; 69pp; English.

XX The present invention describes an isolated amyloid beta peptide or its  
 CC homologue which is selected by a method comprising: (a) determining the  
 CC binding value of each amino acid of a subsequence of amyloid beta peptide  
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)  
 CC determining the resulting score of all amino acids of the subsequence,  
 CC based on the binding value of each amino acid obtained in step (1); and  
 CC (c) comparing the resulting score to a preselected value. Also described:  
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier  
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;  
 CC (3) predicting the reaction of an individual to a vaccine; (4) matching a  
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,  
 CC for immunisation of an individual based on the HLA haplotype of the  
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta  
 CC peptide to an individual based on the HLA haplotype of the individual;  
 CC and (6) preventing the formation or progression of amyloid plaques. The  
 CC amyloid beta peptide has neuroprotective activity, and can be used in  
 CC vaccines. The amyloid beta peptide is useful for preparing a composition  
 CC for preventing the formation or progression of amyloid plaques for  
 CC preventing or treating Alzheimer's disease. The present sequence  
 CC represents an amyloid beta (Abeta) peptide, which is used in an example  
 CC from the present invention.

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 8; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
 DB 1 KLVFFAE 7

RESULT 65

AD135871  
 ID AD135871 standard; peptide; 9 AA.

XX AC AD135871;

XX DT 22-APR-2004 (first entry)

XX DE Amyloid beta peptide SEQ ID NO:25.

XX KW amyloid beta peptide; vaccine; immunisation; neuroprotective;  
 XX KW Alzheimer's disease.

XX OS Synthetic.

XX PN WO2004006861-A2.

XX PD 22-JAN-2004.

XX PF 16-JUL-2003; 2003WO-US022280.

XX PR 17-JUL-2002; 2002US-0396245P.

XX PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.

XX PI Chain DG, Fitzer-Attas C;

XX DR WPI; 2004-122759/12.

XX New amyloid beta peptide, useful for preparing a composition for  
 PT preventing the formation or progression of amyloid plaques for preventing  
 XX or treating Alzheimer's disease.

XX Example 2; SEQ ID NO 25; 69pp; English.

XX The present invention describes an isolated amyloid beta peptide or its  
 CC homologue which is selected by a method comprising: (a) determining the  
 CC binding value of each amino acid of a subsequence of amyloid beta peptide  
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)

CC determining the resulting score of all amino acids of the subsequence,  
 CC based on the binding value of each amino acids obtained in step (1); and  
 CC (c) comparing the resulting score to a preselected value. Also described:  
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier  
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;  
 CC (3) predicting the reaction of an individual to a vaccine; (4) matching a  
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,  
 CC for immunisation of an individual based on the HLA haplotype of the  
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta  
 CC peptide to an individual based on the HLA haplotype of the individual;  
 CC and (6) preventing the formation or progression of amyloid plaques. The  
 CC amyloid beta peptide has neuroprotective activity, and can be used in  
 CC vaccines. The amyloid beta peptide is useful for preparing a composition  
 CC for preventing the formation or progression of amyloid plaques for  
 CC preventing or treating Alzheimer's disease. The present sequence  
 CC represents an amyloid beta (Abeta) peptide, which is used in an example  
 CC from the present invention.

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 8; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVFFAQ 7  
 DB 1 KLVFFAE 7

RESULT 66  
 ADI35903  
 ID ADI35903 standard; peptide; 9 AA.

AC ADI35903;

DT 22-APR-2004 (first entry)

DE Amyloid beta homologue LV/EE HLA-A2.01 epitope SEQ ID NO:57.

KW amyloid beta peptide; vaccine; immunisation; neuroprotective;  
 KW Alzheimer's disease; epitope.

OS Synthetic.

PN WO2004006861-A2.

PD 22-JAN-2004.

PF 16-JUL-2003; 2003WO-US022280.

PR 17-JUL-2002; 2002US-0396245P.

PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.

PI Chain DG, Fitzer-Attas C;

DR WPI; 2004-122759/12.

PT New amyloid beta peptide, useful for preparing a composition for  
 PT preventing the formation or progression of amyloid plaques for preventing  
 PT or treating Alzheimer's disease.

PS Example 3; SEQ ID NO 57; 69pp; English.

CC The present invention describes an isolated amyloid beta peptide or its  
 CC homologue which is selected by a method comprising: (a) determining the  
 CC binding value of each amino acid of a subsequence of amyloid beta peptide  
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)  
 CC determining the resulting score of all amino acids of the subsequence,  
 CC based on the binding value of each amino acids obtained in step (1); and  
 CC (c) comparing the resulting score to a preselected value. Also described:  
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier  
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;

CC (3) predicting the reaction of an individual to a vaccine; (4) matching a  
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,  
 CC for immunisation of an individual based on the HLA haplotype of the  
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta  
 CC peptide to an individual based on the HLA haplotype of the individual;  
 CC and (6) preventing the formation or progression of amyloid plaques. The  
 CC amyloid beta peptide has neuroprotective activity, and can be used in  
 CC vaccines. The amyloid beta peptide is useful for preparing a composition  
 CC for preventing the formation or progression of amyloid plaques for  
 CC preventing or treating Alzheimer's disease. The present sequence  
 CC represents an amyloid beta (Abeta) homologue LV/EE HLA-A2.01 epitope  
 CC peptide, which is used in an example from the present invention.

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 8; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVFFAQ 7  
 DB 1 KLVFFAE 7

RESULT 67  
 AEA51414  
 ID AEA51414 standard; peptide; 9 AA.

AC AEA51414;

DT 08-SEP-2005 (first entry)

DE A 16-23-C peptide immunogen, SEQ ID NO: 45.

KW immunoconjugate; immunostimulant; neuroprotective; neurotropic; virucide;  
 KW cytostatic; amyloidosis; Alzheimers disease; Down's syndrome;  
 KW viral infection; cancer.

OS Unidentified.

PN WO2005058941-A2.

PD 30-JUN-2005.

PF 17-DEC-2004; 2004WO-US044093.

PR 17-DEC-2003; 2003US-0530481P.

PA (ELAN-) ELAN PHARM INC.

PA (AMHP ) WYETH.

PI Arumugham RG, Prasad AK;

DR WPI; 2005-467099/47.

PT Conjugating peptide immunogen by reacting derivatized protein/polypeptide  
 PT carrier with a reactive group of an amino acid of the peptide immunogen  
 PT so that the peptide immunogen is conjugated to derivatized  
 PT protein/polypeptide carrier.

PS Example 10; SEQ ID NO 45; 150pp; English.

CC The present invention relates to methods of producing an immunogenic  
 CC conjugate of a peptide immunogen comprising Abeta peptide or fragments of  
 CC Abeta or analogs with a protein/polypeptide carrier. Given is a method of  
 CC conjugating a peptide immunogen, Abeta peptide, via a reactive group of a  
 CC residue to a protein/polypeptide carrier. The method comprises reacting a  
 CC derivatized protein/polypeptide carrier with a reactive group of an amino  
 CC acid of the Abeta peptide. In conjugating a peptide immunogen, the  
 CC carrier is selected from many substances such as human serum albumin,  
 CC keyhole limpet hemocyanin (KLH), immunoglobulin molecules, thyroglobulin,  
 CC and growth factors or hormones and preferably contains a T-cell epitope,  
 CC or is a bacterial toxoid. The growth factor or hormone is selected from

CC IL-1, IL-2, gamma-interferon, IL-10, GM-CSF, MIP-1alpha, MIP-1beta, or  
 CC RANTES. Described is a method of inducing an immune response in a  
 CC mammalian subject by administering an amount of the immunogenic  
 CC composition to the subject. The conjugate is useful in the manufacture of an  
 CC a medicament for use in the treatment, prophylaxis, or amelioration of an  
 CC amyloidogenic disease. The disease is Alzheimer's disease or Down's  
 CC syndrome. It is also useful for treating viral infection or cancers. The  
 CC present sequence is the A 16-23-C peptide immunogen, SEQ ID NO: 45.  
 XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 9; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 Db 1 KLVFFPAE 7  
 |||||:

## RESULT 68

AEA51417  
 ID AEA51417 standard; peptide; 9 AA.

XX AEA51417;

DT 08-SEP-2005 (first entry)

DE C-A 16-23 peptide immunogen, SEQ ID NO: 48.

XX immunoconjugate; immunostimulant; neuroprotective; virucide;  
 KW cytostatic; amyloidosis; Alzheimers disease; Down's syndrome;  
 KW viral infection; cancer.

XX Unidentified.

XX WO2005058941-A2.

XX 30-JUN-2005.

XX 17-DEC-2004; 2004WO-US044093.

PR 17-DEC-2003; 2003US-0530481P.

XX (ELAN-) ELAN PHARM INC.

PA (AMHP ) WYETH.

XX Arumugham RG, Prasad AK;

XX WPI; 2005-467099/47.

XX Conjugating peptide immunogen by reacting derivatized protein/polypeptide  
 PT carrier with a reactive group of an amino acid of the peptide immunogen  
 PT so that the peptide immunogen is conjugated to derivatized  
 PT protein/polypeptide carrier.

XX Example 10; SEQ ID NO 48; 150pp; English.

XX The present invention relates to methods of producing an immunogenic  
 CC conjugate of a peptide immunogen comprising Abeta peptide or fragments of  
 CC Abeta or analogs with a protein/polypeptide carrier. Given is a method of  
 CC conjugating a peptide immunogen, Abeta peptide, via a reactive group of a  
 CC residue to a protein/polypeptide carrier. The method comprises reacting a  
 CC derivatized protein/polypeptide carrier with a reactive group of an amino  
 CC acid of the Abeta peptide. In conjugating a peptide immunogen, the  
 CC carrier is selected from many substances such as human serum albumin,  
 CC keyhole limpet hemocyanin (KLH), immunoglobulin molecules, thyroglobulin,  
 CC and growth factors or hormones and preferably contains a T-cell epitope,  
 CC or is a bacterial toxoid. The growth factor or hormone is selected from  
 CC IL-1, IL-2, gamma-interferon, IL-10, GM-CSF, MIP-1alpha, MIP-1beta, or  
 CC RANTES. Described is a method of inducing an immune response in a  
 CC mammalian subject by administering an amount of the immunogenic  
 CC composition to the subject. The conjugate is useful in the manufacture of

CC a medicament for use in the treatment, prophylaxis, or amelioration of an  
 CC amyloidogenic disease. The disease is Alzheimer's disease or Down's  
 CC syndrome. It is also useful for treating viral infection or cancers. The  
 CC present sequence is the C-A 16-23 peptide immunogen, SEQ ID NO: 48.

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 9; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 Db 2 KLVFFPAE 8  
 |||||:

## RESULT 69

AEA62825  
 ID AEA62825 standard; peptide; 9 AA.

XX AEA62825;

DT 08-SEP-2005 (first entry)

XX Immunoconjugate Abeta peptide, SEQ ID NO 45.

XX immunoconjugate; immunotherapy; immunotoxin; tumor-associated antigen;  
 KW antigen; antibacterial; virucide; fungicide; antiparasitic;  
 KW neuroprotective; nootropic; cytostatic; Immunotherapy; immunostimulant;  
 KW Alzheimer's disease; cancer.

XX Homo sapiens.

XX WO2005058940-A2.

XX 30-JUN-2005.

XX 17-DEC-2004; 2004WO-US042701.

PR 17-DEC-2003; 2003US-0530480P.

XX (AMHP ) WYETH.

XX Arumugham RG, Prasad AK;

XX WPI; 2005-488538/49.

XX Conjugating peptide immunogen, by derivatizing functional groups of  
 PT protein or polypeptide carrier, reacting reactive group of amino acid  
 PT residue of peptide immunogen with carrier having functional groups, to  
 PT produce conjugate.

XX Example 10; SEQ ID NO 45; 155pp; English.

XX The present invention relates to producing an immunogenic conjugate of a  
 CC peptide immunogen with a protein or polypeptide carrier. Specifically,  
 CC conjugating (M1) the peptide immunogen through a reactive group of an  
 CC amino acid residue to a protein/polypeptide carrier (PC) having  
 CC functional groups, by derivatizing functional groups of PC, reacting  
 CC derivatized PC with a peptide immunogen to produce the conjugate,  
 CC reacting the conjugate with a capping reagent to inactive free, reactive  
 CC unreacted functional groups, so that the conjugate elicits immune  
 CC responses against peptide immunogen. In (M1), the carrier is chosen from  
 CC for example, human serum albumin, keyhole limpet hemocyanin (KLH), and  
 CC immunoglobulin molecules, hepatitis B surface antigen (HBsAg), and  
 CC cholera toxin. The carrier contains a T-cell epitope. The carrier is a  
 CC bacterial or viral protein such as influenza hemagglutinin, and malaria  
 CC circumsporozoite (CS) protein. Preferably, the carrier is C.pneumoniae ORF  
 CC T858. The peptide immunogen can also be an antigen from a malignant  
 CC tumor. Antibacterial; Virucide; Fungicide; Antiparasitic; Neuroprotective  
 CC ; Nootropic; Cytostatic. Immunotherapy. The method is useful for inducing  
 CC an immune response against pathogens, in a mammalian subject, and  
 CC Alzheimer's disease and cancer. The present sequence is a Abeta16-23-C

CC peptide.

XX Sequence 9 AA;

SQ

Query Match 91.2%; Score 31; DB 9; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 |||||:  
 Db 1 KLVFFPAE 7

RESULT 70

AEA62828

ID AEA62828 standard; peptide; 9 AA.

XX

AC AEA62828;

XX

DT 08-SEP-2005 (first entry)

XX

DE Immunoconjugate Abeta peptide, SEQ ID NO 48.

XX

KW Immunoconjugate; immunotherapy; immunotoxin; tumor-associated antigen;  
 KW antigen; antibacterial; virucide; fungicide; antiparasitic;  
 KW neuroprotective; nootropic; cytostatic; immunotherapy; immunostimulant;  
 KW Alzheimer's disease; cancer.

XX

OS Homo sapiens.

XX

PN WO2005058940-A2.

XX

PD 30-JUN-2005.

XX

PF 17-DEC-2004; 2004WO-US042701.

XX

PR 17-DEC-2003; 2003US-0530480P.

XX

PA (AMHP ) WYETH.

XX

PI Arumugham RG, Prasad AK;

XX

DR WPI; 2005-488538/49.

XX

Conjugating peptide immunogen, by derivatizing functional groups of  
 protein or polypeptide carrier, reacting reactive group of amino acid  
 residue of peptide immunogen with carrier having functional groups, to  
 produce conjugate.

XX

PS Example 10; SEQ ID NO 48; 155pp; English.

XX

The present invention relates to producing an immunogenic conjugate of a  
 peptide immunogen with a protein or polypeptide carrier. Specifically,  
 conjugating (M1) the peptide immunogen through a reactive group of an  
 amino acid residue to a protein/polypeptide carrier (PC) having  
 functional groups, by derivatizing functional groups of PC, reacting  
 derivatized PC with a peptide immunogen to produce the conjugate,  
 reacting the conjugate with a capping reagent to produce free, reactive  
 unreacted functional groups, so that the conjugate elicits immune  
 responses against peptide immunogen. In (M1), the carrier is chosen from  
 for example, human serum albumin, keyhole limpet hemocyanin (KLH), and  
 immunoglobulin molecules, hepatitis B surface antigen (HBsAg), and  
 cholera toxin. The carrier contains a T-cell epitope. The carrier is a  
 bacterial or viral protein such as influenza hemagglutinin, and malaria  
 circumsporozoite (CS) protein. Preferably, the carrier is C.pneumoniae ORF  
 T858. The peptide immunogen can also be an antigen from a malignant  
 tumor. Antibacterial; virucide; fungicide; antiparasitic; Neuroprotective  
 ; Nootropic; Cytostatic. Immunotherapy. The method is useful for inducing  
 an immune response against pathogens, in a mammalian subject, and  
 Alzheimer's disease and cancer. The present sequence is a C-Abeta16-23  
 peptide.

XX

SQ Sequence 9 AA;

Query Match 91.2%; Score 31; DB 9; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 |||||:  
 Db 2 KLVFFPAE 8

RESULT 71

AAV79938

ID AAY79938 standard; peptide; 10 AA.

XX

AC AAY79938;

XX

DT 11-MAY-2000 (first entry)

XX

DE Beta-amyloid recognition peptide SEQ ID NO:3.

XX

KW Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;  
 KW Alzheimer's disease; neuroprotective; nootropic.

XX

OS Homo sapiens.

XX

PN US6022859-A.

XX

PD 08-FEB-2000.

XX

PF 14-NOV-1997; 97US-00970833.

XX

PR 15-NOV-1996; 96US-0030840P.

XX

PA (WISC ) WISCONSIN ALUMNI RES FOUND.

XX

PI Murphy RM, Kieselring LL;

XX

DR WPI; 2000-160387/14.

XX

PT Beta-amyloid inhibitor useful for treating Alzheimer's disease.

XX

PS Example; Col 7; 15pp; English.

XX

CC The present invention describes a beta-amyloid inhibitor peptide. Beta-  
 CC amyloid inhibitors have neuroprotective and nootropic properties. The  
 CC inhibitor peptides are useful for the treatment of Alzheimer's disease.  
 CC The present sequence represents a beta-amyloid recognition peptide used  
 CC in the exemplification of present invention

XX

SQ Sequence 10 AA;

XX

Query Match 91.2%; Score 31; DB 3; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 3.1;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7

|||||:

Db 1 KLVFFPAE 7

RESULT 72

AAB46226

ID AAB46226 standard; peptide; 10 AA.

XX

AC AAB46226;

XX

DT 04-APR-2001 (first entry)

XX

DE Human APP derived immunogenic peptide #22.

XX

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.

XX

XX OS Homo sapiens.  
 XX PN WO200072880-A2.  
 XX PD 07-DEC-2000.  
 XX PF 26-MAY-2000; 2000WO-US014810.  
 XX PR 28-MAY-1999; 99US-00322289.  
 XX PA (NEUR-) NEURALAB LTD.  
 XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 XX DR WPI; 2001-032104/04.  
 XX PT Preventing or treating a disease associated with amyloid deposits,  
 XX PT especially Alzheimer's disease, comprises administering amyloid specific  
 XX PT antibody.  
 XX PS Disclosure; Fig 19; 143pp; English.  
 XX CC This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have nootropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease  
 XX SQ Sequence 10 AA;  
 Query Match 91.2%; Score 31; DB 4; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 3.1;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFPAQ 7  
 |||||:  
 Db 3 KLVFFPAE 9  
 RESULT 73  
 AAB46225  
 ID AAB46225 standard; peptide; 10 AA.  
 AC AAB46225;  
 XX DT 04-APR-2001 (first entry)  
 XX DE Human APP derived immunogenic peptide #21.  
 XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.  
 XX OS Homo sapiens.  
 XX PN WO200072880-A2.  
 XX PD 07-DEC-2000.  
 XX PF 26-MAY-2000; 2000WO-US014810.  
 XX PR 28-MAY-1999; 99US-00322289.  
 XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 XX DR WPI; 2001-032104/04.  
 XX PT Preventing or treating a disease associated with amyloid deposits,  
 XX PT especially Alzheimer's disease, comprises administering amyloid specific  
 XX PT antibody.  
 XX PS Disclosure; Fig 19; 143pp; English.  
 XX CC This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have nootropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease  
 XX SQ Sequence 10 AA;  
 Query Match 91.2%; Score 31; DB 4; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 3.1;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFPAQ 7  
 |||||:  
 Db 4 KLVFFPAE 10  
 RESULT 74  
 AAB46228  
 ID AAB46228 standard; peptide; 10 AA.  
 AC AAB46228;  
 XX DT 04-APR-2001 (first entry)  
 XX DE Human APP derived immunogenic peptide #24.  
 XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.  
 XX OS Homo sapiens.  
 XX PN WO200072880-A2.  
 XX PD 07-DEC-2000.  
 XX PF 26-MAY-2000; 2000WO-US014810.  
 XX PR 28-MAY-1999; 99US-00322289.  
 XX PA (NEUR-) NEURALAB LTD.  
 XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 XX DR WPI; 2001-032104/04.  
 XX PT Preventing or treating a disease associated with amyloid deposits,  
 XX PT especially Alzheimer's disease, comprises administering amyloid specific  
 XX PT antibody.  
 XX PS Disclosure; Fig 19; 143pp; English.  
 XX CC This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have neurotropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease  
 XX  
 SQ Sequence 10 AA;

Query Match 91.2%; Score 31; DB 4; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 3.1;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7  
 |||||:  
 Db 1 KLVFFFAE 7

# RESULT 75

AAB46227  
 ID AAB46227 standard; peptide; 10 AA.

XX AAB46227;

XX 04-APR-2001 (first entry)

XX Human APP derived immunogenic peptide #23.

XX Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;  
 XX Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 XX amyloid precursor protein; Alzheimer's disease.

XX Homo sapiens.

XX WO200072880-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014810.

XX 28-MAY-1999; 99US-00322289.

XX (NEUR-) NEURALAB LTD.

XX Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX WPI; 2001-032104/04.

XX Preventing or treating a disease associated with amyloid deposits,  
 XX especially Alzheimer's disease, comprises administering amyloid specific  
 XX antibody.

XX Disclosure; Fig 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have neurotropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 91.2%; Score 31; DB 4; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 3.1;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7  
 |||||:  
 Db 2 KLVFFFAE 8

Search completed: December 29, 2005, 17:33:42  
 Job time : 96.4032 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds  
(without alignments)  
54.137 Million cell updates/sec

Title: US-10-009-122-17  
Perfect score: 29  
Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	186	1	P9835 oryza sativ
2	29	100.0	186	2	P93414 oryza sativ
3	29	100.0	231	2	Q8C6Y8 mus musculus
4	29	100.0	372	2	Q6D7U3 ERWCT
5	29	100.0	373	2	Q7M9N5 WOLSU
6	29	100.0	387	2	Q8K110 BACCZ
7	29	100.0	387	2	Q4MT39 BACCZ
8	29	100.0	387	2	Q63DD4 BACCZ
9	29	100.0	387	2	Q6HKU6 BACCZ
10	29	100.0	387	2	Q73AP3 BACC1
11	29	100.0	387	2	Q81SK9 BACAN
12	29	100.0	410	2	Q8C513 MOUSE
13	29	100.0	442	2	Q9PHV5 CANJE
14	29	100.0	703	2	Q5HYE1 HUMAN
15	29	100.0	721	2	Q6AG25 LEIXX
16	29	100.0	925	2	Q95786 HUMAN
17	29	100.0	925	2	Q5VYT1 HUMAN
18	29	100.0	926	2	Q8Q899 MOUSE
19	29	100.0	940	2	Q9GLV6 FIG
20	29	100.0	1144	1	NOS2 MOUSE
21	29	100.0	1144	2	Q5SXT3 MOUSE
22	29	100.0	1145	2	Q8R410 MOUSE
23	29	100.0	1145	2	Q6P6A0 MOUSE
24	28	96.6	164	2	Q73N39 TREDE
25	28	96.6	203	2	Q6AKN9 DESPS
26	28	96.6	380	2	Q67225 AQUIFX
27	28	96.6	387	2	Q81FH5 BACCR
28	28	96.6	399	2	Q5WPU9 LUTLO
29	28	96.6	450	2	Q4TRF8 SPHPN
30	28	96.6	464	2	Q4S4T5 TETNG
31	28	96.6	606	2	Q91VU5 mus musculus

32	28	96.6	623	2	Q4WBU2 ASPFU
33	28	96.6	630	2	Q5K7E5 CRYNE
34	28	96.6	663	2	Q6RUU2 MOUSE
35	28	96.6	690	2	Q831B2 TROW8
36	28	96.6	698	2	Q83GW3 TROWT
37	28	96.6	760	2	Q5SHW1 CRYNE
38	28	96.6	1265	2	Q6Z091 MOUSE
39	28	96.6	1412	2	Q5F3M1 CHICK
40	28	96.6	1655	2	Q4Q5Q4 LEIMA
41	27	93.1	88	2	Q4LBQ8 SODGL
42	27	93.1	183	2	Q9RQ09 BACTN
43	27	93.1	315	2	Q61C67 CAEBR
44	27	93.1	362	2	Q4HSJ7 CAMUP
45	27	93.1	382	2	Q9V7J0 DROME
46	27	93.1	410	2	Q6L2B4 PICTO
47	27	93.1	447	2	Q59243 PYRHO
48	27	93.1	556	2	Q95S93 DROME
49	27	93.1	556	2	Q9V719 DROME
50	27	93.1	785	2	Q9G082 DROME
51	27	93.1	1384	2	Q68K27 CHLRE
52	27	93.1	1408	2	Q7QEF0 ANOGE
53	27	93.1	1443	2	Q9VPR0 DROME
54	27	93.1	1458	2	Q5BI64 DROME
55	27	93.1	1503	2	Q7KTZ4 DROPH
56	27	93.1	1676	2	Q8A6R7 BACTN
57	26	89.7	33	2	Q9UC33 HUMAN
58	26	89.7	42	2	Q56JU6 GRAGR
59	26	89.7	42	2	Q56JJ7 TURTR
60	26	89.7	42	2	Q7M088 CAVPO
61	26	89.7	52	2	Q8W299 HUMAN
62	26	89.7	55	2	Q82VG8 NITBU
63	26	89.7	57	1	A4_URSM
64	26	89.7	58	1	A4_CANFA
65	26	89.7	58	1	A4_RABIT
66	26	89.7	58	1	A4_SHEEP
67	26	89.7	59	1	A4_BOVIN
68	26	89.7	79	2	Q5JUL8 BACSK
69	26	89.7	79	2	Q35463 CRIGR
70	26	89.7	81	1	MOAD_ECOLI
71	26	89.7	81	2	Q9APP7_9BACT
72	26	89.7	81	2	Q57RF2 SALCH
73	26	89.7	81	2	Q65TTO MANSCH
74	26	89.7	81	2	Q7N6P4 PHOIL
75	26	89.7	81	2	Q8D897_VIBUH
76	26	89.7	81	2	Q9KT78_VIBCH
77	26	89.7	81	2	Q83S38 SHIFL
78	26	89.7	81	2	Q7MM72_VIBVY
79	26	89.7	81	2	Q8X807_ECO57
80	26	89.7	83	2	Q5PG40_SALPA
81	26	89.7	83	2	Q82886_SALTI
82	26	89.7	83	2	Q8ZQO0_SALTY
83	26	89.7	85	2	Q87MY3_VIBPA
84	26	89.7	109	2	Q6YVX4_ORYSA
85	26	89.7	113	2	Q8JH58_CHESE
86	26	89.7	137	2	Q7UPR1_RHOBA
87	26	89.7	141	2	Q5LGT9_BACFN
88	26	89.7	141	2	Q64XP1_BACFR
89	26	89.7	143	2	Q8EMC6_OCEIH
90	26	89.7	152	2	Q9STZ9_ARATH
91	26	89.7	163	2	Q5PBG6_ANAMM
92	26	89.7	193	2	Q980V9_SULSO
93	26	89.7	195	2	Q7N3A0_PHOIL
94	26	89.7	207	1	HIS2_CAMJE
95	26	89.7	207	2	Q4HDT2_CAMCO
96	26	89.7	207	2	Q5HS17_CAMUR
97	26	89.7	218	2	Q8BPV5_MOUSE
98	26	89.7	221	2	Q6AMY5_DESPS
99	26	89.7	229	2	Q8VY56_ARATH
100	26	89.7	231	2	Q9SV79_ARATH
101	26	89.7	252	2	Q73M22_TREDE
102	26	89.7	264	2	Q9FGJ8_ARATH
103	26	89.7	265	2	Q4SV83_TETNG
104	26	89.7	293	1	Y844_ARCFU

Q4WBU2	aspergillus
Q5K7E5	cryptococcus
Q6RUU2	mus musculus
Q831B2	tropheryma
Q83GW3	cryptococcus
Q5SHW1	mus musculus
Q6Z091	mus musculus
Q5F3M1	gallus gall
Q4Q5Q4	leishmania
Q4LBQ8	sodalis glo
Q9RQ09	bacteroides
Q61C67	caenorhabdi
Q4HSJ7	campylobact
Q9V7J0	drosophila
Q6L2B4	picophilus
Q59243	pyrococcus
Q95S93	drosophila
Q9V719	drosophila
Q9G082	drosophila
Q68K27	chlamydomon
Q7QEF0	anopheles g
Q9VPR0	drosophila
Q5BI64	drosophila
Q7KTZ4	drosophila
Q8A6R7	bacteroides
Q9UC33	homo sapien
Q56JU6	grampus gri
Q56JJ7	tursiops tr
Q7M088	cavia porce
Q8W299	homo sapien
Q82VG8	nitrosomona
Q29199	u alzheimer
Q28280	c alzheimer
Q28748	o alzheimer
Q28757	o alzheimer
Q28053	b alzheimer
Q5WJ18	bacillus cl
Q35463	cricketulus
P30748	escherichia
Q9APP7	uncultured
Q57RF2	salmonella
Q65TTO	mannheimia
Q7N6P4	photobacteri
Q8D897	vibrio vuln
Q9KT78	vibrio chol
Q83S38	shigella fl
Q7MM72	vibrio vuln
Q8X807	escherichia
Q5PG40	salmonella
Q82886	salmonella
Q8ZQO0	salmonella
Q87MY3	vibrio para
Q6YVX4	oryza sativ
Q8JH58	chelydrea se
Q7UPR1	rhodospirell
Q5LGT9	bacteroides
Q64XP1	bacteroides
Q8EMC6	oceanobacil
Q9STZ9	arabidopsis
Q5PBG6	anaplasma m
Q980V9	sulfolobus
Q7N3A0	photobacteri
Q9PM71	campylobact
Q4HDT2	campylobact
Q5HS17	campylobact
Q8BPV5	mus musculus
Q6AMY5	desulfotale
Q8VY56	arabidopsis
Q9SV79	arabidopsis
Q73M22	treponema d
Q9FGJ8	arabidopsis
Q4SV83	tetradodon n
Q29414	archaeoglob



105	26	89.7	294	2	Q97XW2_SULSO	Q97XW2 sulfolobus	178	26	89.7	751	2	Q6RH28_CANFA	Q6rh28 canis famil
106	26	89.7	294	2	Q62HR5_BURMA	Q62hrs burkholderi	179	26	89.7	751	2	Q56JK5_CANFA	Q56jk5 canis famil
107	26	89.7	300	2	Q9XU61_CABEL	Q9xu61 caenorhabdi	180	26	89.7	751	2	Q4R4R8_MACFA	Q4r4r8 macaca fasc
108	26	89.7	314	2	Q7S8K9_NEUCR	Q7s8k9 neurospora	181	26	89.7	751	2	Q9DGJ7_CHICK	Q9dgj7 gallus gall
109	26	89.7	330	2	Q9PG18_XYLFA	Q9pg18 xylolla fas	182	26	89.7	754	2	Q4RY33_TETNG	Q4ry33 tetraodon n
110	26	89.7	339	1	MURG_THEME	Q9wy74 thermotoga	183	26	89.7	759	2	Q4S0J4_TETNG	Q4soj4 tetraodon n
111	26	89.7	349	2	Q9XU59_CABEL	Q9xu59 caenorhabdi	184	26	89.7	770	1	A4_CAVFO	Q60495 c amyloid b
112	26	89.7	352	2	Q9XGY6_SIMCH	Q9xgy6 simmondsia	185	26	89.7	770	1	A4_HUMAN	P05067 h amyloid b
113	26	89.7	352	2	Q87EP8_XYLFT	Q8xep8 xylolla fas	186	26	89.7	770	1	A4_MACFA	P53601 m amyloid b
114	26	89.7	357	2	Q8U460_PYRFU	Q8u460 pyrococcus	187	26	89.7	770	1	A4_MOUSE	P12023 m amyloid b
115	26	89.7	357	2	Q8UUI8_BRARE	Q8uui8 brachydanio	188	26	89.7	770	1	A4_PANTR	P51580 p amyloid b
116	26	89.7	366	2	Q8PPL1_XANNC	Q8ppl1 xanthomonas	189	26	89.7	770	1	A4_PIG	P79307 p amyloid b
117	26	89.7	370	2	Q65SJ1_MANSM	Q65sj1 manheimia	190	26	89.7	770	1	A4_RAT	P08592 r amyloid b
118	26	89.7	374	2	Q7MAT1_WOLSU	Q7mat1 wolliella s	191	26	89.7	770	2	Q6RH30_CANFA	Q6rh30 canis famil
119	26	89.7	384	2	Q8BPC7_MOUSE	Q8bpc7 mus musculus	192	26	89.7	770	2	Q56JK6_CANFA	Q56jk6 canis famil
120	26	89.7	391	2	Q4NSU7_THRPA	Q4nsu7 theileria p	193	26	89.7	770	2	Q532T3_MOUSE	Q532t3 mus musculu
121	26	89.7	395	2	Q95WD9_9DIPT	Q95wd9 phlebotomus	194	26	89.7	770	2	Q547B7_RAT	Q547b7 rattus norv
122	26	89.7	403	2	Q5L117_GEOKA	Q5l117 geobacillus	195	26	89.7	780	1	A4_TETFL	Q73683 tetraodon f
123	26	89.7	404	2	Q4UY85_XANCP	Q4uy85 xanthomonas	196	26	89.7	817	2	Q6QP9_VIBVU	Q6qp9 vibrio vuln
124	26	89.7	404	2	Q8P597_XANCP	Q8p597 xanthomonas	197	26	89.7	817	2	Q87FQ8_VIBPU	Q87fq8 vibrio para
125	26	89.7	428	2	Q9MIQ8_ARATH	Q9miq8 arabidopsis	198	26	89.7	817	2	Q8D4P2_VIBVU	Q8d4p2 vibrio vuln
126	26	89.7	443	2	Q4RHQ1_CAMCO	Q4rhq1 campylobact	199	26	89.7	817	2	Q9KNF1_VIBCH	Q9knf1 vibrio chol
127	26	89.7	461	2	Q89329_9POTV	Q89329 zucchini ye	200	26	89.7	840	2	Q7MG92_VIBVY	Q7mg92 vibrio vuln
128	26	89.7	467	2	Q4L319_STAHO	Q4l319 staphylococ	201	26	89.7	939	2	Q6CET0_YARLI	Q6cet0 yarrowia li
129	26	89.7	469	2	Q4Y318_PLACH	Q4y318 plasmodium	202	26	89.7	955	2	Q8QRZ2_9POTV	Q8qrz2 calla lily
130	26	89.7	470	2	Q7T910_9POTV	Q7t910 zucchini ye	203	26	89.7	962	2	Q4NTK2_9DELT	Q4ntk2 anaeromyxob
131	26	89.7	472	2	Q6UUS0_BRARE	Q6uus0 brachydanio	204	26	89.7	1016	2	Q05912_9POTV	Q05912 zucchini ye
132	26	89.7	477	1	YFUM_RHOCA	P26176 rhodobacter	205	26	89.7	1056	2	Q6FKH6_CANGA	Q6fkh6 candida gla
133	26	89.7	488	2	Q52NV6_9POTV	Q52nv6 zucchini ye	206	26	89.7	1083	2	Q81311_PLAF7	Q81311 plasmodium
134	26	89.7	490	2	Q7T911_9POTV	Q7t911 zucchini ye	207	26	89.7	1497	2	Q95YH6_DROME	Q95yh6 drosophila
135	26	89.7	490	2	Q7T912_9POTV	Q7t912 zucchini ye	208	26	89.7	1571	2	Q95YH7_DROME	Q95yh7 drosophila
136	26	89.7	493	2	Q5K4D4_9POTV	Q5k4d4 soybean mos	209	26	89.7	1571	2	Q8MSQ4_DROME	Q8msq4 drosophila
137	26	89.7	493	2	Q5K4D5_9POTV	Q5k4d5 soybean mos	210	26	89.7	1612	2	Q9VE37_DROME	Q9ve37 drosophila
138	26	89.7	496	2	Q5K4D0_9POTV	Q5k4d0 dahehen mos	211	26	89.7	1916	2	Q8QKU4_9POTV	Q8qku4 zucchini ye
139	26	89.7	508	2	Q5GV85_XANOR	Q5gv85 xanthomonas	212	26	89.7	3080	1	POLG_ZTMVC	P18479 z genome po
140	26	89.7	520	2	Q9K207_CHLPN	Q9k207 chlamydia p	213	26	89.7	3080	2	Q6WN47_9POTV	Q6wn47 zucchini ye
141	26	89.7	534	2	Q93296_CHICK	Q93296 gallus gall	214	26	89.7	3080	2	Q6WN48_9POTV	Q6wn48 zucchini ye
142	26	89.7	554	2	Q7P777_FUSNV	Q7p777 fusobacteri	215	26	89.7	3080	2	Q6WN49_9POTV	Q6wn49 zucchini ye
143	26	89.7	559	2	Q9PVL1_CHICK	Q9pvl1 gallus gall	216	26	89.7	3080	2	Q6Y2U7_9POTV	Q6y2u7 zucchini ye
144	26	89.7	594	2	Q9JSK0_CHLPN	Q9jsk0 chlamydia p	217	26	89.7	3080	2	Q7T908_9POTV	Q7t908 zucchini ye
145	26	89.7	603	2	Q9XIQ9_THEME	Q9xiq9 thermotoga	218	26	89.7	3080	2	Q7T914_9POTV	Q7t914 zucchini ye
146	26	89.7	609	2	Q6CFJ3_YARLI	Q6cfj3 yarrowia li	219	26	89.7	3083	1	POIG_ZTMVS	P03979 z genome po
147	26	89.7	612	2	Q919E7_BRARE	Q919e7 brachydanio	220	26	89.7	3105	2	Q7OXR2_9POTV	Q7oxr2 soybean mos
148	26	89.7	613	2	Q8HML1_9TELE	Q8hml1 hiodon alos	221	25	86.2	40	2	Q91FF3_DERVH	Q91ff3 chilo iride
149	26	89.7	614	2	Q94YP6_9TELE	Q94yp6 osteoglossu	222	25	86.2	66	2	Q728F0_IRSVH	Q728f0 desulfovibr
150	26	89.7	615	2	Q50285_ENTHI	Q50285 entamoeba h	223	25	86.2	74	1	Y131_MYCGE	P47377 mycoplasma
151	26	89.7	617	2	Q9Z9B2_CHLPN	Q9z9b2 chlamydia p	224	25	86.2	81	2	Q6D3D0_ERWCT	Q6d3d0 erwinia car
152	26	89.7	617	2	Q8RDN8_FUSNV	Q8rdn8 fusobacteri	225	25	86.2	89	2	Q8JVF2_LACLC	Q8jvf2 lactococcus
153	26	89.7	634	2	Q7SD58_NEUCR	Q7sd58 neurospora	226	25	86.2	104	2	Q5LXX2_STRT1	Q5lxx2 streptococc
154	26	89.7	638	2	Q5B2V4_EMENI	Q5b2v4 aspergillus	227	25	86.2	104	2	Q5M2H4_STRT2	Q5m2h4 streptococc
155	26	89.7	670	2	Q8GX2_RHILO	Q8gx2 rhizobium l	228	25	86.2	105	2	Q64CV5_9ARCH	Q64cv5 uncultured
156	26	89.7	678	2	Q7Z2T1_BRARE	Q7z2t1 brachydanio	229	25	86.2	107	2	Q59MN1_CANAL	Q59mn1 candida alb
157	26	89.7	682	2	Q64DY0_9ARCH	Q64dy0 uncultured	230	25	86.2	107	2	Q8E222_STRAS	Q8e222 streptococc
158	26	89.7	693	2	Q98SG0_XENLA	Q98sg0 xenopus lae	231	25	86.2	107	2	Q8E7H9_STRAS	Q8e7h9 streptococc
159	26	89.7	695	2	Q64BX4_9ARCH	Q64bx4 uncultured	232	25	86.2	109	2	Q9X292_THEME	Q9x292 thermotoga
160	26	89.7	695	2	Q5R477_PONFY	Q5r477 pongo pygma	233	25	86.2	122	2	Q4Y0Z7_PLACH	Q4y0z7 plasmodium
161	26	89.7	695	2	Q6RH29_CANFA	Q6rh29 canis famil	234	25	86.2	124	2	Q61N30_CAEER	Q61n30 caenorhabdi
162	26	89.7	695	2	Q56JK3_CANFA	Q56jk3 canis famil	235	25	86.2	125	2	Q6U9U2_9CAUD	Q6u9u2 bacterioph
163	26	89.7	695	2	Q6GR78_MOUSE	Q6gr78 mus musculu	236	25	86.2	125	2	Q56F01_9CAUD	Q56f01 aeromonas p
164	26	89.7	695	2	Q9DGJ8_CHICK	Q9dgj8 gallus gall	237	25	86.2	128	2	Q6LGS9_PHOPR	Q6lgs9 photobacter
165	26	89.7	695	2	Q98SF9_XENLA	Q98sf9 xenopus lae	238	25	86.2	136	2	Q18208_CAEEL	Q18208 caenorhabdi
166	26	89.7	695	2	Q7ZXQ0_XENLA	Q7zxq0 xenopus lae	239	25	86.2	141	2	Q8U3A1_PYRFU	Q8u3a1 pyrococcus
167	26	89.7	714	2	Q56JK4_CANFA	Q56jk4 canis famil	240	25	86.2	143	2	Q91Y69_MESAU	Q91y69 mesocricetu
168	26	89.7	733	2	Q6PQ05_RAT	Q6pq05 rattus norv	241	25	86.2	145	2	Q5USA9_9PEZI	Q5usa9 monacropor
169	26	89.7	737	1	A4_FUGRU	Q93279 fugu rubrip	242	25	86.2	146	2	Q9V0B4_PYFAB	Q9v0b4 pyrococcus
170	26	89.7	738	2	Q6NUZ1_BRARE	Q6nuz1 brachydanio	243	25	86.2	148	2	Q17202_CAEEL	Q17202 caenorhabdi
171	26	89.7	738	2	Q90W28_BRARE	Q90w28 brachydanio	244	25	86.2	156	2	Q8DN20_STRR6	Q8dn20 streptococc
172	26	89.7	747	2	Q91963_9PIPI	Q91963 xenopus ap	245	25	86.2	157	2	Q97N92_STRPN	Q97n92 streptococc
173	26	89.7	749	2	Q56JK2_STECO	Q56jk2 stenella co	246	25	86.2	156	2	Q8XNL2_CLOPE	Q8xnl2 clostridium
174	26	89.7	749	2	Q6NRR1_XENLA	Q6nrr1 xenopus lae	247	25	86.2	159	2	Q58626_PYRHO	Q58626 pyrococcus
175	26	89.7	750	2	Q6DJB6_XENTR	Q6djb6 xenopus tro	248	25	86.2	161	2	Q32197_9LILI	Q32197 eichornia
176	26	89.7	751	1	A4_SAI8C	Q95241 c amyloid b	249	25	86.2	162	2	Q9N284_BOVIN	Q9n284 bos taurus
177	26	89.7	751	2	Q6GSC0_HUMAN	Q6gsc0 homo sapien	250	25	86.2	163	2	Q32164_9LILI	Q32164 eichornia

251 25 86.2 163 2 Q32179 9LILI Q32179 eichhornia  
 252 25 86.2 163 2 Q32190 9LILI Q32190 eichhornia  
 253 25 86.2 163 2 Q32201 9LILI Q32201 eichhornia  
 254 25 86.2 163 2 Q32202 9LILI Q32202 eichhornia  
 255 25 86.2 163 2 Q32210 9LILI Q32210 eichhornia  
 256 25 86.2 163 2 Q32390 9LILI Q32390 heteranther  
 257 25 86.2 163 2 Q32419 9LILI Q32419 heteranther  
 258 25 86.2 163 2 Q32424 9LILI Q32424 heteranther  
 259 25 86.2 163 2 Q32430 9LILI Q32430 heteranther  
 260 25 86.2 163 2 Q32441 9LILI Q32441 heteranther  
 261 25 86.2 163 2 Q32556 9LILI Q32556 monochoria  
 262 25 86.2 163 2 Q32579 9LILI Q32579 monochoria  
 263 25 86.2 163 2 Q32648 9LILI Q32648 monochoria  
 264 25 86.2 163 2 Q32802 9LILI Q32802 pontederia  
 265 25 86.2 163 2 Q32892 9LILI Q32892 pontederia  
 266 25 86.2 163 2 Q32915 9LILI Q32915 pontederia  
 267 25 86.2 164 2 Q31Y15 BACAN Q31Y15 bacillus an  
 268 25 86.2 165 2 Q37011 PONCO Q37011 pontederia  
 269 25 86.2 172 2 Q33PK3 ORISA Q33PK3 oriza sativ  
 270 25 86.2 180 2 Q3NLQ4 ZYMMO Q3NLQ4 zymomonas m  
 271 25 86.2 188 2 Q3W2G3 ORISA Q3W2G3 oriza sativ  
 272 25 86.2 188 2 Q7VR27 CANBF Q7VR27 candidatus  
 273 25 86.2 188 2 Q67835 AQUAE Q67835 aquifex aeo  
 274 25 86.2 190 2 Q32WB8 RHIME Q32WB8 rhizobium m  
 275 25 86.2 194 2 Q37G46 CLOAB Q37G46 clostridium  
 276 25 86.2 196 2 Q6HVS9 BACAN Q6HVS9 bacillus an  
 277 25 86.2 196 2 Q4U6V3 9VIRU Q4U6V3 potato viru  
 278 25 86.2 197 2 Q7VR77 CANBF Q7VR77 candidatus  
 279 25 86.2 198 2 Q46025 CORDI Q46025 corynebacte  
 280 25 86.2 198 2 Q847W0 VIBPA Q847W0 vibrio para  
 281 25 86.2 198 2 Q3NGT3 CORDI Q3NGT3 corynebacte  
 282 25 86.2 198 2 Q87168 VIBPA Q87168 vibrio para  
 283 25 86.2 199 2 Q7MFJ3 VIBVY Q7MFJ3 vibrio vuln  
 284 25 86.2 200 1 COAB LISIN Q2Bf2 listeria in  
 285 25 86.2 200 2 Q73L44 TREDE Q73L44 treponema d  
 286 25 86.2 202 2 Q7P578 FUSNV Q7P578 fusobacteri  
 287 25 86.2 202 2 Q8RE19 FUSNV Q8RE19 fusobacteri  
 288 25 86.2 208 2 Q3QBU5 9ACTO Q3QBU5 nonomuraea  
 289 25 86.2 210 2 Q8T312 DROME Q8T312 drosophila  
 290 25 86.2 217 2 Q84019 PSECL Q84019 pseudomonas  
 291 25 86.2 218 2 Q5CYB3 CRYPV Q5CYB3 cryptospori  
 292 25 86.2 218 2 Q5CIV9 CRWHO Q5CIV9 cryptospori  
 293 25 86.2 220 2 Q5Z2T4 PEMVM Q5Z2T4 peanut mott  
 294 25 86.2 228 2 Q51V22 MAGGR Q51V22 magnaporthe  
 295 25 86.2 229 2 Q70Z41 9VIRU Q70Z41 potato viru  
 296 25 86.2 229 2 Q7TD31 9VIRU Q7TD31 potato viru  
 297 25 86.2 229 2 Q7TD37 9VIRU Q7TD37 potato viru  
 298 25 86.2 230 2 Q7RDM3 PLAYO Q7RDM3 plasmodium  
 299 25 86.2 231 2 Q637W5 BACCZ Q637W5 bacillus ce  
 300 25 86.2 232 2 Q84601 CHLTR Q84601 chlamydia t

## ALIGNMENTS

RESULT 1  
 GL19 ORISA  
 ID GL19 ORISA STANDARD; PRT; 186 AA.  
 AC P29835;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE 19 kDa globulin precursor (Alpha-globulin).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoideae; Oryza.  
 ON NCBI\_TaxID=4530;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
 RC STRAIN=cv. Japonica / Nipponbare; TISSUE=Endosperm;  
 RX MEDLINE=92119226; PubMed=1731968;  
 RA Shorrosh B.S., Wen L., Zen K.C., Huang J.K., Pan J.S., Hermodson M.A.,

Tanaka K., Muthukrishnan S., Reeck G.R.;  
 "A novel cereal storage protein: molecular genetics of the 19 kDa  
 Globulin of rice."  
 Plant Mol. Biol. 18:151-154 (1992).  
 [2]  
 NUCLEOTIDE SEQUENCE OF 5-186.  
 RC STRAIN=cv. Japonica / Lemont; TISSUE=Endosperm;  
 RX MEDLINE=93277591; PubMed=8503935;  
 RA Krishnan H.B., Pueppke S.G.;  
 "Nucleotide sequence of an abundant rice seed globulin: homology with  
 the high molecular weight glutelins of wheat, rye and triticale."  
 Biochem. Biophys. Res. Commun. 193:460-466(1993).  
 RL - FUNCTION: Seed storage protein.  
 CC - SIMILARITY: Belongs to the 2S seed storage albumins family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC  
 CC EMBL; X63990; CAA45400.1; -; mRNA.  
 DR EMBL; L12252; AAA72362.1; ALT\_INIT; mRNA.  
 DR PIR; S20024; WMEZ19.  
 DR HSP; P24565; IPNB.  
 DR Gramene; P29835; -.  
 DR InterPro; IPR001419; AAI.  
 DR InterPro; IPR001419; Glutenin.  
 DR PANTHER; PTHR14054; Glutenin; 1.  
 DR Pfam; PF00234; Tryp alpha amyl; 1.  
 DR PRINTS; PR00210; GLUTENIN.  
 DR SMART; SM00499; AAI; 1.  
 DR Direct protein sequencing; Seed storage protein; Signal;  
 DR Storage protein.  
 FT SIGNAL 1 22 Potential.  
 FT CHAIN 23 186 19 kDa globulin.  
 SQ SEQUENCE 186 AA; 21050 MW; 9E09BA74CB0B6810 CRC64;  
 Query Match 100.0%; Score 29; DB 1; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KWVFFA 6  
 Db |||||  
 4 KWVFFA 9  
 RESULT 2  
 P93414 ORISA  
 ID P93414 ORISA PRELIMINARY; PRT; 186 AA.  
 AC P93414;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE 26 kDa globulin (Alpha-globulin).  
 GN Name=P001D04.16; Synonyms=QJ1057\_B02.5;  
 OS Oryza sativa (Japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoideae; Oryza.  
 ON NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Endosperm;  
 RX MEDLINE=96235139; PubMed=8666249; DOI=10.1016/0378-1119(95)00887-X;  
 RA Nakase M., Hotta H., Adachi T., Aoki N., Nakamura R., Masumura T.,  
 Tanaka K., Matsuda T.;  
 "Cloning of the rice seed alpha-globulin-encoding gene: sequence  
 similarity of the 5'-flanking region to those of the genes encoding  
 wheat high molecular-weight glutenin and barley D hordein."  
 Gene 170:223-226(1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,  
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,  
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,  
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,  
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,  
 RA Wu H.-P., Shaw J.-F.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RN NUCLEOTIDE SEQUENCE.

RP Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,  
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,  
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,  
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,  
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,  
 RA Wu H.-P., Shaw J.-F.;  
 RT "Oryza sativa BAC QJ1057.B02 genomic sequence.";  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

DR ENBL; D50643; BAA03308.1; -; Genomic DNA.

DR ENBL; AC130605; AA044292.1; -; Genomic DNA.

DR ENBL; AC13332; AAT93857.1; -; Genomic DNA.

DR PIR; JC4784; JC4784.

DR HSP; P24565; IPNB.

DR Gramene; P93414; -.

DR GO; GO:0045735; F:nutrient reservoir activity; IEA.

DR InterPro; IPR003612; AAI.

DR InterPro; IPR001419; Glutinin.

DR PIR; PF00234; Trp alpha amyl 1.

DR PRINTS; PR00210; GLUTENIN.

DR SMART; SM00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

DR SWART; SN00499; AAT1.

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Heart;  
 RC The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Heart;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RX Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Heart;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Heart;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Heart;  
 RC STRAIN=C57BL/6J; TISSUE=Heart;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai C., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; AK052871; BAC35183.1; -; mRNA.  
 DR MGI; MGI:2442858; Ddx58.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004386; F:helicase activity; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR InterPro; IPR011545; DEAD/DEAH\_N.  
 DR Pfam; PF00270; DEAD; 1.  
 DR SMART; SM00487; DEXDC; 1.  
 DR Helicase; Hypothetical protein.  
 FT NON\_TER 231 231  
 SQ SEQUENCE 231 AA; 25524 MW; 1D191607390D7FBB CRC64;

Query Match 100.0%; Score 29; DB 2; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 Db 4 KVVFFA 9  
 RESULT 3  
 ID Q8C6Y8\_MOUSE PRELIMINARY; PRT; 231 AA.  
 AC Q8C6Y8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched  
 DE library, clone:ID830015B12 product:hypothetical DEAD/DEAH box helicase  
 DE containing protein, full insert sequence. (Fragment).  
 GN Names=Ddx58;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Heart;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Heart;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,

Query Match 100.0%; Score 29; DB 2; Length 231;

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||  
Db 145 KVVFFA 150

## RESULT 4

Q6D7U3 ERWCT  
ID Q6D7U3 ERWCT PRELIMINARY; PRT; 372 AA.  
AC Q6D7U3  
DT 25-OCT-2004 (TRENBLrel. 28, Created)  
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE Hydrogenase isoenzymes formation protein.  
GN Name=hypD; OrderedLocusNames=KCA1232;  
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pectobacterium.  
OX NCBI\_TaxID=29471;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=SCBI 1043 / ATCC BAA-672;  
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;  
RA Bell K.S., Sebatia M., Pritchard L., Holden M.T.G., Hyman L.J.,  
RA Holleva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,  
RA Atkin R., Basen N., Brooks K., Chillingworth T., Clark K., Doggett J.,  
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,  
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,  
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;  
RT "Genome sequence of the enterobacterial phytopathogen Erwinia  
carotovora subsp. atroseptica and characterization of virulence  
factors";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).  
DR EMBL; BX50851; CAG74142.1; -; Genomic\_DNA.  
DR InterPro; IPR002780; HypD.  
DR Pfam; PF01924; HypD; 1.  
DR TIGRFAMs; TIGR005622; Hydrgn\_mat\_hypD; 1.  
DR PIRSF; PIRSF005622; Hydrgn\_mat\_hypD; 1.  
KW Complete proteome.  
SQ SEQUENCE 372 AA; 41130 MW; A001A18AC015B620 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 372;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||  
Db 139 KVVFFA 144

## RESULT 5

Q7M9N5 WOLSU  
ID Q7M9N5 WOLSU PRELIMINARY; PRT; 373 AA.  
AC Q7M9N5  
DT 01-MAR-2004 (TRENBLrel. 26, Created)  
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE HYDROGENASE PROTEIN.  
GN Name=HYPD; OrderedLocusNames=WS0793;  
OS Wolinella succinogenes.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Wolinella.  
OX NCBI\_TaxID=844;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=DSMZ 1740;  
RX MEDLINE=22982897; PubMed=14500908; DOI=10.1073/pnas.1932838100;  
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,  
RA Nandakumar R., Gross R., Robinus A., Keller H., Jagtap P., Linke B.,  
RA Meyer F., Lederer H., Schuster S.C.;  
RT "Complete genome sequence and analysis of Wolinella succinogenes";

Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).  
DR EMBL; BX571659; CA09906.1; -; Genomic\_DNA.  
DR InterPro; IPR002780; HypD.  
DR Pfam; PF01924; HypD; 1.  
DR PIRSF; PIRSF005622; Hydrgn\_mat\_hypD; 1.  
DR TIGRFAMs; TIGR00075; hypD; 1.  
KW Complete proteome.

SQ SEQUENCE 373 AA; 41793 MW; 3B7815EDB25790A6 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 373;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||  
Db 138 KVVFFA 143

## RESULT 6

Q9KI10 BACCE  
ID Q9KI10 BACCE PRELIMINARY; PRT; 387 AA.  
AC Q9KI10;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE GerN.  
GN Name=gerN;  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC10876;  
RX MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;  
RA Thackray P.D., Behravan J., Southworth T.W., Moir A.;  
RT "GerN, an antipporter homologue important in germination of Bacillus  
cereus endospores";  
RL J. Bacteriol. 183:476-482 (2001).  
DR EMBL; AF246294; AAF91326.1; -; Genomic DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0008324; F:cation transporter activity; IEA.  
DR GO; GO:0015299; F:solute:hydrogen antipporter activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006885; P:regulation of pH; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR004771; K\_eff.  
DR InterPro; IPR006153; Na\_H\_porter.  
DR Pfam; PF00999; Na\_H\_Exchange; 1.  
DR TIGRFAMs; TIGR00932; 2a37; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 387 AA; 41093 MW; 40DE45B71B715D01 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||  
Db 184 KVVFFA 189

## RESULT 7

Q4MT39 BACCE  
ID Q4MT39 BACCE PRELIMINARY; PRT; 387 AA.  
AC Q4MT39;  
DT 13-SEP-2005 (TRENBLrel. 31, Created)  
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
DE Na+/H+ antipporter.  
GN ORFNames=BCE\_G9241\_1647;  
OS Bacillus cereus G9241.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

```

OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CR ENBL; AAE01000008; EMBL15336.1; -; Genomic DNA.
SQ SEQUENCE 387 AA; 41122 MW; 15CC136E79912C38 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 8
Q63DD4_BACCZ
ID Q63DD4_BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18770.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 9
Q63DD4_BACCZ
ID Q63DD4_BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18770.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 9

```

```

Q6HKU6_BACHK
ID Q6HKU6_BACHK PRELIMINARY; PRT; 387 AA.
AC Q6HKU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN; OrderedLocusNames=BT9727_1493;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017355; AAT63168.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41076 MW; DFECD90985F951 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 10
Q73AP3_BACCI
ID Q73AP3_BACCI PRELIMINARY; PRT; 387 AA.
AC Q73AP3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Germination protein gerN.
GN OrderedLocusNames=BCB1729;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017269; AAS40658.1; -; Genomic DNA.
DR TIGR; BCB1729; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.

```

```

DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FEBA3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 11
O81SK9_BACAN PRELIMINARY; PRT; 387 AA.
AC O81SK9; Q610U3; Q6KUP8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Germination protein GenN.
OS OrderedLocustNames=BA1639, GBAA1639;
OC Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilestone J., Wu M.,
RA Kolony J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";
RL EMBL; AB017029; AAT25572.1; -; Genomic DNA.
DR EMBL; AB017334; AAT30749.1; -; Genomic DNA.
DR EMBL; AE017225; AAT53839.1; -; Genomic DNA.
DR TIGR; BA1639; -.
DR TIGR; GBAA1639; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0008324; F: cation transporter activity; IEA.
DR GO; GO:0015299; F: solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR GO; GO:0006885; P: regulation of pH; IEA.

GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 40932 MW; D59F6A08A283BCA3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 12
O8CS13_MOUSE PRELIMINARY; PRT; 410 AA.
AC O8CS13;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430573D20 product:hypothetical DEAD/DEAH box
DE helicase containing protein, full insert sequence.
GN Name=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085650; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai J., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]

```



```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Tashiro T., Hatada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIGEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AK078287; BAC37205.1; -; mRNA.
DR Ensembl; ENSMUSG0000040296; Mus musculus.
DR MGI; MGI:242858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDC; 1.
DR Helicase; Hypothetical protein, Nuclear protein.
SQ SEQUENCE 410 AA; 46841 MW; ECC9E3D2D2BC5FE0 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 293 KVVFFA 298
|||||

RESULT 13
Q9PHV5_CAMJTE PRELIMINARY; PRT; 442 AA.
AC Q9PHV5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Putative integral membrane protein.
GN OrderedLocusNames=Cj0560;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OC NCBI_TaxID=197;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; ALU39075; CAB75196.1; -; Genomic_DNA.
DR FIC; H81402; H81402.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; P:anion transporter activity; IEA.
DR GO; GO:0015238; P:drug transporter activity; IEA.
DR GO; GO:0008855; P:multidrug transport; IEA.
DR InterPro; IPR002114; HPr_SerP_S.
DR InterPro; IPR002528; MateP.
DR Pfam; PF01554; MateP; 1.
DR TIGRFAMs; TIGR00797; matP; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
SQ SEQUENCE 442 AA; 49452 MW; 38EA04E7AB1A8F3E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 313 KVVFFA 318
|||||

RESULT 14
Q5HYE1_HUMAN PRELIMINARY; PRT; 703 AA.
AC Q5HYE1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFZp686N19181 (fragment).
GN Name=DKFZp686N19181;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Skin endothel;
RG The German cDNA Consortium;
RA Foustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX647917; CAI46068.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Hypothetical protein.
FT NON_TER 703
SQ SEQUENCE 703 AA; 80308 MW; 3CF7500F4F955586 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 703;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 KVWFFA 6  
 Db 247 KVWFFA 252

## RESULT 15

Q6AG25 LEIXX  
 ID Q6AG25 LEIXX PRELIMINARY; PRT; 721 AA.  
 AC Q6AG25;  
 DT 25-OCT-2004 (TremBLrel. 28, Created)  
 DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)  
 DE ATP-dependent RNA helicase.  
 GN OrderedLocusNames=Lxx07490;  
 OS Leifsonia xyl (subsp. xyl).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococcales; Microbacteriaceae; Leifsonia.  
 OC NCBI\_TaxID=59736;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CTCB07;  
 RX PubMed=15305603;  
 RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,  
 RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R., C.Y.,  
 RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,  
 RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,  
 RA Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorri H.A.,  
 RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,  
 RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,  
 RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,  
 RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,  
 RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.;  
 RA "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia  
 RT xyl subsp. xyl.";  
 RL Mol. Plant-Microbe Interact. 17:827-836(2004).  
 DR EMBL; AB016822; AAT8670.1; -; Genomic\_DNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004386; F:helicase activity; IEA.  
 DR InterPro; IPR011545; DEAD/DEAH\_N.  
 DR InterPro; IPR001650; Helicase\_C.  
 DR Pfam; PF00270; DEAD; 1.  
 DR SMART; SM00487; DEXDC; 1.  
 DR SMART; SM00490; HELIC; 1.  
 KW Complete proteome; DNA-binding; Helicase; Hydrolase.  
 SQ SEQUENCE 721 AA; 7860 MW; 73F5D2A8435BADE3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 721;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVWFFA 6  
 Db 564 KVWFFA 569

## RESULT 16

O95786 HUMAN  
 ID O95786\_HUMAN PRELIMINARY; PRT; 925 AA.  
 AC O95786;  
 DT 01-MAY-1999 (TremBLrel. 10, Created)  
 DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)  
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
 DE RNA helicase.  
 GN Name=DDX58; Synonyms=RIG-I;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Sun Y.W.;  
 RT "RIG-I, a human homolog gene of RNA helicase, is induced by retinoic  
 RT acid during the differentiation of acute promyelocytic leukemia  
 RT cell.";  
 RL Thesis (1997), Shanghai Institute of Hematology, Rui-Jin Hospital,  
 RL Shanghai Second Medical University.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RA Yi-Wu S.;  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF038963; AAD19826.1; -; mRNA.  
 DR Ensembl; ENSG00000107201; Homo sapiens.  
 DR HGNC; HGNC:19102; DDX58.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004386; F:helicase activity; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR011545; DEAD/DEAH\_N.  
 DR InterPro; IPR001650; Helicase\_C.  
 DR Pfam; PF00270; DEAD; 1.  
 DR Pfam; PF00271; Helicase\_C; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR SMART; SM00487; DEXDC; 1.  
 DR SMART; SM00490; HELIC; 1.  
 KW Helicase.  
 SQ SEQUENCE 925 AA; 106613 MW; 5922B4F3D0F00D4 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVWFFA 6  
 Db 292 KVWFFA 297

## RESULT 17

O5VYTI HUMAN  
 ID O5VYTI\_HUMAN PRELIMINARY; PRT; 925 AA.  
 AC O5VYTI;  
 DT 01-FEB-2005 (TremBLrel. 29, Created)  
 DT 01-FEB-2005 (TremBLrel. 29, Last sequence update)  
 DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)  
 DE OTTHUMP00000021185.  
 GN Name=RP11-334P12.2; ORFNames=RP11-334P12.2-001;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Doggett S.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RA Sehra H.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL; AL353671; CAH71251.1; -; Genomic\_DNA.  
 DR EMBL; AL161783; CAH72600.1; -; Genomic\_DNA.  
 DR EMBL; AL161783; CAH71251.1; JOINED; Genomic\_DNA.  
 DR EMBL; AL353671; CAH72600.1; JOINED; Genomic\_DNA.  
 DR Ensembl; ENSG00000107201; Homo sapiens.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004386; F:helicase activity; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR InterPro; IPR011545; DEAD/DEAH\_N.  
 DR InterPro; IPR001650; Helicase\_C.  
 DR Pfam; PF00270; DEAD; 1.  
 DR Pfam; PF00271; Helicase\_C; 1.



```

DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase; Hydrolase; Nuclear protein.
SQ SEQUENCE 925 AA; 106600 MW; BF0D501C395BAE25 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 925;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |||||
Db 292 KVVFFA 297

RESULT 18
Q60899 MOUSE
ID Q60899_MOUSE PRELIMINARY; PRT; 926 AA.
AC Q60899
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DEAD/H box polypeptide RIG-I.
GN Names=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wei J., Gu J.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY53221; AAS59532.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR006935; ResIII.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF04851; ResIII; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
SQ SEQUENCE 926 AA; 105877 MW; 632462010107698E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 926;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |||||
Db 293 KVVFFA 298

RESULT 19
Q9GLV6_PIG
ID Q9GLV6_PIG PRELIMINARY; PRT; 940 AA.
AC Q9GLV6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Names=RHIV-1;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhang X., Wang C., Schook L.B., Hawken R.J., Rutherford M.S.;

```

```

RT "An RNA helicase, RHIV -1, induced by porcine reproductive and
RT respiratory syndrome virus (PRRSV) is mapped on porcine chromosome
RT 10q13."
RL Microb. Pathog. 28:267-278(2000).
CC -1- SURCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF181119; AG09428.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase; Hydrolase; Nuclear protein; Repeat.
SQ SEQUENCE 940 AA; 107584 MW; 118CA910B0AF7821 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |||||
Db 290 KVVFFA 295

RESULT 20
NOS2_MOUSE
ID NOS2_MOUSE STANDARD; PRT; 1144 AA.
AC P29477; O70515; O70516;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (iNOS) (Macrophage NOS) (MAC-NOS).
GN Name=Nos2; Synonyms=Inos1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92229444; PubMed=1373522;
RA Xie Q.-W., Cho H.J., Calaycay J., Mumford R.A., Swiderek K.M.,
RA Lee T.D., Ding A., Troso T., Nathan C.;
RT "Cloning and characterization of inducible nitric oxide synthase from
RT mouse macrophages."
RL Science 256:225-228(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92357701; PubMed=1379716;
RA Lowenstein C.J., Glatz C.S., Bredt D.S., Snyder S.H.;
RT "Cloned and expressed macrophage nitric oxide synthase contrasts with
RT the brain enzyme."
RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92210618; PubMed=1372907;
RA Lyons C.R., Orloff G.J., Cunningham J.M.;
RT "Molecular cloning and functional expression of an inducible nitric
RT oxide synthase from a murine macrophage cell line."
RL J. Biol. Chem. 267:6370-6374(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96088781; PubMed=7503239;
RA Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;
RT "Role of NF-kappa B in the regulation of inducible nitric oxide
RT synthase in an MTL cell line."
RL Am. J. Physiol. 269:F718-F729(1995).
RN [5]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-211; LEU-967 AND PHE-968.

```

RC STRAIN=B10.S/J, BALB/cBYJ, DBA/2J, NOD/LtJ, and SJL/J; TISSUE=Spleen;  
RX MEDLINE=99370037; PubMed=10438970;  
RA Blankenhorn E.P.;  
RA "Sequence polymorphisms in the chemokines Sclay (TCA-3), Sclay2  
RT (monocyte chemoattractant protein (MCP)-1), and Sclay2 (MCP-5) are  
RT candidates for eae7, a locus controlling susceptibility to monophasic  
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";  
RL J. Immunol. 163:2262-2266(1999).  
[6]  
RN EFFECT OF ASPIRIN.  
RC TISSUE=Macrophage;  
RX MEDLINE=95372392; PubMed=7544010;  
RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,  
RA Weissmann G., Abramson S.B.;  
RT "The mode of action of aspirin-like drugs: effect on inducible nitric  
RT oxide synthase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).  
[7]  
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.  
RX MEDLINE=97477482; PubMed=9334294; DOI=10.1126/science.278.5337.425;  
RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,  
RA Stuehr D.J., Tainer J.A.;  
RT "The structure of nitric oxide synthase oxygenase domain and inhibitor  
RT complexes.";  
RL Science 278:425-431(1997).  
[8]  
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.  
RX MEDLINE=98182450; PubMed=9516116; DOI=10.1126/science.279.5359.2121;  
RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,  
RA Tainer J.A.;  
RT "Structure of nitric oxide synthase oxygenase dimer with pterin and  
RT substrate.";  
RL Science 279:2121-2126(1998).  
[9]  
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.  
RX MEDLINE=20031637; PubMed=10562539; DOI=10.1093/emboj/18.22.6260;  
RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,  
RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;  
RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin  
RT hook and pterin-binding segment in dimerization and  
RT tetrahydrobiopterin interaction.";  
RL EMBO J. 18:6260-6270(1999).  
[10]  
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.  
RX MEDLINE=20031638; PubMed=10562539; DOI=10.1093/emboj/18.22.6271;  
RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,  
RA Tainer J.A., Stuehr D.J., Getzoff E.D.;  
RT "N-terminal domain swapping and metal ion binding in nitric oxide  
RT synthase dimerization.";  
RL EMBO J. 18:6271-6281(1999).  
[11]  
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.  
RX MEDLINE=20233702; PubMed=10769116; DOI=10.1021/bi992409a;  
RA Crane B.R., Arvai A.S., Ghosh S., Getzoff E.D., Stuehr D.J.,  
RA Tainer J.A.;  
RT "Structures of the N(omega)-hydroxy-L-arginine complex of inducible  
RT nitric oxide synthase oxygenase dimer with active and inactive  
RT pterins.";  
RL Biochemistry 39:4608-4621(2000).  
[12]  
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF TRP-457 MUTANTS.  
RX MEDLINE=21526413; PubMed=11669619; DOI=10.1021/bi011183k;  
RA Aoyagi M., Arvai A.S., Ghosh S., Stuehr D.J., Tainer J.A.,  
RA Getzoff E.D.;  
RT "Structures of tetrahydrobiopterin binding-site mutants of inducible  
RT nitric oxide synthase oxygenase dimer and implicated roles of  
RT Trp457.";  
RL Biochemistry 40:12826-12832(2001).  
[13]  
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.  
RX MEDLINE=22235496; PubMed=12437346; DOI=10.1021/bi026313j;  
RA Rosenfeld R.J., Garcin E.D., Panda K., Andersson G., Aberg A.,

RA Wallace A.V., Morris G.M., Olson A.J., Stuehr D.J., Tainer J.A.,  
RA Getzoff E.D.;  
RT "Conformational changes in nitric oxide synthases induced by  
RT chlorzoxazone and nitroindazoles: crystallographic and computational  
RL analyses of inhibitor potency.";  
RL Biochemistry 41:13915-13925(2002).  
[14]  
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 77-495.  
RX MEDLINE=22351717; PubMed=12464241; DOI=10.1016/S0003-9861(02)00555-6;  
RA Fedorov R., Ghosh D.K., Schlichting I.;  
RT "Crystal structures of cyanide complexes of P450cam and the oxygenase  
RT domain of inducible nitric oxide synthase - structural models of the  
RT short-lived oxygen complexes.";  
RL Arch. Biochem. Biophys. 409:25-31(2003).  
CC -1- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule  
CC with diverse functions throughout the body. In macrophages, NO  
CC mediates tumoricidal and bactericidal actions.  
CC -1- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline +  
CC nitric oxide + n NADP(+).  
CC -1- COFACTOR: Heme.  
CC -1- COFACTOR: FAD. Binds 1 mole of FAD.  
CC -1- COFACTOR: FMN. Binds 1 mole of FMN.  
CC -1- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric  
CC form of the enzyme.  
CC -1- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin  
CC inhibits expression and function of this enzyme and effects may be  
CC exerted at the level of translational/posttranslational  
CC modification and directly on the catalytic activity.  
CC -1- SUBUNIT: Homodimer. Binds SLC9A3R1 (By similarity).  
CC -1- TISSUE SPECIFICITY: Macrophages.  
CC -1- INDUCTION: By treatment with endotoxins or cytokines.  
CC -1- SIMILARITY: Belongs to the NOS family.  
CC -1- SIMILARITY: Contains 1 flavodoxin-like domain.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
-----  
DR EMBL; M87039; AAA39315.1; -; mRNA.  
DR EMBL; M92649; -; NOT ANNOTATED CDS; mRNA.  
DR EMBL; M84373; AAA39834.1; -; mRNA.  
DR EMBL; U43428; AAC52356.1; -; mRNA.  
DR EMBL; AF065919; AAC17914.1; -; mRNA.  
DR EMBL; AF065920; AAC17915.1; -; mRNA.  
DR EMBL; AF065921; AAC17916.2; -; mRNA.  
DR EMBL; AF065922; AAC17917.2; -; mRNA.  
DR EMBL; AF065923; AAC17918.2; -; mRNA.  
DR PIR; A43271; A43271.  
DR PDB; 1DD7; X-ray; A=114-498.  
DR PDB; 1DF1; X-ray; A/B=77-499.  
DR PDB; 1DWV; X-ray; A/B=77-496.  
DR PDB; 1DWH; X-ray; A/B=77-496.  
DR PDB; 1DXX; X-ray; A/B=77-496.  
DR PDB; 1JWJ; X-ray; A/B=66-498.  
DR PDB; 1JWK; X-ray; A/B=66-498.  
DR PDB; 1MBD; X-ray; A/B=65-498.  
DR PDB; 1MBE; X-ray; A/B=65-498.  
DR PDB; 1MBH; X-ray; A/B=65-498.  
DR PDB; 1MBL; X-ray; A/B=65-498.  
DR PDB; 1M9T; X-ray; A/B=77-495.  
DR PDB; 1N2N; X-ray; A/B=77-495.  
DR PDB; 1NOC; X-ray; A=115-498.  
DR PDB; 1NOD; X-ray; A/B=77-499.  
DR PDB; 1NOS; X-ray; @=115-498.  
DR PDB; 1QOM; X-ray; A/B=65-498.  
DR PDB; 1QW4; X-ray; A/B=77-495.  
DR PDB; 1QW5; X-ray; A/B=77-495.  
DR PDB; 1R35; X-ray; A/B=66-498.  
DR PDB; 1VAF; X-ray; A/B=77-495.  
DR PDB; 2BHJ; X-ray; A=77-498.  
DR PDB; 2NOD; X-ray; A/B=77-499.

```
DR PDB; 2NOS; X-ray; @=115-498.
DR PDB; 3NOD; X-ray; A/B=77-499.
DR InterAct; P29477; -.
DR Ensembl; ENSMUSG00000020826; Mus musculus.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; TAS.
DR GO; GO:0020037; F:heme binding; NAS.
DR GO; GO:0020037; F:heme binding; NAS.

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFFFA 6
Db 514 KVFFFA 519

RESULT 21
Q5SXT3 MOUSE
ID Q5SXT3_MOUSE PRELIMINARY; PRT; 1144 AA.
AC Q5SXT3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Nitric oxide synthase 2, inducible, macrophage (Inducible nitric oxide
synthase)
GN NamesNos2; ORFNamesRP23-341J22.2-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RA Hopkins B.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCES.
RC STRAIN=CD-1;
RA Coxe F., Levacher B., Rique H., Leopold O., Boutin J.A.,
RA Gallizzi J.-P.;
RT "Genomic structure of the murine inducible nitric oxide synthase (i-
RT NOS) gene."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL592185; CAI25275.1; -; Genomic_DNA.
DR EMBL; AF427516; AAL24076.1; -; Genomic_DNA.
SQ SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFFFA 6
Db 514 KVFFFA 519

RESULT 22
Q8R410 MOUSE
ID Q8R410_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q8R410;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN NamesNos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

DR PDB; 2NOS; X-ray; @=115-498.
DR PDB; 3NOD; X-ray; A/B=77-499.
DR InterAct; P29477; -.
DR Ensembl; ENSMUSG00000020826; Mus musculus.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; NAS.
DR GO; GO:0020037; F:heme binding; NAS.

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFFFA 6
Db 514 KVFFFA 519

RESULT 23
Q6P6A0 MOUSE
ID Q6P6A0_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q6P6A0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nos2 protein.
GN NameNos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
```

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;  
 RA Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC062378; AAH62378.1; -; mRNA.  
 DR HSSP; P29477; 1JWK.  
 DR MGI; MGI:97361; Nos2.  
 DR GO; GO:0030863; C:cortical cytoskeleton; IDA.  
 DR GO; GO:0048471; C:perinuclear region; IDA.  
 DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0042803; F:protein homodimerization activity; IDA.  
 DR GO; GO:0042742; P:defense response to bacteria; IMP.  
 DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.  
 DR GO; GO:0001666; P:response to hypoxia; IDA.  
 DR GO; GO:0006801; P:superoxide metabolism; IMP.  
 DR InterPro; IPR003097; FAD binding.  
 DR InterPro; IPR001094; Flavodoxin like.  
 DR InterPro; IPR008254; Flav nitox synth.  
 DR InterPro; IPR001709; FPN\_Cyt\_redtse.  
 DR InterPro; IPR012144; NOS.  
 DR InterPro; IPR004030; NO synthase.  
 DR InterPro; IPR001433; Oxid FAD/NAD(P).  
 DR Pfam; PF00667; FAD binding\_1; 1.  
 DR Pfam; PF00258; Flavodoxin\_1; 1.  
 DR Pfam; PF00175; NAD binding\_1; 1.  
 DR Pfam; PF02898; NO synthase; 1.  
 DR PIRSF; PIRSF000333; NOS; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.  
 DR PROSITE; PS60001; NOS; UNKNOWN 1.  
 SQ SEQUENCE 1145 AA; 130671 MW; C26E09F53923295 CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 1145;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVVFPA 6  
 Db 515 KVVFPA 520  
 RESULT 24  
 ID Q73N39 TREDE PRELIMINARY; PRT; 164 AA.  
 AC Q73N39;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Membrane protein, putative.  
 GN OrderedLocusNames=TDE1317;  
 OS Treponema denticola.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
 OC NCBI\_TaxID=158;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 35405 / DSM 14222;  
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;  
 RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,  
 RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,  
 RA Salengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,  
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,  
 RA Gebregeorgis E., Geer K., Teagave G., Malek J.A., Ayodeji B.,  
 RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,  
 RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,  
 RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;  
 RT "Comparison of the genome of the oral pathogen Treponema denticola  
 RT with other spirochete genomes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).  
 DR EMBL; AE017250; AAS11834.1; -; Genomic\_DNA.  
 DR TIGR; TDE1317; -.  
 KW Complete proteome.  
 SQ SEQUENCE 164 AA; 18968 MW; 27E92778DDA9117C CRC64;  
 Query Match 96.6%; Score 28; DB 2; Length 164;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVVFPA 6  
 Db 50 KVVFPA 55  
 RESULT 25  
 Q6AKE9 DESPS  
 ID Q6AKE9 DESPS PRELIMINARY; PRT; 203 AA.  
 AC Q6AKE9;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Related to McbG protein.  
 GN OrderedLocusNames=DP2447;  
 OS Desulfotalea psychrophila.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;  
 OC Desulfobulbaceae; Desulfotalea.  
 OC NCBI\_TaxID=84980;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=LSV54 / DSM 12343;  
 RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;  
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,  
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,  
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,  
 RA Klenk H.-P.;  
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium  
 RT from permanently cold Arctic sediments.";  
 RL Environ. Microbiol. 6:887-902 (2004).  
 DR EMBL; CR522870; CAG37176.1; -; Genomic\_DNA.  
 DR InterPro; IPR001646; Sipeptide\_repeat.  
 DR Pfam; PF00805; Pentapeptide; 3.  
 KW Complete proteome.  
 SQ SEQUENCE 203 AA; 23270 MW; 2EA1CD022861292D CRC64;  
 Query Match 96.6%; Score 28; DB 2; Length 203;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVVFPA 6  
 Db 52 KVVFPA 57  
 RESULT 26  
 O67225 AQUAE  
 ID O67225 AQUAE PRELIMINARY; PRT; 380 AA.  
 AC O67225;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```
DE Hydrogenase expression/formation protein HypD.
GN Name=hypD; OrderedLocusNames=AQ_1157;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AB000726; AAC07185.1; -; Genomic_DNA.
DR PIR; F70399; F70399.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrgn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 141 KVIFFA 146

RESULT 27
Q81FH5_BACCR PRELIMINARY; PRT; 387 AA.
ID Q81FH5;
AC Q81FH5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Na+/H+ antiporter Napa (Inosine-dependent germination).
GN OrderedLocusNames=BC1612;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candolon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AB017003; AAP08591.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41037 MW; 907C03E6BA150B4A CRC64;

Query Match 96.8%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

us-10-009-122-17.rup

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 184 KIVFFA 189

RESULT 28
Q5WPU9_LUTLO PRELIMINARY; PRT; 399 AA.
ID Q5WPU9;
AC Q5WPU9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 43.2 kDa salivary protein.
GN ORFNames=LJTM11.Clu9;
OS Lutzomyia longipalpis (Sand fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
OC Psychodidae; Lutzomyia; Lutzomyia.
OX NCBI_TaxID=7200;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Salivary gland;
RX PubMed=15371479; DOI=10.1242/jeb.01185;
RA Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
RT "Identification of the most abundant secreted proteins from the
RT salivary glands of the sand fly Lutzomyia longipalpis, vector of
RT Leishmania chagasi.";
RL J. Exp. Biol. 207:3717-3729(2004).
DR EMBL; AY445935; AAS05318.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
SQ SEQUENCE 399 AA; 45277 MW; F4E19F115794AAE8 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 399;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 305 KVIFFA 310

RESULT 29
Q4TRF8_9SPHN PRELIMINARY; PRT; 450 AA.
ID Q4TRF8;
AC Q4TRF8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Membrane protein.
GN ORFNames=ELI0568;
OS Erythrobacter litoralis HTCC2594.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=314225;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC2594;
RA Giavannoni S.J., Cho J.-C., Ferrera S., Johnson J., Kravitz S.,
RA Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
RA Friedman R., Venter J.C.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAG0100001; EAL76762.1; -; Genomic DNA.
SQ SEQUENCE 450 AA; 50280 MW; 077F448E75ADF977 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 KVVFPA 6
Db 116 KIVFPA 121

RESULT 30
Q4S4T5_TETNG PRELIMINARY; PRT; 464 AA.
ID Q4S4T5_TETNG PRELIMINARY; PRT; 464 AA.
AC Q4S4T5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAF14738, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0024047001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jabin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Reest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RN Nature 431:946-957(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014738; CAG04347.1; -; Genomic_DNA.
FT NON TER 464 464
SQ SEQUENCE 464 AA; 53213 MW; 0F9FF81DB193CE5C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 464;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 304 KIVFPA 309

RESULT 31
Q91VU5_MOUSE PRELIMINARY; PRT; 606 AA.
ID Q91VU5_MOUSE PRELIMINARY; PRT; 606 AA.
AC Q91VU5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Wdccc2 protein.
GN Name=Af661311; Synonyms=Wdccc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/Fl;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/Fl;
RG NTH MGC Project;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009019; AAH09019.1; -; mRNA.
DR Ensembl; ENSMUSG0000024169; Mus musculus.
DR MGI; MGI:2146906; A1661311.
DR GO; GO:0005488; Fibrinogen; IEA.
DR InterPro; IPR011990; TPR-like helical.
SQ SEQUENCE 606 AA; 70992 MW; 4BB6057E07ADA16C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 606;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 376 KIVFPA 381

RESULT 32
Q4WB22_ASFPF PRELIMINARY; PRT; 623 AA.
ID Q4WB22_ASFPF PRELIMINARY; PRT; 623 AA.
AC Q4WB22;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Afu8g06810;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman N., Fodorova N., Fodorova N., Feldblyum T.V., Fischer R.,
RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris H., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafon A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,

```

RA Rabbinitovitch E., Rawlins N., Rajandream M.-A., Reichard U.,  
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,  
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,  
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
RA White C., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,  
RA Machida M., Hall N., Barrell B., Denning D.W.;  
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus  
RT Aspergillus fumigatus.";  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAHF01000013; EAL85442.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 623 AA; 72379 MW; 08795F0DEF6C18E2 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 623;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
||:||||  
DB 96 KVIFFA 101

RESULT 33  
Q5K7E5\_CRYNE PRELIMINARY; PRT; 630 AA.  
AC Q5K7E5;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DE Hypothetical protein.  
GN ORFNames=CN00130;  
OS Cryptococcus neoformans var. neoformans JEC21.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
OX NCBI\_TaxID=214684;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JEC21;  
RA Loftus B.J., Fung B., Roncaglia P., Vamathevan J., Utterback T.,  
RA Van Aken S., Fraser C.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=JEC21;  
RX PubMed=15653466; DOI=10.1126/science.1103773;  
RA Loftus B.J., Fung B., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
RA D'Souza C.A., Fox D.S., Gribberg V., Fu J., Fukushima M., Haas B.J.,  
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,  
RA Kwon-Chung K.J., Lengler K.B., Maiti R., Marra M.A., Marra R.E.,  
RA Mathewson C.A., Mitchell T.G., Perlea M., Riggs F.R., Salzberg S.L.,  
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,  
RA Fraser C.M., Hyman R.W.;  
RT "The genome of the basidiomycetous yeast and human pathogen  
RT Cryptococcus neoformans.";  
RL Science 307:1321-1324 (2005).  
DR EMBL; AS017356; AAW47004.1; -; Genomic\_DNA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0046872; F:metal ion binding; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR InterPro; IPR007219; Fungal trans.  
DR InterPro; IPR001138; Fungi\_Trcsrp\_N.  
DR Pfam; PF04082; Fungal\_trans; 1.

DR Pfam; PF00172; Zn\_clus; 1.  
DR PRINTS; PR00054; FUNGALZNCYS.  
DR SMART; SM00066; GAL4; 1.  
DR PROSITE; PS00463; ZN2\_CV6\_FUNGAL\_1; 1.  
DR PROSITE; PS50048; ZN2\_CV6\_FUNGAL\_2; 1.  
KW Complete proteome; DNA-binding; Hypothetical protein; Metal-binding;  
KW Nuclear protein; Transcription; Transcription regulation; Zinc.  
SQ SEQUENCE 630 AA; 68912 MW; 730A7C02A87D6B3B CRC64;

Query Match 96.6%; Score 28; DB 2; Length 630;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
||:||||  
DB 572 KVIFFA 577

RESULT 34  
Q6RUU2\_MOUSE PRELIMINARY; PRT; 663 AA.  
AC Q6RUU2;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE Hypothetical protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Brathwaite M., Waelz P., Dudekula D., Nagaraja R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY491413; AAS21643.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 663 AA; 77192 MW; CEB02E3EED356F1C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 663;  
Best Local Similarity 83.3%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
||:||||  
DB 433 KVIFFA 438

RESULT 35  
Q83IB2\_TROW8 PRELIMINARY; PRT; 690 AA.  
AC Q83IB2;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Putative helicase regulator.  
GN OrderedLocNames=TW130;  
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OX Micrococccineae; Cellulomonadaceae; Tropheryma.  
OX NCBI\_TaxID=218496;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22495039; PubMed=12606174; DOI=10.1016/S0140-6736(03)12597-4;  
RA Bentley S.D., Maitwald M., Murphy L.D., Pallen M.J., Yeats C.A.,  
RA Dover L.G., Norbertczak H.T., Besta G.S., Quail M.A., Harris D.E.,  
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,  
RA Barrell B.G., Parkhill J., Relman D.A.;  
RT "Sequencing and analysis of the genome of the Whipple's disease  
RT bacterium Tropheryma whipplei.";  
RL Lancet 361:637-644 (2003).  
DR EMBL; BX251410; CAD66810.1; -; Genomic\_DNA.



DR GO: 0005524; F:ATP binding; IEA.  
 DR GO: 0003677; F:DNA binding; IEA.  
 DR GO: 0004386; F:Helicase activity; IEA.  
 DR InterPro: IPR011545; DEAD/DEAH\_N.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR InterPro: IPR000330; SNF2\_N\_  
 DR Pfam: PF00271; Helicase\_C\_1.  
 DR Pfam: PF00176; SNF2\_N; 1.  
 DR SMART: SM00487; DEXDC; 1.  
 DR SMART: SM00490; HELIC; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 690 AA; 76266 MW; CD3633B94B669B32 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 690;  
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 :|||  
 Db 526 KIVFFA 531

## RESULT 36

Q83GW3 TROWT  
 ID Q83GW3; TROWT PRELIMINARY; PRT; 698 AA.  
 AC Q83GW3;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE DNA helicase.  
 GN OrderedLocustNames=TW118;  
 OS Tropheryma whipplei (strain Twist) (Whipple's bacillus).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococcineae; Cellulomonadaceae; Tropheryma.  
 OX NCBI\_TaxID=203267;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Twist;  
 RX MEDLINE=22784088; PubMed=12902375;  
 RA Raoult D., Ogata H., Audic S., Robert C., Suhre K., Drancourt M.,  
 RA Claverie J.-M.;  
 RT "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a  
 RT reduced genome.";  
 RL Genome Res. 13:1800-1809(2003).  
 DR ENBL; AE016850; AAC4215.1; -; Genomic\_DNA.  
 DR GO: 0005524; F:ATP binding; IEA.  
 DR GO: 0003677; F:DNA binding; IEA.  
 DR GO: 0004386; F:Helicase activity; IEA.  
 DR InterPro: IPR011545; DEAD/DEAH\_N.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR Pfam: PF00271; Helicase\_C\_1.  
 DR Pfam: PF00176; SNF2\_N; 1.  
 DR SMART: SM00487; DEXDC; 1.  
 DR SMART: SM00490; HELIC; 1.  
 KW Complete proteome; Helicase.  
 SQ SEQUENCE 698 AA; 77193 MW; 6D104BF533CDDE72 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 698;  
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 :|||  
 Db 534 KIVFFA 539

## RESULT 37

Q55HW1 CRYNE  
 ID Q55HW1 CRYNE PRELIMINARY; PRT; 760 AA.  
 AC Q55HW1;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 DE ORFNames=CNBN0110;  
 GN Cryptococcus neoformans var. neoformans B-3501A.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=283643;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B-3501A;  
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
 RA Wickes B.L., Fu J., Davis R.W.;  
 RT "Cryptococcus neoformans serotype D sequencing.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABY01000066; EAL17182.1; -; Genomic\_DNA.  
 DR GO: 0005634; C:nucleus; IEA.  
 DR GO: 0003700; F:transcription factor activity; IEA.  
 DR GO: 0008270; F:zinc ion binding; IEA.  
 DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO: 0006350; P:transcription; IEA.  
 DR DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;  
 KW Transcription; Transcription regulation; Zinc.  
 SQ SEQUENCE 760 AA; 84062 MW; 735C53C64AB54619 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 760;  
 Best Local Similarity 83.3%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 :|||  
 Db 702 KIVFFA 707

## RESULT 38

Q6ZQ91 MOUSE  
 ID Q6ZQ91 MOUSE PRELIMINARY; PRT; 1265 AA.  
 AC Q6ZQ91;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE MKIAA0590 protein (Fragment).  
 GN Name=MKIAA0590;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX PubMed=14621295;  
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,  
 RA Saga Y., Nagase T., Ohara O., Koga H.;  
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:  
 RT iii. the complete nucleotide sequences of 500 mouse KIAA-homologous  
 RT cDNAs identified by screening of terminal sequences of cDNA clones  
 RT randomly sampled from size-fractionated libraries.";  
 RL DNA Res. 10:167-180(2003).  
 DR ENBL; AK129167; BAC97977.1; -; mRNA.  
 DR NON TER 1  
 FT SEQUENCE 1265 AA; 143403 MW; C9C157ABE80FF928 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1265;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 :|||  
 Db 1081 KIVFFA 1086



```
RESULT 39
Q5F3M1 CHICK PRELIMINARY; PRT; 1412 AA.
AC Q5F3M1_
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.13m2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Rutter S., Blagodatski A., Kostovska D., Kotter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851629; CAH65263.1; -; mRNA.
DR InterPro; IPR001680; WD40.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE 1412 AA; 158448 MW; FA0050885B274747 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1412;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1225 KIVFFA 1230

RESULT 40
Q4Q5Q4 LEIMA PRELIMINARY; PRT; 1655 AA.
AC Q4Q5Q4_
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=ImjF32.0310;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CF005269; CAJ08491.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1655 AA; 181249 MW; 2B5317E9ED469A55 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1655;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1397 KIVFFA 1402
```

```
RESULT 41
Q4LBQ8 SODGL PRELIMINARY; PRT; 88 AA.
AC Q4LBQ8_
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Chey protein.
GN Name=chey;
OS Sodalis glossinidius.
OC Plasmid pSG4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PLASMID=pSG4;
RA Darby A.C., Lagnel J., Matthew C.Z., Bourtzis K., Maudlin I.,
RA Welburn S.C.;
RT "Extrachromosomal DNA of the symbiont Sodalis glossinidius.";
RL J. Bacteriol. 187:5003-5007(2005).
DR EMBL; AJ868439; CAI59440.1; -; Genomic_DNA.
DR EMBL; AJ868438; CAI59427.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 88 AA; 10177 MW; F4168F2A56B8D0AC CRC64;

Query Match 93.1%; Score 27; DB 2; Length 88;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 42 KIIFFA 47

RESULT 42
Q9RQ09 BACTIN PRELIMINARY; PRT; 183 AA.
AC Q9RQ09_07C422;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE RNA polymerase sigma factor SigZ-like protein (RNA polymerase ECF-type
DE sigma factor).
GN Name=sigZ; OrderedLocusNames=BT1278;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482;
RX MEDLINE=99380605; PubMed=10449780; DOI=10.1073/pnas.96.17.9833;
RX Hooper L.V., Xu J., Falk P.G., Midtvedt T., Gordon J.I.;
RT "A molecular sensor that allows a gut commensal to control its
RT nutrient foundation in a competitive ecosystem.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9833-9838(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482; ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RX Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AF137263; AAF01488.1; -; Genomic_DNA.
DR EMBL; AE016931; AAO76385.1; -; Genomic_DNA.
DR GO; GO:0016987; F:sigma factor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007627; Sigma70_r2.
```

DR InterPro; IPR011991; Wing\_hlx\_DNA\_bd.  
DR Pfam; PF04542; Sigma70\_r2; 1.  
KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;  
KW Nucleotidyltransferase; Sigma factor; Transcription;  
KW Transcription regulation; Transferase.  
SQ SEQUENCE 183 AA; 22042 MW; 6B24DABC99BEC643 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 183;  
Best Local Similarity 66.7%; Pred. No. 3.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:|:|  
Db 172 KIIFFA 177

## RESULT 43

Q61C67 CAEBR  
ID Q61C67\_CAEBR PRELIMINARY; PRT; 315 AA.  
AC Q61C67;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein CBG13055 (Fragment).  
GN Name=CBG13055;  
OS Caenorhabditis briggsae.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6238;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RG The C.briggsae Sequencing Consortium;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CAAC01000061; CAB67532.1; -; Genomic DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsin.  
DR Pfam; PF00001; 7cm 1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN  
DR PROSITE; PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Hypothetical protein; Receptor;  
KW Transducer; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 315  
SQ SEQUENCE 315 AA; 35855 MW; 579B59D0D1874512 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 315;  
Best Local Similarity 66.7%; Pred. No. 5.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:|:|  
Db 117 KIIFFA 122

## RESULT 44

Q4HS77 CAMUP  
ID Q4HS77\_CAMUP PRELIMINARY; PRT; 362 AA.  
AC Q4HS77;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hydrogenase expression/formatation protein HypD.  
GN Name=hypD; ORFNames=CUP0294;  
OS Campylobacter upsaliensis RM3195.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Campylobacteraceae; Campylobacter.  
OX NCBI\_TaxID=306264;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=RM3195;  
RA Pouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Raeko D.A.,  
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,  
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,  
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,  
RA Nelson K.E.;  
RT "Major structural and novel potential virulence mechanisms from the  
RT genomes of multiple Campylobacter species";  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAEJ01000002; EAL53713.1; -; Genomic DNA.  
SQ SEQUENCE 362 AA; 40365 MW; 15B0A8B12D60CAED CRC64;

Query Match 93.1%; Score 27; DB 2; Length 362;  
Best Local Similarity 66.7%; Pred. No. 6.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:|:|  
Db 132 KIIFFA 137

## RESULT 45

Q9V7J0 DROME  
ID Q9V7J0\_DROME PRELIMINARY; PRT; 382 AA.  
AC Q9V7J0; Q9GQ81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE C98421-PB, isoform B (Aspartyl beta-hydroxylase variant 2).  
GN Name=Asph; ORFNames=C98421;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RR MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muszy D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M., Pan S.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celnik S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a Genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX Berkeley *Drosophila* Genome Project;  
RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Paclet B., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;  
RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,  
RA O'Neill K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,  
RA Friedman P.A.;  
RT "Aspartyl beta-hydroxylase (Asph) and an evolutionarily conserved  
RT isoform of Asph missing the catalytic domain share exons with  
RT junctin.";  
RL J. Biol. Chem. 275:39543-39554(2000).  
DR EMBL; AF003808; AAF58063.2; -; Genomic\_DNA.  
DR EMBL; AF289494; AAG40807.1; -; mRNA.  
DR Ensembl; CG8421; *Drosophila melanogaster*.  
DR FlyBase; FBgn0034075; Asph.  
DR FlyBase; FBgn0034075; Asph.  
SQ SEQUENCE 382 AA; 43287 MW; 6085C03AEBFC5E8B CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 382;  
Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6  
Db 53 KIIFPA 58  
RESULT 46  
Q6L2B4\_PICTO  
ID Q6L2B4\_PICTO PRELIMINARY; PRT; 410 AA.  
AC Q6L2B4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Lipopolysaccharide N-acetylglucosaminyltransferase.  
GN OrderedLocusNames=PT00303;  
OS *Picrophilus torridus*.  
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;  
OC Picrophilaceae; Picrophilus.  
OX NCBI\_TaxID=82076;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=DSM 9790 / ATCC 700027;  
RA PubMed=15184674; DOI=10.1073/pnas.0401356101;  
RA Fueterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,  
RA Schepers B., Dock C., Antranikian G., Liebl W.;  
RT "Genome sequence of *Picrophilus torridus* and its implications for life  
RT around pH 0.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).  
DR EMBL; AE017261; AAT42888.1; -; Genomic DNA.  
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . .; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.  
DR InterPro; IPR001296; Glyco\_trans\_1.  
DR Pfam; PF00534; Glycosyl\_transf\_1; I.  
KW Complete proteome; Glycosyltransferase; Transferase.  
SQ SEQUENCE 410 AA; 48120 MW; C192F0152E66E9B0 CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 410;  
Best Local Similarity 66.7%; Pred. No. 6.8e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVFPPA 6  
Db 235 KIIFPA 240  
RESULT 47  
O59243\_PYRHO  
ID O59243\_PYRHO PRELIMINARY; PRT; 447 AA.  
AC O59243;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein PH1606.  
GN OrderedLocusNames=PH1606;  
OS *Pyrococcus horikoshii*.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=53953;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=OT3;  
RX MEDLINE=98344137; PubMed=9679194;  
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kuehida N., Oguchi A.,  
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
RA Masuchi Y., Shizuya H., Kikuchi H.;  
RT "Complete sequence and gene organization of the genome of a hyper-  
RT thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";  
RL DNA Res. 5:55-76(1998).  
DR EMBL; BA000001; BAA30718.1; -; Genomic\_DNA.  
DR PIR; F71039; F71039.  
DR GO; GO:0016020; C:membrane; IEA.

```

DR GO: GO:0005355; F:glucose transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000803; GLUC transporter.
DR PRINTS; PR00172; GLUCRNSPORT.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 447 AA; 51173 MW; 509FA5A302D3B059 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 447;
Best Local Similarity 66.7%; Pred. No. 7.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPPA 6
Db 207 KIIFPA 212

RESULT 48
ID Q95S93 DROME PRELIMINARY; PRT; 556 AA.
AC Q95S93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GMS02239P.
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RA EMBL; AY060905; AAL28453.1; -; mRNA.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 556 AA; 63089 MW; 95D82EAC57D11FB8 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 556;
Best Local Similarity 66.7%; Pred. No. 8.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPPA 6
Db 53 KIIFPA 58

RESULT 49
Q9V719 DROME PRELIMINARY; PRT; 556 AA.
AC Q9V719;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8421-PD, isoform D (CG8421-pe, isoform e).
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

```

```

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RT Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22426070; PubMed=12537573;
RA Xaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22426069; PubMed=12537572;
RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RA Berkeley Drosophila Genome Project;
RG Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,

```

```

RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RG NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -I- INTERACTION:
CC O46085:EG:63B12.5; NDExp=1; IntAct=EBI-123244, EBI-151469;
DR EMBL; AB003808; AAF58064.2; -; Genomic_DNA.
DR IntAct; Q9V719; -;
DR Ensembl; CG8421; Drosophila melanogaster.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; Asph.
SQ SEQUENCE 556 AA; 63144 MW; B420980CB6C357A CRC64;

Query Match 93.1%; Score 27; DB 2; Length 556;
Best Local Similarity 66.7%; Pred.No. 8.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6 PRT; 785 AA.
DB 53 KLIFFA 58

RESULT 50
Q9Q82 DROME PRELIMINARY; PRT; 785 AA.
AC Q9Q82;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Aspartyl beta-hydroxylase variant 1 (CG8421-PA, isoform A).
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
RA O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
RA Friedman P.A.;
RT "Aspartyl beta-hydroxylase (Asph) and an evolutionarily conserved
RT isoform of Asph missing the catalytic domain share exons with
RT junctin.";
RL J. Biol. Chem. 275:39543-39554 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champagne B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Doudna K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

```

```

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Spradling A.C., Simpson M., Skupski M.P., Smith T.,
RA Spier R.A., Sideris E.W., Zhong W., Zhou G., Zhao Q., Zheng L.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasegarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou S., Zhu X.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnik S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnik S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF289493; AAG40806.1; -; mRNA.
RL EMBL; AE003808; AAM70947.1; -; Genomic DNA.
DR Ensembl; CG8421; Drosophila melanogaster.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004597; F:peptide-aspartate beta-dioxygenase activity; IEA.
DR GO; GO:0018193; P:peptidyl-amino acid modification; IEA.

```

```

DR InterPro; IPR007803; Asp Arg_Hydrox.
DR InterPro; IPR006025; Pept_M_En_BS.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like helical.
DR Pfam; PF05118; Asp Arg_Hydrox; 1.
DR PROSITE; PS05293; TPR_REGION; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 785 AA; 89643 MW; 30A8DFC6836f7f71 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 785;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 53 KIIFFA 58

RESULT 51
Q68K27 CHLRE
ID Q68K27 CHLRE PRELIMINARY; PRT; 1384 AA.
AC Q68K27;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Intracellular transport particle protein 140.
GN Name=IFT140;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadales; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Walker B.L., Hou Y., Dentler W.L., Witman G.B., Pazour G.J.;
RT "Intraflagellar transport protein IFT140."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AY866103; AA95430.1; -, mRNA.
DR GO; GO:0019861; C:flagellum; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 5.
DR TIGRfam; TIGR00756; PPR; 2.
DR PROSITE; PS0082; WD_REPEATS_2; 1.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Flagellum.
SQ SEQUENCE 1384 AA; 154603 MW; 5D3E70C8440DABCD CRC64;

Query Match 93.1%; Score 27; DB 2; Length 1384;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1154 KIIFFA 1159

RESULT 52
Q7QEF0 ANOGA
ID Q7QEF0 ANOGA PRELIMINARY; PRT; 1408 AA.
AC Q7QEF0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000001545 (Fragment).
GN ORFNames=ENSANGG0000001308;
OS Anopheles gambiae str. FEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL "Anopheles gambiae re-annotation.";
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008847; EAA06855.1; -, Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
FT NON TER 1408 1408
SQ SEQUENCE 1408 AA; 157382 MW; FF63317DAB976DB2 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 1408;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1212 KIIFFA 1217

RESULT 53
Q9VPR0 DROME
ID Q9VPR0 DROME PRELIMINARY; PRT; 1443 AA.
AC Q9VPR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG11838-PA, isoform A.
GN Names=Ose93; ORFNames=CG11838;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RX Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballev R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Foeiser C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hradec N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.S., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

```



RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Waeserman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirekas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
RT *melanogaster* euchromatic genome sequence";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirekas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX Berkeley *Drosophila* Genome Project;  
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirekas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003589; RAFL51483.1; -; Genomic\_DNA.  
DR FlyBase; FBgn0031262; Ose93.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR011990; TPR-like\_helical.  
DR InterPro; IPR001680; WD40.  
DR SMART; SM00320; WD40; 3.  
DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
KW Repeat.  
SQ SEQUENCE 1443 AA; 163136 MW; A8C5997678040B88 CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 1443;  
Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|::|||

Db 1204 KIIFFA 1209  
RESULT 54  
Q5BI64 DROME PRELIMINARY; PRT; 1458 AA.  
ID Q5BI64;  
AC Q5BI64;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DE LP14662p.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; *Drosophila*.  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Berkeley;  
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,  
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; EF021360; AAX33508.1; -; mRNA.  
DR InterPro; IPR011990; TPR-like\_helical.  
DR InterPro; IPR001680; WD40.  
DR PROSITE; PS006878; WD\_REPEATS\_1; UNKNOWN 1.  
DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
KW Repeat.  
SQ SEQUENCE 1458 AA; 163133 MW; 2D704C9970E541EC CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 1458;  
Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|::|||

Db 1219 KIIFFA 1224  
RESULT 55  
Q7KTZ4 DROME PRELIMINARY; PRT; 1503 AA.  
ID Q7KTZ4;  
AC Q7KTZ4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE CG11838-PB, Isoform B.  
GN Name=Ose93; ORFNames=CG11838;  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; *Drosophila*.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfaffner B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davesport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fostier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Markulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*;"  
RL Science 287:2185-2195(2000).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence;"  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celinker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomics perspective;"  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review;"  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RN NUCLEOTIDE SEQUENCE.  
RG Berkeley *Drosophila* Genome Project;  
RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence;"  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.  
RN [6]  
RN NUCLEOTIDE SEQUENCE.  
RG FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AE003589; AAS6435.1; -; Genomic DNA.  
DR InterPro; IPR011990; TPR-like\_helical.  
DR InterPro; IPR001680; WD40.  
DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
DR PROSITE; PS00294; WD\_REPEATS\_REGION; 1.  
KW Repeat.

SQ SEQUENCE 1503 AA; 167957 MW; A0DD3F532590486 CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 1503;  
Best Local Similarity 66.7%; Pred. No. 2.2e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
Db 1264 KIIFPA 1269  
RESULT 56  
Q8A6R7\_BACTN  
ID Q8A6R7\_BACTN PRELIMINARY; PRT; 1676 AA.  
AC Q8A6R7;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Conserved protein, with weak BamHI domain.  
GN OrderedLocustNames-BT1809;  
OS Bacteroides thetaiotaomicron.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=818;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RX STRAIN=VPI-5482 / ATCC 29148;  
RC MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;  
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
RA Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis;"  
RL Science 299:12074-2076(2003).  
RL EMBL; AE016933; AA076916.1; -; Genomic DNA.  
DR InterPro; IPR002048; EF-hand.  
DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 1676 AA; 193673 MW; 28065878C0F6C961 CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 1676;  
Best Local Similarity 66.7%; Pred. No. 2.4e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
Db 1656 KIIFPA 1661  
RESULT 57  
Q9UC33\_HUMAN  
ID Q9UC33\_HUMAN PRELIMINARY; PRT; 33 AA.  
AC Q9UC33;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Beta-amyloid peptide (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN PROTEIN SEQUENCE.  
RX MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;  
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,  
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;  
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from  
RT biological fluids;"  
RL Nature 359:325-327(1992).  
DR HSP; Q16019; IBA4.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.



DR PRINTS; PR00204; BETAAMYLOID.  
SQ SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 33;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFA 6  
|:|||||  
Db 16 KLVFFFA 21

RESULT 58  
Q56JJ6 GRAGR  
ID Q56JJ6 GRAGR PRELIMINARY; PRT; 42 AA.  
AC Q56JJ6;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Amyloid beta protein (Fragment).  
OS Grampus griseus (Risso's dolphin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;  
OC Odontoceti; Delphinidae; Grampus.  
OX NCBI\_TaxID=83653;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Gallego C., Sarasa M.;  
RT "The molecular machinery of Alzheimer's disease in the dolphin.";  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY926589; AAX81918.1; -; mRNA.  
FT NON\_TER 1  
FT NON\_TER 42  
FT NON\_TER 42  
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFA 6  
|:|||||  
Db 16 KLVFFFA 21

RESULT 59  
Q56JJ7 TURTR  
ID Q56JJ7 TURTR PRELIMINARY; PRT; 42 AA.  
AC Q56JJ7;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Amyloid beta protein (Fragment).  
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;  
OC Odontoceti; Delphinidae; Tursiops.  
OX NCBI\_TaxID=9739;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Gallego C., Sarasa M.;  
RT "The molecular machinery of Alzheimer's disease in the dolphin.";  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY926588; AAX81917.1; -; mRNA.  
FT NON\_TER 1  
FT NON\_TER 42  
FT NON\_TER 42  
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFA 6  
|:|||||

Db 16 KLVFFFA 21

RESULT 60  
Q7M088 CAVPO  
ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.  
AC Q7M088;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Beta-amyloid protein (Fragment).  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
OC Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=93290653; PubMed=7685598;  
RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,  
RA Kamiya H., Ohno M.;  
RT "Receptor-mediated specific biological activity of a beta-amyloid  
protein fragment for NK-1 substance p receptors.";  
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).  
DR PIR; PNO512; PNO512.  
DR HSSP; Q16019; 1IYT.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00204; BETAAMYLOID.  
FT NON\_TER 1  
FT NON\_TER 42  
FT NON\_TER 42  
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFA 6  
|:|||||  
Db 16 KLVFFFA 21

RESULT 61  
Q8WZ99 HUMAN  
ID Q8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.  
AC Q8WZ99;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Amyloid protein (Fragment).  
GN Name=APP;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;  
RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,  
RA Ninomiya H., Saïdo TC., Hashimoto T., Iwatsubo T., Nakashima K.;  
RT "Novel amyloid precursor protein gene missense mutation (D678N) in  
probable familial Alzheimer's disease.";  
RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).  
DR EMBL; AB066441; BAB71958.2; -; mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00204; BETAAMYLOID.  
FT NON\_TER 1

```

PT  NON TER      52      52
SQ  SEQUENCE     52 AA;  5597 MW;  3F0E8E9EC18011AD CRC64;

Query Match      89.7%; Score 26; DB 2; Length 52;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KVVFPA 6
Db  16 KLVFPA 21

RESULT 62
Q82VG8_NITEU
ID  Q82VG8_NITEU PRELIMINARY; PRT; 55 AA.
AC  Q82VG8;
DT  01-JUN-2003 (TrEMBLrel. 24, Created)
DT  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Hypothetical protein.
DE  OrderedLocusNames=NE1120;
OS  Nitrosomonas europaea.
OC  Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC  Nitrosomonadaceae; Nitrosomonas.
OX  NCBI_TaxID=915;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC 19718 / IPO 14298;
RX  MEDLINE=22586410; PubMed=12700255;
RA  DOI=10.1128/JB.185.5.2759-2773.2003;
RA  Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA  Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA  Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT  "Complete genome sequence of the ammonia-oxidizing bacterium and
RT  obligate chemolithoautotroph Nitrosomonas europaea.";
RL  J. Bacteriol. 185:2759-2773 (2003).
DR  EMBL; BX321859; CAD85031.1; -; Genomic_DNA.
DR  InterPro; IPR009760; DUF1328.
DR  Pfam; PF07043; DUF1328; 1.
DR  PIRSF; PIRSF036466; UCP036466; 1.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 55 AA; 5845 MW; 4F6839F53BE308C CRC64;

Query Match      89.7%; Score 26; DB 2; Length 55;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KVVFPA 6
Db  32 KLVFPA 37

RESULT 63
A4_UR5MA
ID  A4_UR5MA STANDARD; PRT; 57 AA.
AC  Q29149;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE  beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE  Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE  C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE  fragment 57)] (Fragment).
GN  Name=APP;
OS  Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC  Ursus.
OX  NCBI_TaxID=29073;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Brain;

MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
Brain Res. Mol. Brain Res. 10:299-305 (1991).
-|- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
-|- SUBCELLULAR LOCATION: Type I membrane protein.
-|- SIMILARITY: Belongs to the APP family.

This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; X56128; CAA39593.1; -; mRNA.
PIR; B60045; B60045.
HSSP; P08592; INMJ.
InterPro; IPR008155; A4_APP.
InterPro; IPR001255; Beta-APP.
PANTHER; PTHR10083:SP6; Beta-APP; 1.
Pfam; PF03494; Beta-APP; 1.
PRINTS; PR00204; BETAAMYL0ID.
PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
KW  Amyloid; Transmembrane.
FT  CHAIN <1..5 Soluble APP-beta (By similarity).
FT  CHAIN 6..57 CTF-alpha (By similarity).
FT  CHAIN 6..47 Beta-amyloid protein 42 (By similarity).
FT  CHAIN 6..45 Beta-amyloid protein 40 (By similarity).
FT  CHAIN 46..57 Gamma-CTF(59) (By similarity).
FT  CHAIN 48..57 Gamma-CTF(57) (By similarity).
FT  TOPO_DOM <1..33 Extracellular (Potential).
FT  TRANSMEM 34..57 Potential.
FT  NON_TER 1..1
FT  NON_TER 57..57
SQ  SEQUENCE 57 AA; 6172 MW; 84209D8E8A82DFA CRC64;

Query Match      89.7%; Score 26; DB 1; Length 57;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KVVFPA 6
Db  21 KLVFPA 26

RESULT 64
A4_CANFA
ID  A4_CANFA STANDARD; PRT; 58 AA.
AC  Q28280;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE  beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE  Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE  C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE  fragment 57)] (Fragment).
GN  Name=APP;
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC  Canis.
OX  NCBI_TaxID=9615;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Kidney;
RX  MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

```

```

RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56125; CAA39590.1; -, mRNA.
DR HSSP; P08592; INMU.
DR Ensembl; ENSCAFG0000008557; Canis familiaris.
DR InterPro; IPR001255; A4_APP.
DR PANTHER; PTHR10083:SP6; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PTHRI0083:SP6; Beta-APP; 1.
DR PROSITE; PS00320; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >58 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;

Query Match 89.7%; Score 26; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 22 KLVFFA 27

RESULT 65
A4_RABIT
ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

```

```

RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56129; CAA39594.1; -, mRNA.
DR HSSP; P08592; INMJ.
DR InterPro; IPR008155; A4_APP.
DR PANTHER; PTHR10083:SP6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88BBA82D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 66
A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

```



```

Query Match      89.7%; Score 26; DB 2; Length 79;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   ||:||||
DB 3 KLVFFA 8

RESULT 69
O35463 CRIGR
ID O35463 CRIGR PRELIMINARY; PRT; 79 AA.
AC O35463
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).
GN Name=beta APP;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Samdamurti K., Plinix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF030413; AAB86608.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 79;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   ||:||||
DB 36 KLVFFA 41

RESULT 70
MOAD_ECOLI
ID MOAD_ECOLI STANDARD; PRT; 81 AA.
AC P30748; P77422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Molybdopterine converting factor subunit 1 (MPT synthase subunit 1)
DE (Molybdopterine synthase subunit 1) (Molybdenum cofactor biosynthesis
DE protein D) (Molybdopterine converting factor small subunit).
GN Name=moaD; Synonyms=chlA4, chlM; OrderedLocusNames=b0784;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K12 / MC4100;
RX MEDLINE=93368423; PubMed=8361352;
RA Rivers S.L., McNairn E., Blasco F., Giordano G., Boxer D.H.;
RT "Molecular genetic analysis of the moa operon of Escherichia coli K-12
RT required for molybdenum cofactor biosynthesis.";
RL Mol. Microbiol. 8:1071-1081(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;

```

```

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP PROTEIN SEQUENCE OF 1-15, CHARACTERIZATION, AND MASS SPECTROMETRY.
RX MEDLINE=93293873; PubMed=8514782;
RA Pitterle D.M., Rajagopalan K.V.;
RT "The biosynthesis of molybdopterine in Escherichia coli. Purification
RT and characterization of the converting factor.";
RL J. Biol. Chem. 268:13499-13505(1993).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS).
RX MEDLINE=20577273; PubMed=11135669; DOI=10.1038/83034;
RA Rudolph M.J., Wuebbens M.M., Rajagopalan K.V., Schindelin H.;
RT "Crystal structure of molybdopterine synthase and its evolutionary
RT relationship to ubiquitin activation.";
RL Nat. Struct. Biol. 8:42-46(2001).
CC -!- FUNCTION: Converts molybdopterine precursor Z into molybdopterine.
CC This requires the incorporation of two sulfur atoms into precursor
CC Z to generate a dithiolene group. The sulfur atoms are provided by
CC the active form of the small subunit, whose activation involves
CC the acquisition of sulfur and the activity of moeB/chlN.
CC -!- PATHWAY: Molybdenum cofactor biosynthesis.
CC -!- SUBUNIT: Heterodimer of 2 moaD subunits and 2 moaE subunits.
CC -!- INTERACTION: Belongs to the moaD family.
CC P30749:moaE; NbExp=1; IntAct=EBI-554366; EBI-554376;
CC POA7K2:rpLL; NbExp=1; IntAct=EBI-554366; EBI-543702;
CC -!- INDUCTION: By anaerobiosis, repressed by the molybdenum cofactor.
CC -!- MASS SPECTROMETRY: MW=8773.6; MW_ERR=0.2; METHOD=Electrospray;
CC RANGE=1-81; NOTE=Ref. 4.
CC -!- SIMILARITY: Belongs to the moaD family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X70420; CAA49864.1; -; Genomic DNA.
CC EMBL; U00096; AAC73871.1; -; Genomic DNA.
CC EMBL; D90716; BAA35442.1; -; Genomic DNA.
CC P18; H64814; H64814.
CC PDB; 1PM0; X-ray; D=1-81.
CC PDB; 1FMA; X-ray; D=1-81.
CC PDB; 1JW9; X-ray; D=1-81.
CC PDB; 1JWA; X-ray; D=1-81.
CC PDB; 1JWB; X-ray; D=1-81.
CC PDB; 1NVI; X-ray; D=3-81.
CC IntAct; P30748; -.
CC EchoBASE; EBI554; -.
CC EcoGene; EG11597; moaD.
CC InterPro; IPR010034; MoaD.
CC InterPro; IPR003749; This.
CC Pfam; PF02597; This; 1.
CC TIGRFAMs; TIGR01682; moaD; 1.
CC 3D-structure; Complete proteome; Direct protein sequencing;
KW

```

KW Molybdenum cofactor biosynthesis.  
 FT CONFLICT 9 9 Q -> B (in Ref. 4).  
 FT CONFLICT 45 45 A -> R (in Ref. 1).  
 FT STRAND 2 6  
 FT HELIX 8 14  
 FT STRAND 18 21  
 FT STRAND 27 27  
 FT STRAND 36 36  
 FT TURN 37 37  
 FT HELIX 40 45  
 FT TURN 46 46  
 FT TURN 48 49  
 FT STRAND 52 55  
 FT TURN 56 57  
 FT STRAND 58 59  
 FT TURN 62 63  
 FT STRAND 65 65  
 FT TURN 68 69  
 FT STRAND 71 75  
 SQ SEQUENCE 81 AA; 8758 MW; 1E0A440520EE82F4 CRC64;  
 Query Match 89.7%; Score 26; DB 1; Length 81;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 ||:||||  
 Db 3 KVLFFA 8

RESULT 71  
 Q9APP7\_9BACT PRELIMINARY; PRT; 81 AA.  
 AC Q9APP7;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative molybdenum cofactor biosynthesis protein D.  
 GN Name=moa;  
 OS uncultured bacterium pCosHE1.  
 OC Bacteria; environmental samples.  
 NCBI\_TaxID=143796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20575196; PubMed=11133432; DOI=10.1128/AEM.67.1.89-99.2001;  
 RA Entcheva P., Liebl W., Johann A., Hartsch T., Streit W.R.;  
 RT "Direct cloning from enrichment cultures, a reliable strategy for  
 isolation of complete operons and genes from microbial consortia.";  
 RL Appl. Environ. Microbiol. 67:89-99(2001).  
 DR EMBL; AF250774; AAG60573.1; -; Genomic\_DNA.  
 DR HSSP; P30748; 1JW9.  
 DR SMR; Q9APP7; 1-81.  
 DR GO; GO:0006777; P:Mo-molybdopter in cofactor biosynthesis; IEA.  
 DR GO; GO:0006790; P:sulfur metabolism; IEA.  
 DR InterPro; IPR010034; MoaD.  
 DR InterPro; IPR003749; This.  
 DR Pfam; PF02597; This; 1.  
 DR TIGRFAMs; TIGR01682; moaD; 1.  
 SQ SEQUENCE 81 AA; 8739 MW; 21361C1FCA3AA24C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 ||:||||  
 Db 3 KVLFFA 8

RESULT 72  
 Q57RF2\_SALCH PRELIMINARY; PRT; 81 AA.  
 ID Q57RF2\_SALCH PRELIMINARY;  
 AC Q57RF2;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Molybdopter in biosynthesis protein.  
 GN Name=moa; OrderedLocusNames=SC0803;  
 OS Salmonella cholerae-suis (Salmonella enterica).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 NCBI\_TaxID=591;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=SC-B67;  
 RX PubMed=15781495;  
 RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,  
 Wang H.-S., Lee Y.-S.;  
 RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a  
 highly invasive and resistant zoonotic pathogen.";  
 RL Nucleic Acids Res. 33:1690-1698(2005).  
 DR EMBL; AE017220; AAX64709.1; -; Genomic\_DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 81 AA; 8772 MW; 5821119685621426 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 ||:||||  
 Db 3 KVLFFA 8

RESULT 73  
 Q65TT0\_MANSN PRELIMINARY; PRT; 81 AA.  
 ID Q65TT0\_MANSN PRELIMINARY;  
 AC Q65TT0;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE MoaD protein.  
 GN Name=moa; OrderedLocusNames=MS1023;  
 OS Mannheimia succiniciproducens (strain MBEL55E).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Mannheimia.  
 NCBI\_TaxID=221988;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15378067; DOI=10.1038/nbt1010;  
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,  
 Kim C.H., Jeong H., Hur C.G., Kim J.J.;  
 RT "The genome sequence of the capnophilic rumen bacterium Mannheimia  
 succiniciproducens.";  
 RL Nat. Biotechnol. 22:1275-1281(2004).  
 DR EMBL; AE016827; AAU37630.1; -; Genomic DNA.  
 DR GO; GO:0006777; P:Mo-molybdopter in cofactor biosynthesis; IEA.  
 DR GO; GO:0006790; P:sulfur metabolism; IEA.  
 DR InterPro; IPR010034; MoaD.  
 DR InterPro; IPR003749; This.  
 DR Pfam; PF02597; This; 1.  
 DR TIGRFAMs; TIGR01682; moaD; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 81 AA; 8617 MW; E529ED840985D661 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 ||:||||  
 Db 3 KVLFFA 8

RESULT 74  
 Q7N6P4\_PHOLL

ID Q7N6P4\_PHOILL PRELIMINARY; PRT; 81 AA.  
AC Q7N6P4;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Molybdopterin.  
DE Molybdopterin.  
GN Name-moad; OrderedLocusNames=plu1501;  
OS Photorhabdus luminescens (subsp. laumondii).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Photorhabdus.  
OX NCBI\_TaxID=141679;  
RN [1]\_TaxID=141679;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=TT01;  
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;  
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,  
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,  
RA Dasea E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,  
RA Medigue C., Lanois A., Powell K., Siguer P., Vincent R., Wingate V.,  
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;  
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus  
RT luminescens.";  
RT Nat. Biotechnol. 21:1307-1313 (2003).  
DR EMBL; BX571864; CAE13794.1; -; Genomic\_DNA.  
DR HSSP; P30748; 1JW9.  
DR PhotoList; plu1501; -.  
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.  
DR GO; GO:0006790; P:sulfur metabolism; IEA.  
DR InterPro; IPR010034; Moad.  
DR InterPro; IPR003749; This.  
DR Pfam; PF02597; This; 1.  
DR TIGRFAMs; TIGR01682; moad; 1.  
KW Complete proteome.  
SQ SEQUENCE 81 AA; 8886 MW; 6646B5932531F136 CRC64;  
  
Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
Db ||:||||  
3 KVLFFA 8  
  
RESULT 75  
Q8D897\_VIBVU PRELIMINARY; PRT; 81 AA.  
ID Q8D897\_VIBVU PRELIMINARY; PRT; 81 AA.  
AC Q8D897;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Molybdenum cofactor biosynthesis protein D.  
GN OrderedLocusNames=VW13085;  
OS Vibrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=672;  
RN [1]\_TaxID=672;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CMCP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
RA Choy H.E.;  
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";  
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AS016807; AAO11408.1; -; Genomic\_DNA.  
DR HSSP; P30748; 1JW9.  
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.  
DR GO; GO:0006790; P:sulfur metabolism; IEA.  
DR InterPro; IPR010034; Moad.  
DR InterPro; IPR003749; This.  
DR Pfam; PF02597; This; 1.  
DR TIGRFAMs; TIGR01682; moad; 1.  
KW Complete proteome.

SQ SEQUENCE 81 AA; 8731 MW; 4BE52C0ABDE06418 CRC64;  
  
Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
Db ||:||||  
3 KVLFFA 8  
  
Search completed: December 29, 2005, 17:47:29  
Job time : 79.1936 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 15.129 Seconds  
(without alignments)  
44.518 Million cell updates/sec

Title: US-10-009-122-2  
Perfect score: 34  
Sequence: 1 KKLVFFA 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : PIR\_80.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	91.2	447	2 F71039	hypothetical prote
2	30	88.2	33	2 S23094	beta-amyloid prote
3	30	88.2	42	2 P00512	beta-amyloid prote
4	30	88.2	57	2 A60045	Alzheimer's diseas
5	30	88.2	57	2 F60045	Alzheimer's diseas
6	30	88.2	57	2 D60045	Alzheimer's diseas
7	30	88.2	57	2 G60045	Alzheimer's diseas
8	30	88.2	57	2 G60045	Alzheimer's diseas
9	30	88.2	57	2 B60045	Alzheimer's diseas
10	30	88.2	82	2 P04138	Alzheimer's diseas
11	30	88.2	346	2 D81288	probable fucose sy
12	30	88.2	359	2 C94983	hypothetical prote
13	30	88.2	380	2 F70399	hydrogenase expres
14	30	88.2	479	2 F96285	F9L1.11 protein -
15	30	88.2	586	1 RNEGB1	DNA-directed RNA p
16	30	88.2	655	2 G36524	protein TIN5.9 [i
17	30	88.2	695	1 A47995	Alzheimer's diseas
18	30	88.2	695	2 A27485	Alzheimer's diseas
19	30	88.2	695	2 S00550	Alzheimer's diseas
20	30	88.2	747	2 JH0773	Alzheimer's diseas
21	30	88.2	770	1 ORH044	Alzheimer's diseas
22	29	85.3	96	2 A05035	translation initia
23	29	85.3	109	2 B72213	conserved hypothet
24	29	85.3	152	2 T06645	hypothetical prote
25	29	85.3	176	1 I64161	cytochrome c bioge
26	29	85.3	231	2 H85138	hypothetical prote
27	29	85.3	316	2 AH1155	membrane proteins
28	29	85.3	316	2 AC1514	membrane protein h
29	29	85.3	352	2 T48903	wax synthase [impo

30	29	85.3	421	2 D81374	probable oxidoredu
31	29	85.3	428	2 T48008	hypothetical prote
32	29	85.3	484	2 E64432	spore coat polysac
33	29	85.3	593	2 T21510	hypothetical prote
34	29	85.3	610	2 T23836	hypothetical prote
35	29	85.3	763	2 C86733	penicillin-binding
36	29	85.3	774	2 F96639	protein Tif9, 8 [im
37	29	85.3	1016	2 S30236	genome polypeptid
38	28	82.4	123	2 H90367	hypothetical prote
39	28	82.4	214	2 T47892	hypothetical prote
40	28	82.4	218	2 H72361	conserved hypothet
41	28	82.4	236	2 S18783	exotoxin type A pr
42	28	82.4	236	2 S18786	hypothetical prote
43	28	82.4	245	2 B69841	streptococcal pyro
44	28	82.4	250	1 A26152	exotoxin type A pr
45	28	82.4	251	1 S29659	hypothetical prote
46	28	82.4	254	2 T28170	hypothetical prote
47	28	82.4	276	2 B82243	hypothetical prote
48	28	82.4	293	2 D69355	hypothetical prote
49	28	82.4	294	2 H90318	glycerol kinase (g
50	28	82.4	315	2 A70313	NADH2 dehydrogenas
51	28	82.4	321	2 H71729	hypothetical prote
52	28	82.4	333	2 A95039	sugar binding tran
53	28	82.4	355	2 B97909	transcription regu
54	28	82.4	383	2 AF1893	hydrogenase expres
55	28	82.4	528	2 T50330	hypothetical prote
56	28	82.4	605	2 T33750	hypothetical prote
57	28	82.4	1016	2 JQ0498	genome polypeptid
58	28	82.4	1133	2 T03302	P-type ATPase - Te
59	27	79.4	41	2 T07329	hypothetical prote
60	27	79.4	91	2 H97796	RP534 protein homo
61	27	79.4	110	2 A10493	probable membrane
62	27	79.4	147	2 T24057	hypothetical prote
63	27	79.4	208	2 D70134	flagellar biosynth
64	27	79.4	211	2 JC4540	transcription init
65	27	79.4	215	2 S74602	hypothetical prote
66	27	79.4	231	2 C64703	hypothetical prote
67	27	79.4	263	2 G97198	HAD superfamily hy
68	27	79.4	266	2 F97176	HAD superfamily hy
69	27	79.4	300	2 T26245	hypothetical prote
70	27	79.4	313	2 T25850	hypothetical prote
71	27	79.4	313	2 T23207	hypothetical prote
72	27	79.4	315	2 T28942	hypothetical prote
73	27	79.4	326	2 S76400	hypothetical prote
74	27	79.4	329	2 D88109	protein T24E12.6 [
75	27	79.4	331	2 S51490	chaperone (cpn60)
76	27	79.4	334	2 T20562	hypothetical prote
77	27	79.4	349	2 T26247	hypothetical prote
78	27	79.4	352	2 S51893	hypothetical prote
79	27	79.4	363	2 F70195	UDP-N-acetylglucos
80	27	79.4	377	2 AB0715	probable membrane
81	27	79.4	379	2 T39743	hydrogenase homolo
82	27	79.4	412	2 S23208	mRNA maturase b12
83	27	79.4	420	2 B97276	glycoyltransferas
84	27	79.4	423	2 E90569	conserved hypothet
85	27	79.4	446	2 D95061	sensor histidine k
86	27	79.4	487	2 AB2269	hypothetical prote
87	27	79.4	556	2 D96791	hypothetical prote
88	27	79.4	572	2 H96685	probable AMP-bindi
89	27	79.4	601	2 H69274	probable long-chain
90	27	79.4	613	2 F69424	conserved hypothet
91	27	79.4	629	2 AE2497	hypothetical prote
92	27	79.4	689	2 S74764	hypothetical prote
93	27	79.4	754	2 T06249	protoporphyrin IX
94	27	79.4	758	2 T02925	protoporphyrin IX
95	27	79.4	778	2 B86218	protein T27G7.20 [
96	27	79.4	855	2 S46050	probable purine nu
97	27	79.4	1174	2 H84982	exodeoxyribonuclea
98	27	79.4	1175	2 D85089	hypothetical prote
99	27	79.4	1285	2 B72420	hypothetical prote
100	27	79.4	3066	1 JQ1661	genome polypeptid
101	27	79.4	3066	1 JQ1662	genome polypeptid
102	27	79.4	4466	1 S17231	dynein beta heavy





249 25 73.5 334 2 I64220  
250 25 73.5 334 2 C84984  
251 25 73.5 337 2 S08459  
252 25 73.5 341 2 A64383  
253 25 73.5 343 1 C70418  
254 25 73.5 346 2 B86715  
255 25 73.5 346 2 G96643  
256 25 73.5 347 2 T20618  
257 25 73.5 348 2 B64552  
258 25 73.5 364 2 C72402  
259 25 73.5 366 2 T32598  
260 25 73.5 367 2 G95158  
261 25 73.5 374 2 S53829  
262 25 73.5 384 2 A51636  
263 25 73.5 384 2 H64161  
264 25 73.5 385 2 G98024  
265 25 73.5 388 2 B89777  
266 25 73.5 402 2 B86038  
267 25 73.5 402 2 D91191  
268 25 73.5 404 2 A54871  
269 25 73.5 405 2 A70146  
270 25 73.5 406 2 AC2267  
271 25 73.5 408 2 B72238  
272 25 73.5 408 2 C96984  
273 25 73.5 422 2 A98318  
274 25 73.5 422 2 AD2965  
275 25 73.5 423 2 S48817  
276 25 73.5 431 2 A82470  
277 25 73.5 433 2 T17654  
278 25 73.5 435 2 AD1340  
279 25 73.5 435 2 A81711  
280 25 73.5 440 1 OMWY  
281 25 73.5 443 2 T45574  
282 25 73.5 444 2 F96838  
283 25 73.5 446 2 A81721  
284 25 73.5 453 2 T75206  
285 25 73.5 471 2 T21102  
286 25 73.5 472 1 S55379  
287 25 73.5 472 2 A60330  
288 25 73.5 474 2 T34193  
289 25 73.5 475 2 B90545  
290 25 73.5 481 2 I56246  
291 25 73.5 481 2 B86285  
292 25 73.5 495 2 T31944  
293 25 73.5 497 2 T32090  
294 25 73.5 500 2 H91283  
295 25 73.5 500 2 B86125  
296 25 73.5 500 2 S56489  
297 25 73.5 507 2 C82901  
298 25 73.5 510 2 E71695  
299 25 73.5 513 2 A80021  
300 25 73.5 513 2 E71683

## ALIGNMENTS

RESULT 1  
F71039  
hypothetical protein PH1606 - Pyrococcus horikoshii  
C/Species: Pyrococcus horikoshii  
C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 05-Oct-2004  
C/Accession: F71039  
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A/Reference number: A71000; MUID:98344137; PMID:9679194  
A/Accession: F71039  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-447 <KAW>  
A/Cross-references: UNIPROT:059243; UNIPARC:UPI00000630DB; GB:AP000006; NID:g326133; PI

A;Experimental source: strain OT3  
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C/Genetics:  
A/Gene: PH1606  
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1142  
Query Match 91.2%; Score 31; DB 2; Length 447;  
Best Local Similarity 71.4%; Pred. No. 25; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KKLVEFA 7  
Db 206 KKLVEFA 212  
||:||||  
||:||||  
RESULT 2  
S23094  
beta-amyloid protein precursor - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
C/Accession: S23094  
R;Kojima, S.; Omori, M.  
FEBS Lett. 304, 57-60, 1992  
A/Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
A/Reference number: S23094; MUID:92316198; PMID:1618299  
A/Accession: S23094  
A/Molecule type: protein  
A/Residues: 1-33 <KOJ>  
A/Cross-references: UNIPARC:UPI00001777PB  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
Query Match 88.2%; Score 30; DB 2; Length 33;  
Best Local Similarity 85.7%; Pred. No. 4.1;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KKLVEFA 7  
Db 20 QKLVEFA 26  
:|||||  
:|||||  
RESULT 3  
PN0512  
beta-amyloid protein - guinea pig (fragment)  
C/Species: Cavia porcellus (Guinea pig)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: PN0512  
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno,  
Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
A/Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragm  
A/Reference number: PN0512; MUID:93290653; PMID:7685598  
A/Accession: PN0512  
A/Molecule type: protein  
A/Residues: 1-42 <SHI>  
A/Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C/Keywords: alternative splicing; amyloid  
Query Match 88.2%; Score 30; DB 2; Length 42;  
Best Local Similarity 85.7%; Pred. No. 5.1;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KKLVEFA 7  
Db 15 QKLVEFA 21  
:|||||  
:|||||  
RESULT 4  
A60045  
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C/Species: Canis lupus familiaris (dog)  
C/Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C/Accession: A60045  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

```

Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 5
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:G1895; PIDN:CAA39592.1; PID:
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 6
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 7
E60045

```

```

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 8
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 9
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:G2165; PIDN:
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||

```

Db 20 QKLVFFA 26

RESULT 10

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995

C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor

A;Reference number: PQ0438; MUID:93075180; PMID:1445331

A;Accession: PQ0438

A;Molecule type: DNA

A;Residues: 1-82 <DAV>

R;Johnstone, E.M.; Chaney, M.O.; Norris, P.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: C60045

A;Molecule type: mRNA

A;Residues: 12-68 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56129

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 88.2%; Score 30; DB 2; Length 82;

Best Local Similarity 85.7%; Pred. No. 9.3; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 1;

Qy 1 KKLVFFA 7

Db 31 QKLVFFA 37

RESULT 11

D81288

probable fucose synthetase Cj1428c [imported] - Campylobacter jejuni (strain NCTC 11168)

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C;Accession: D81288

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: D81288

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-346 <PAR>

A;Cross-references: UNIPROT:Q9PMW9; UNIPARC:UPI00000C1F0E; GB:AL1139078; GB:AL111168; NID

C;Genetics:

A;Gene: fcl; Cj1428c

Query Match 88.2%; Score 30; DB 2; Length 346;

Best Local Similarity 100.0%; Pred. No. 34; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0;

Qy 1 KKLVFF 6

Db 100 KKLVFF 105

RESULT 12

C84983

hypothetical protein mlta [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 05-Oct-2004

C;Accession: C84983

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.

A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: C84983

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-359 <STO>

A;Cross-references: UNIPARC:UPI000005E5B6; GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: mlta; BU458

C;Superfamily: membrane-bound lytic murein transglycosylase A homolog

Query Match 88.2%; Score 30; DB 2; Length 359;

Best Local Similarity 71.4%; Pred. No. 35; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 2;

Qy 1 KKLVFFA 7

Db 196 KKLIFFS 202

RESULT 13

F70399

hydrogenase expression/formation protein HypD - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

C;Accession: F70399

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; G

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: F70399

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-380 <AQF>

A;Cross-references: UNIPROT:O67225; UNIPARC:UPI0000056543; GB:AE000726; NID:G2983612; P

A;Experimental source: strain VF5

C;Genetics:

A;Gene: hypD

C;Superfamily: [NiFe]-hydrogenase maturation factor, HypD type

Query Match 88.2%; Score 30; DB 2; Length 380;

Best Local Similarity 71.4%; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 2;

Qy 1 KKLVFFA 7

Db 140 KKVIFFA 146

RESULT 14

F86285

F9L1.11 protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: F86285

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizlar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: F86285

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-479 <STO>

A;Cross-references: UNIPROT:Q9XI52; UNIPARC:UPI000000A9ASC; GB:AE005172; NID:G5103814; PIDN:G5103814;  
 C;Genetics:  
 A;Map position: 1

Query Match 88.2%; Score 30; DB 2; Length 479;  
 Best Local Similarity 71.4%; Pred. No. 45;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 |||||  
 Db 36 KKLVPFA 42

RESULT 15  
 RNEGB1  
 DNA-directed RNA polymerase (EC 2.7.7.6) beta'-1 chain - Euglena gracilis chloroplast  
 C;Species: chloroplast Euglena gracilis  
 C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
 C;Accession: S19258; S09211; S34555; S34922  
 R;Hallick, R.B.  
 submitted to the EMBL Data Library, November 1989  
 A;Reference number: S19258  
 A;Accession: S19258  
 A;Molecule type: DNA  
 A;Residues: 1-586 <HAL>  
 A;Cross-references: UNIPROT:P23580; UNIPARC:UPI000013471B; EMBL:X17191; NID:g11501; PIDN:G11501;  
 A;Experimental source: strain Pringsheim Z  
 R;Yepiz-Plascencia, G.M.; Radebaugh, C.A.; Hallick, R.B.  
 Nucleic Acids Res. 18, 1869-1878, 1990  
 A;Title: The Euglena gracilis chloroplast rpoB gene. Novel gene organization and transcription  
 A;Reference number: S09210; MUID:90245579; PMID:2110656  
 A;Accession: S09211  
 A;Molecule type: DNA  
 A;Residues: 1-23 <YEP>  
 A;Cross-references: UNIPARC:UPI00001726CE; EMBL:X17191  
 R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann, R.  
 submitted to the EMBL Data Library, January 1993  
 A;Description: The complete sequence of the Euglena gracilis chloroplast genome (tentative)  
 A;Reference number: S34494  
 A;Accession: S34555  
 A;Molecule type: DNA  
 A;Residues: 1-586 <HAL>  
 A;Cross-references: UNIPARC:UPI000013471B; EMBL:X70810; NID:g415327; PIDN:CAA50137.1; PIDN:CAA50137.1;  
 R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmann, R.  
 Nucleic Acids Res. 21, 3537-3544, 1993  
 A;Title: Complete sequence of Euglena gracilis chloroplast DNA.  
 A;Reference number: S34862; MUID:93347989; PMID:8346031  
 A;Accession: S34922  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-586 <HAL>  
 A;Cross-references: UNIPARC:UPI000013471B; EMBL:X70810; NID:g415327; PIDN:CAA50137.1; PIDN:CAA50137.1;  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993  
 C;Genetics:  
 A;Gene: rpoC1  
 A;Genome: chloroplast  
 A;Intons: 35/3; 104/2; 126/1; 176/2; 185/3; 267/1; 309/3; 361/1; 406/3; 515/3; 569/3  
 C;Superfamily: chloroplast DNA-directed RNA polymerase beta'-1 chain  
 C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 88.2%; Score 30; DB 1; Length 586;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 6  
 |||||  
 Db 564 KKLVPFA 569

RESULT 16  
 G96524  
 protein TIN15.9 [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
 C;Accession: G96524  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: G96524  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-655 <STO>  
 A;Cross-references: UNIPROT:Q9LP77; UNIPARC:UPI00000A1D67; GB:AE005173; NID:g8778688; PIDN:G8778688;  
 C;Genetics:  
 A;Gene: TIN15.9  
 A;Map position: 1  
 C;Superfamily: Receptor-like protein kinase

Query Match 88.2%; Score 30; DB 2; Length 655;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 6  
 |||||  
 Db 352 KKLVPFA 357

RESULT 17  
 A49795  
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C;Species: Macaca fascicularis (crab-eating macaque)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: A49795  
 R;Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.  
 Am. J. Pathol. 138, 1423-1435, 1991  
 A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
 A;Reference number: A49795; MUID:91273117; PMID:1905108  
 A;Accession: A49795  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-695 <POD>  
 A;Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:g342062; PIDN:AAA36829.1; PIDN:AAA36829.1;  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C;Keywords: alternative splicing

Query Match 88.2%; Score 30; DB 1; Length 695;  
 Best Local Similarity 85.7%; Pred. No. 63;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 :|||||  
 Db 611 KKLVPFA 617

RESULT 18  
 A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N;Alternate names: proteinase nexin II  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
 C;Accession: A27485; S19727; I49485  
 R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor  
 A;Reference number: A27485; MUID:88106489; PMID:3322280  
 A;Accession: A27485  
 A;Molecule type: mRNA  
 A;Residues: 1-695 <YAM>

A;Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN:  
A;Experimental source: brain  
R;de Strooper, B.; van Leuven, F.; van den Bergh, H.  
Biochim. Biophys. Acta 1129, 141-143, 1991  
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
A;Reference number: S19727; MUID:92096458; PMID:1756177  
A;Accession: S19727  
A;Molecule type: mRNA  
A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
A;Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379  
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, M.; Hattori, H.; Hattori, M.; Sakaki, Y.  
Gene 112, 189-195, 1992  
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
A;Reference number: 149485; MUID:92209998; PMID:1555768  
A;Accession: 149485  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-19 <RES>  
A;Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:  
C;Genetics:  
A;Map position: 16C3  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 88.2%; Score 30; DB 2; Length 695;  
Best Local Similarity 85.7%; Pred. No. 63;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 611 QKLVPFA 617

RESULT 19  
S00550  
Alzheimer's disease amyloid beta protein precursor - rat  
N;Alternate names: beta-A4 amyloid protein  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: S00550; A1245; A39820; S46251  
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
EMBO J. 7, 1365-1370, 1988  
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
A;Reference number: S00550; MUID:88313583; PMID:2900758  
A;Accession: S00550  
A;Molecule type: mRNA  
A;Residues: 1-695 <SH1>  
A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648; NID:g55616; PIDN:  
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.  
Science 241, 223-226, 1988  
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
A;Reference number: A41245; MUID:88264430; PMID:2968652  
A;Accession: A41245  
A;Molecule type: Protein  
A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
A;Cross-references: UNIPARC:UPI0000177FD  
A;Note: evidence for heparan sulfate attachment  
R;Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.  
PEBS Lett. 349, 109-116, 1994  
A;Title: The beta-A4 amyloid precursor protein binding to copper.  
A;Reference number: S46251; MUID:94320627; PMID:7913895  
A;Contents: annotation; copper binding sites  
A;Note: rat peptides were isolated but not sequenced  
R;Potempa, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
J. Biol. Chem. 266, 8464-8469, 1991  
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
A;Reference number: A39820; MUID:91217087; PMID:1673681  
A;Accession: A39820  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 18-32 <POT>  
A;Cross-references: UNIPARC:UPI0000177FE  
A;Experimental source: brain

C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is a  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
F;625-648/Domain: transmembrane #status predicted <TM>

Query Match 88.2%; Score 30; DB 2; Length 695;  
Best Local Similarity 85.7%; Pred. No. 63;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 611 QKLVPFA 617

RESULT 20  
JH0773  
Alzheimer's disease amyloid beta protein precursor - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
C;Accession: JH0773  
R;Okado, H.; Okamoto, H.  
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental  
A;Reference number: JH0773; MUID:93129227; PMID:1282805  
A;Accession: JH0773  
A;Molecule type: mRNA  
A;Residues: 1-747 <OKA>  
A;Cross-references: UNIPARC:UPI00000FC80; GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:  
A;Experimental source: larva  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C;Keywords: alternative splicing; amyloid  
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 88.2%; Score 30; DB 2; Length 747;  
Best Local Similarity 85.7%; Pred. No. 67;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 663 QKLVPFA 669

RESULT 21  
QRH04  
Alzheimer's disease amyloid beta protein precursor [validated] - human  
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi  
N;Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascula  
protein precursor splice form APP(770)  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
C;Accession: S02260; S05194; A32277; A32260; A35486; I39452; I39451; I39453; I59562; A4  
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S  
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Be  
Nucleic Acids Res. 17, 517-522, 1989  
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded  
A;Reference number: S02260; MUID:89128427; PMID:2783775  
A;Accession: S02260  
A;Molecule type: DNA  
A;Residues: 1-288, 'V', 365-770 <LEM1>  
A;Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466  
A;Note: alternative splice form APP(695)  
R;Lemaire, H.G.  
submitted to the EMBL Data Library, November 1988  
A;Reference number: S05194  
A;Accession: S05194  
A;Molecule type: DNA  
A;Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
A;Cross-references: UNIPARC:UPI000016A6FC; EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PJ:  
A;Note: alternative splice form APP(695)  
R;La Fauti, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prot  
A;Reference number: A32277; MUID:89165870; PMID:2538123



A;Accession: A32277  
 A;Molecule type: DNA  
 A;Residues: 1-75 <LAF>  
 A;Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:G341202; PIDN:AAAC13  
 R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, P.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity  
 A;Reference number: A33260; MUID:89392030; PMID:2675937  
 A;Accession: A33260  
 A;Molecule type: DNA  
 A;Residues: 656-737 <JOH>  
 A;Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:gl78863; PIDN:AAAS1768.1; PID:  
 R;Pirelli, F.; Levy, E.; van Duinen, S.G.; Bote, G.T.A.M.; Luyendijk, W.; Frangione, B.  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
 A;Reference number: A35486; MUID:90321244; PMID:2196878  
 A;Accession: A35486  
 A;Molecule type: DNA  
 A;Residues: 672-710 <PRE1>  
 A;Cross-references: UNIPARC:UPI000016A5176  
 A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 87, 257-263, 1990  
 A;Title: Genomic organization of the human amyloid beta-protein precursor gene.  
 A;Reference number: I39451; MUID:90236318; PMID:2110105  
 A;Accession: I39452  
 A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL  
 A;Molecule type: DNA  
 A;Residues: 1-770 <YOS1>  
 A;Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:gl78613; PIDN:AAB59502.1; PID:  
 A;Accession: I39451  
 A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL  
 A;Molecule type: DNA  
 A;Residues: 1-530, 'OWLMPVLPAPFAWEAKVGR' <YOS2>  
 A;Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:gl78608; PIDN:AAB59501.1; PID:  
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 102, 291-292, 1991  
 A;Reference number: A59020; MUID:91340168; PMID:1908403  
 A;Contents: annotation; erratum  
 A;Note: revised physical map for reference I39451  
 R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine  
 Science 248, 1124-1126, 1990  
 A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh  
 A;Reference number: I39453; MUID:90260663; PMID:2111584  
 A;Accession: I39453  
 A;Status: translated from GB/EMBL/DBBJ  
 A;Molecule type: DNA  
 A;Residues: 656-737 <LEV>  
 A;Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:gl78618; PIDN:AAAS1727.1; PID:  
 A;Note: a mutation with 693-Gln is presented  
 R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer  
 A;Reference number: I59562; MUID:92022553; PMID:1925564  
 A;Accession: I59562  
 A;Status: translated from GB/EMBL/DBBJ  
 A;Molecule type: DNA  
 A;Residues: 689-716, 'F', 718-737 <MUR>  
 A;Cross-references: UNIPARC:UPI000011F7EA; GB:S57665; NID:G236720; PIDN:AAB19991.1; PID:  
 R;Kamino, K.; Orr, H.T.; Payami, H.; Wijesman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,  
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,  
 Am. J. Hum. Genet. 51, 998-1014, 1992  
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the  
 A;Reference number: A44017; MUID:93035397; PMID:1415269  
 A;Accession: A44017  
 A;Molecule type: DNA  
 A;Residues: 687-692, 'G', 694-718 <KAM1>  
 A;Cross-references: UNIPARC:UPI000011F7EB; GB:S45135; NID:G257377; PIDN:AAB23645.1; PID:  
 A;Experimental source: familial Alzheimer disease family SB  
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)  
 A;Accession: B44017  
 A;Molecule type: DNA  
 A;Residues: 687-718 <KAM2>

A;Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:G257379; PIDN:AAB23646.1; PID:  
 A;Experimental source: familial Alzheimer disease family LIT  
 A;Note: this sequence has a silent mutation  
 R;Kang, J.; Lenaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
 Nature 325, 733-736, 1987  
 A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
 A;Reference number: A03134; MUID:87144572; PMID:2881207  
 A;Accession: A03134  
 A;Molecule type: mRNA  
 A;Residues: 1-288, 'V', 365-770 <KAN>  
 A;Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:  
 A;Note: alternative splice form APP(695)  
 R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular  
 A;Reference number: A29030; MUID:87231371; PMID:3035574  
 A;Accession: A29030  
 A;Molecule type: mRNA  
 A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A;Cross-references: UNIPARC:UPI000016A545; GB:M15765; NID:gl78539; PIDN:AAAS1722.1; PID:  
 A;Note: the authors translated the codon GAG for residue 647 as Asp  
 R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
 Science 235, 877-880, 1987  
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
 A;Reference number: A47584; MUID:87120328; PMID:3810169  
 A;Accession: A47584  
 A;Molecule type: mRNA  
 A;Residues: 674-756, 'S', 758-770 <GOL>  
 A;Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:gl78706; PIDN:AAA35540.1; PID:  
 A;Experimental source: brain  
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
 Science 235, 880-884, 1987  
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
 A;Reference number: A47585; MUID:87120329; PMID:2949367  
 A;Accession: A47585  
 A;Molecule type: mRNA  
 A;Residues: 674-703 <TAN1>  
 A;Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:gl77957; PIDN:AAAS1564.1; PID:  
 R;Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
 EMBO J. 7, 949-957, 1988  
 A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
 A;Reference number: S02638; MUID:88296437; PMID:2900137  
 A;Accession: S02638  
 A;Molecule type: mRNA  
 A;Residues: 672-678 <DVR>  
 A;Cross-references: UNIPARC:UPI0000035AB0  
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
 Nature 331, 528-530, 1988  
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
 A;Reference number: S00707; MUID:88122640; PMID:2893290  
 A;Accession: S00707  
 A;Molecule type: mRNA  
 A;Residues: 286-344, 'I', 365-366 <TAN2>  
 A;Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PFI  
 A;Experimental source: promyelocytic leukemia cell line HL60  
 A;Note: alternative splice form APP(751)  
 R;Ponté, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; D-  
 Nature 331, 525-527, 1988  
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi  
 A;Reference number: S00925; MUID:88122639; PMID:2893289  
 A;Accession: S00925  
 A;Molecule type: mRNA  
 A;Residues: 1-344, 'I', 365-770 <PO2>  
 A;Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CAA3  
 A;Note: alternative splice form APP(751)  
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor  
 A;Reference number: A38949; MUID:88122641; PMID:2893291  
 A;Accession: A38949  
 A;Molecule type: mRNA  
 A;Residues: 287-367 <KIT>

A;Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:9  
 A;Experimental source: Glioblastoma cell line  
 A;Note: alternative splice form APP(770)  
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtori  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p  
 A;Reference number: A30320  
 A;Accession: A30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 284-288, 'V', 365-770 <VIT1>  
 A;Cross-references: UNIPARC:UPI0000174094  
 A;Accession: B30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 122-288, 'V', 365-770 <VIT2>  
 A;Cross-references: UNIPARC:UPI0000174094  
 A;Accession: C30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 606-770 <VIT3>  
 A;Cross-references: UNIPARC:UPI0000174094  
 R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br  
 A;Reference number: A31087; MUID:88124954; PMID:2893379  
 A;Accession: A31087  
 A;Molecule type: mRNA

Query Match 88.2%; Score 30; DB 1; Length 770;  
 Best Local Similarity 85.7%; Pred. No. 69;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFFA 7  
 :|||||  
 Db 686 QKLVEFFA 692

RESULT 22  
 A05035  
 translation initiation factor IP-1 homolog - common tobacco chloroplast (fragment)  
 N;Alternate names: hypothetical protein 96  
 C;Species: chloroplast Nicotiana tabacum (common tobacco)  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
 C;Accession: A05035  
 R;Sugiura, M.  
 submitted to the EMBL Data Library, August 1986  
 A;Reference number: A00149  
 A;Accession: A05035  
 A;Molecule type: DNA  
 A;Residues: 1-96 <SUG>  
 A;Cross-references: UNIPROT:P12136; UNIPARC:UPI000012D24A; EMBL:Z00044; NID:g11807; PID:  
 A;Experimental source: cv. Bright Yellow 4  
 R;Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Matsubayashi, T.; Za  
 Deno, H.; Kamogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Tohdoh, N.; Sh  
 EMBO J. 5, 2043-2049, 1986  
 A;Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene or  
 A;Reference number: A38013  
 A;Contents: annotation; gene organization, sites, features  
 C;Genetics:  
 A;Genome: chloroplast  
 C;Superfamily: translation initiation factor IF-1  
 C;Keywords: chloroplast; protein biosynthesis

Query Match 85.3%; Score 29; DB 2; Length 96;  
 Best Local Similarity 83.3%; Pred. No. 18;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFF 6  
 :|||||  
 Db 83 KKLVEFF 88

RESULT 23  
 B72213  
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)  
 C;Species: Thermotoga maritima  
 C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C;Accession: B72213  
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke  
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
 C.M.  
 Nature 399, 323-329, 1999  
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se  
 A;Reference number: A72200; MUID:99287316; PMID:10360571  
 A;Accession: B72213  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-109 <ARN>  
 A;Cross-references: UNIPROT:Q9X292; UNIPARC:UPI000000C120B; GB:AE001815; GB:AE000512; NI  
 A;Experimental source: strain MSB8  
 C;Genetics:  
 A;Gene: TM1771  
 C;Superfamily: Bacillus subtilis conserved hypothetical protein yghY

Query Match 85.3%; Score 29; DB 2; Length 109;  
 Best Local Similarity 71.4%; Pred. No. 20;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFFA 7  
 :|||||  
 Db 18 KKLVEFFA 24

RESULT 24  
 T06645  
 hypothetical protein T20K18.220 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C;Accession: T06645  
 R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Me  
 submitted to the Protein Sequence Database, April 1999  
 A;Reference number: Z15790  
 A;Accession: T06645  
 A;Molecule type: DNA  
 A;Residues: 1-152 <BEV>  
 A;Cross-references: UNIPROT:Q9ST29; UNIPARC:UPI000000A0722; EMBL:AL049640; GSPDB:GN00062  
 A;Experimental source: cultivar Columbia; BAC clone T20K18  
 C;Genetics:  
 A;Gene: ATSP:T20K18.220  
 A;Map position: 4  
 A;Introns: 87/3; 109/3  
 C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 85.3%; Score 29; DB 2; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKLVEFFA 7  
 :|||||  
 Db 9 KKLVEFFA 14

RESULT 25  
 I64161  
 cytochrome c biogenesis protein CycX homolog H10935 [similarity] - Haemophilus influenza  
 C;Species: Haemophilus influenzae  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: I64161  
 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,  
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,  
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
 Science 269, 496-512, 1995  
 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
 A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A;Reference number: A64000; MUID:95350630; PMID:7542800



```

A;Accession: I64161
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-176 <TIGR>
A;Cross-references: UNIPROT:P44943; UNIPARC:UPI0000130501; GB:U32775; GB:L42023; NID:g15
A;Note: best homolog was a hypothetical protein from Escherichia coli
C;Superfamily: cytochrome c biogenesis protein Cyck
C;Keywords: redox-active disulfide
F;75-78/Disulfide bonds: redox-active #status predicted

Query Match      85.3%; Score 29; DB 1; Length 176;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFF 6
   |||||
Db 3 KKLIF 8

RESULT 26
H85138
hypothetical protein AT4g12900 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85138
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-231 <STO>
A;Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI00000A7E0E; GB:NC_001268; NID:g7267992; E
C;Genetics:
A;Gene: AT4g12900
A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match      85.3%; Score 29; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFFA 7
   |||||
Db 12 KLVFFA 17

RESULT 27
AH1155
membrane proteins homolog lmo0648 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C;Accession: AH1155
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1155
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <GLA>
A;Cross-references: UNIPROT:Q9Y985; UNIPARC:UPI0000055175; GB:NC_003210; PIDN:CAC98726.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0648
C;Superfamily: divalent cation transporter, CorA type

Query Match      85.3%; Score 29; DB 2; Length 316;

```

```

Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
   |||||
Db 182 KSLVFFA 188

RESULT 28
AC1514
membrane protein homolog lin0651 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C;Accession: AC1514
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1514
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <GLA>
A;Cross-references: UNIPROT:Q92E10; UNIPARC:UPI00000CC2E0; GB:ALS92022; PIDN:CAC95883.1.
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0651
C;Superfamily: divalent cation transporter, CorA type

Query Match      85.3%; Score 29; DB 2; Length 316;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
   |||||
Db 182 KSLVFFA 188

RESULT 29
T48903
wax synthase [imported] - Simmondsia chinensis
C;Species: Simmondsia chinensis
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T48903
R;Iardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W
Plant Physiol. 122, 645-655, 2000
A;Title: Purification of a jojoba embryo wax synthase, cloning of its cDNA and production
A;Reference number: Z25002
A;Accession: T48903
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <LAR>
A;Cross-references: UNIPROT:Q9XGY6; UNIPARC:UPI00000A1C81; EMBL:AF149919; PIDN:AAD38041

Query Match      85.3%; Score 29; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFFA 7
   |||||
Db 135 KLVFFA 140

RESULT 30
DB1374
probable oxidoreductase ferredoxin-type electron transport protein Cj0991c [imported] -
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: DB1374
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Baaham, D.; Chillin

```

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
 Nature 403, 665-668, 2000  
 A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp  
 A;Reference number: A81250; MUID:20150912; PMID:10688204  
 A;Accession: D81374  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: UNIPROT:Q9PNU9; UNIPARC:UPI00000C1DC0; GB:AL111168; NID  
 A;Experimental source: serotype O2, strain NCTC 11168  
 C;Genetics:  
 A;Gene: Cj0991c  
 C;Superfamily: glycolate oxidase, iron-sulfur subunit

Query Match 85.3%; Score 29; DB 2; Length 421;  
 Best Local Similarity 83.3%; Pred. No. 68;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6  
 |||:|  
 Db 98 KKLIFP 103

RESULT 31  
 T48008  
 hypothetical protein T17J13.120 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 31-Dec-2004  
 A;Accession: T48008  
 R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,  
 submitted to the Protein Sequence Database, February 2000  
 A;Reference number: Z24482  
 A;Accession: T48008  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-428 <RIB>  
 A;Cross-references: UNIPROT:Q9MIQ8; UNIPARC:UPI00000489B7; EMBL:AL138651  
 A;Experimental source: cultivar Columbia; BAC clone T17J13  
 C;Genetics:  
 A;Map position: 3  
 A;Introns: 137/3  
 A;Note: T17J13.120  
 C;Superfamily: N-hydroxycinnamoyl/benzoyl transferase

Query Match 85.3%; Score 29; DB 2; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KLVPPA 7  
 |||:|  
 Db 271 KLVPPA 276

RESULT 32  
 E6432  
 spore coat polysaccharide biosynthesis protein G homolog - *Methanococcus jannaschii*  
 C;Species: *Methanococcus jannaschii*  
 C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 A;Accession: E6432  
 R;Buit, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
 Reisch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
 Science 273, 1058-1073, 1996  
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C  
 A;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*  
 A;Reference number: A64300; MUID:96337999; PMID:8688087  
 A;Accession: E6432  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-484 <BUL>  
 A;Cross-references: UNIPROT:Q58462; UNIPARC:UPI0000139F8D; GB:U67549; GB:L77117; NID:928  
 C;Genetics:  
 A;Map position: REV1004535-1003081

Query Match 85.3%; Score 29; DB 2; Length 484;  
 Best Local Similarity 83.3%; Pred. No. 77;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6  
 |||:|  
 Db 98 KKLIFP 103

## RESULT 33

T21510

hypothetical protein F28F8.4 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

A;Accession: T21510

R;McMurray, A.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19432

A;Accession: T21510

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-593 &lt;WIL&gt;

A;Cross-references: UNIPROT:O17849; UNIPARC:UPI0000080E55; EMBL:Z81071; PIDN:CAB03015.1

A;Experimental source: clone F28F8

C;Genetics:

A;Gene: CESP:F28F8.4

A;Map position: 5

A;Introns: 33/2; 61/2; 202/3; 265/3; 294/2

## Query Match

85.3%; Score 29; DB 2; Length 593;

Best Local Similarity 83.3%; Pred. No. 93;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6

|||:|

Db 264 KKLIFP 269

## RESULT 34

T23836

hypothetical protein M88.6a - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

A;Accession: T23836

R;Sulston, J.

submitted to the EMBL Data Library, June 1994

A;Reference number: Z19806

A;Accession: T23836

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-610 &lt;WIL&gt;

A;Cross-references: UNIPROT:Q21604; UNIPARC:UPI000007610B; EMBL:Z34802; PIDN:CAA84337.1

A;Experimental source: clone M88

C;Genetics:

A;Gene: CESP:M88.6a

A;Map position: 3

A;Introns: 40/3; 60/2; 101/3; 216/2; 290/1; 427/3; 471/1; 560/3

## Query Match

85.3%; Score 29; DB 2; Length 610;

Best Local Similarity 83.3%; Pred. No. 95;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6

|||:|

Db 370 KKLIFP 375

## RESULT 35

C86733

penicillin-binding protein [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL140;C;Species: *Lactococcus lactis* subsp. *lactis*

C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004

C;Accession: C86733  
R;Solotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarma, K.; Weissbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: C86733  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-763 <STO>  
A;Cross-references: UNIPROT:Q9CH71; UNIPARC:UPI00000C6923; GB:AE005176; PID:g12723796; F  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: pbpX

Query Match 85.3%; Score 29; DB 2; Length 763;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6  
|||:|  
DB 6 KKLIFP 11

RESULT 36  
F96639  
protein TIF9.8 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
C;Accession: F96639  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: F96639  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-774 <STO>  
A;Cross-references: UNIPROT:O64777; UNIPARC:UPI00000A26B1; GB:AE005173; NID:g3056587; PI  
C;Genetics:  
A;Gene: TIF9.8  
A;Map position: 1  
C;Superfamily: S-locus receptor-like kinase SRK; protein kinase homology; S-locus-specif

Query Match 85.3%; Score 29; DB 2; Length 774;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 7  
|||:|  
DB 4 KRIVPFA 10

RESULT 37  
S30236  
genome polyprotein - zucchini yellow mosaic virus (strain Singapore) (fragment)  
N;Contains: coat protein; nuclear inclusion protein a; RNA-directed RNA polymerase (EC 2  
C;Species: zucchini yellow mosaic virus, ZYMV  
A;Variety: strain Singapore  
C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: S30236  
R;Wu, M.; Yeong, C.Y.; Lee, S.C.; Wong, S.M.  
Nucleic Acids Res. 21, 1317, 1993  
A;Title: Nucleotide sequence of the 3' half of zucchini yellow mosaic virus (Singapore i  
A;Reference number: S30236; MUID:93219099; PMID:8464715  
A;Accession: S30236  
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA  
A;Residues: 1-1016 <WUM>  
A;Cross-references: UNIPROT:Q05912; UNIPARC:UPI00000ECC69; EMBL:X68509; NID:g288233; PI  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992  
C;Superfamily: tobacco etch virus genome polyprotein  
C;Keywords: coat protein; genome-linked protein; nucleotidyltransferase; phosphoprotein,  
F;9-61/Product: VPg protein #status predicted <VPG>  
F;62-494/Product: nuclear inclusion protein a #status predicted <NIA>  
F;495-1010/Product: RNA-directed RNA polymerase #status predicted <POL>  
F;1011-1016/Product: coat protein (fragment) #status predicted <COP>  
F;125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 85.3%; Score 29; DB 2; Length 1016;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVVFA 7  
|||:|  
DB 837 KLVVFA 842

RESULT 38  
H90367  
hypothetical protein SSO2013 [imported] - *Sulfolobus solfataricus*  
C;Species: *Sulfolobus solfataricus*  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: H90367  
R;She, Q.; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: *Sulfolobus solfataricus* complete genome.  
A;Reference number: A99139  
A;Accession: H90367  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-123 <KUR>  
A;Cross-references: UNIPROT:Q97WV1; UNIPARC:UPI0000064642; GB:AE006641; NID:gl3815291; F  
C;Genetics:  
A;Gene: SSO2013

Query Match 82.4%; Score 28; DB 2; Length 123;  
Best Local Similarity 85.7%; Pred. No. 38;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
|||:|  
DB 114 KKLVIFA 120

RESULT 39  
T47892  
hypothetical protein T4C21.220 - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T47892  
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa  
W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24479  
A;Accession: T47892  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-214 <CHO>  
A;Cross-references: UNIPROT:Q9LYZ2; UNIPARC:UPI000009DAB0; EMBL:AL162295  
A;Experimental source: cultivar Columbia; BAC clone T4C21  
C;Genetics:  
A;Map position: 3  
A;Introns: 46/2; 65/2; 106/2; 128/3; 159/3; 197/3  
A;Note: T4C21.220

Query Match 82.4%; Score 28; DB 2; Length 214;  
Best Local Similarity 71.4%; Pred. No. 63;

```

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLVPFA 7
    :|||:|
Db 18 KKLVPFA 24

RESULT 40
H72361
C:Species: Thermotoga maritima (strain MSB8)
C:Spec: conserved hypothetical protein - Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: H72361
R;Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: H72361
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <ARN>
A;Cross-references: UNIPROT:Q9WZ39; UNIPARC:UPI00000C13EB; GB:AE001731; GB:AE000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0569

Query Match 82.4%; Score 28; DB 2; Length 218;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLVPFF 6
    :|||:|
Db 20 KKLVPFF 25

RESULT 41
S18783
A;Title: exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isol
N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes phage
A;Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MG
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S18783; S18793; S18794; S18801; S18798
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18783
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEA>
A;Cross-references: UNIPARC:UPI00000BOA72; EMBL:X61568; NID:947289; PIDN:CAA43766.1; PID
A;Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18793
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEA>
A;Cross-references: UNIPARC:UPI00000BOA72; EMBL:X61569; NID:947313; PIDN:CAA43767.1; PID
A;Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18794
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEZ>
A;Cross-references: UNIPARC:UPI00000BOA72; EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID
A;Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18801
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

```

```

A;Residues: 1-236 <NEY>
A;Cross-references: UNIPARC:UPI00000BOA72; EMBL:X61572; NID:947333; PIDN:CAA43770.1; PI
A;Experimental source: strain MGAS624 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18798
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEO>
A;Cross-references: UNIPARC:UPI00000BOA72; EMBL:X61571; NID:947323; PIDN:CAA43769.1; PI
A;Experimental source: strain MGAS495 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 82.4%; Score 28; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLVPFF 6
    :|||:|
Db 1 KKLVPFF 6

RESULT 42
S18786
A;Title: exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 iso
N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes phage
A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain
isolate United Kingdom; strain MGAS496 isolate Germany
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18786
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEA>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61562; NID:947299; PIDN:CAA43760.1; PI
A;Experimental source: strain MGAS251 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18788
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEZ>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61563; NID:947301; PIDN:CAA43761.1; PI
A;Experimental source: strain MGAS256 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18790
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEV>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61564; NID:947305; PIDN:CAA43762.1; PI
A;Experimental source: strain MGAS285 isolate Colorado unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18792
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEO>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61565; NID:947311; PIDN:CAA43763.1; PI
A;Experimental source: strain MGAS250 isolate California unassigned phage

```

A;Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage  
A;Accession: S18795  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-236 <NEH>  
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61566; NID:G47317; PIDN:CAA43764.1; PID  
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phage  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18799  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-236 <NES>  
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61567; NID:G47325; PIDN:CAA43765.1; PID  
A;Experimental source: strain MGAS496 isolate Germany unassigned phage  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
C;Genetics:  
A;Gene: speA2  
C;Superfamily: enterotoxin B  
C;Keywords: exotoxin  
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>  
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>  
  
Query Match 82.4%; Score 28; DB 2; Length 236;  
Best Local Similarity 83.3%; Pred. No. 69;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KKLVPF 6  
||:||||  
Db 1 KKMVFF 6  
  
RESULT 43  
B69841  
Hypothetical protein yitQ - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: B69841  
R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bexter  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galled  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mauda, S.; Maueel  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:198044033; PMID:9384377  
A;Accession: B69841  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-245 <KUN>  
A;Cross-references: UNIPROT:O06752; UNIPARC:UPI0000060186; GB:Z99109; GB:AL009126; NID:G  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: yitQ  
C;Superfamily: Bacillus subtilis hypothetical protein yitQ  
  
Query Match 82.4%; Score 28; DB 2; Length 245;  
Best Local Similarity 85.7%; Pred. No. 71;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 KKLVPFA 7  
|||||  
Db 179 KKLVPFA 185

## RESULT 44

A26152  
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.  
N;Alternate names: scarlet fever toxin; scarlet fever toxin  
C;Species: Streptococcus sp.  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A26152  
R;Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.  
Mol. Gen. Genet. 203, 354-356, 1986  
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta  
A;Reference number: A26152; MUID:86284313; PMID:3526093  
A;Accession: A26152  
A;Molecule type: DNA  
A;Residues: 1-250 <JOH>  
A;Cross-references: UNIPROT:P08095; UNIPARC:UPI000017021E  
C;Superfamily: enterotoxin B  
C;Keywords: exotoxin

Query Match 82.4%; Score 28; DB 1; Length 250;  
Best Local Similarity 83.3%; Pred. No. 73;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6

||:||||

Db 9 KKMVFF 14

## RESULT 45

S29659  
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12  
N;Alternate names: erythrogenic toxin; scarlet fever toxin  
C;Species: Streptococcus pyogenes phage T12  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800  
R;Weeks, C.R.; Ferretti, J.J.  
Infect. Immun. 52, 144-150, 1986  
A;Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g  
A;Reference number: S29659; MUID:86166804; PMID:3514452  
A;Accession: S29659  
A;Molecule type: DNA  
A;Residues: 1-251 <WES>  
A;Cross-references: UNIPARC:UPI0000135DD7; GB:U04053; EMBL:M19350; NID:gl877426; PIDN:AA  
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.  
J. Exp. Med. 174, 1271-1274, 1991  
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod  
A;Reference number: S18782; MUID:92044323; PMID:1940804  
A;Accession: S18782  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 9-244 <NEL>  
A;Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61560; NID:G47287; PIDN:CAA43758.1; PID  
A;Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18784  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 9-244 <NEA>  
A;Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61556; NID:G47291; PIDN:CAA43754.1; PID  
A;Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18785  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 9-244 <NEZ>  
A;Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61559; NID:G47293; PIDN:CAA43757.1; PID  
A;Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18791  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 9-244 <NEY>  
A;Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61555; NID:G47309; PIDN:CAA43753.1; PID  
A;Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18796  
A;Status: Nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 9-244 <NEO>  
A;Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61557; NID:G47319; PIDN:CAA43755.1; PIDN:CAA43755.2  
A;Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18797  
A;Status: Nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 9-244 <NEH>  
A;Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61558; NID:G47321; PIDN:CAA43756.1; PIDN:CAA43756.2  
A;Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18800  
A;Status: Nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 9-228 <NES>  
A;Cross-references: UNIPARC:UPI00001701AF; EMBL:X61554; NID:G47327; PIDN:CAA43752.1; PIDN:CAA43752.2  
A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
C;Genetics:  
A;Gene: speA; speB  
C;Superfamily: enterotoxin B  
C;Keywords: exotoxin  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-251/Product: exotoxin type A #status predicted <MAT>  
Query Match 82.4%; Score 28; DB 1; Length 251;  
Best Local Similarity 83.3%; Pred. No. 73;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPFF 6  
||:||||  
DB 9 KKLVPFF 14  
||:||||  
RESULT 46  
T28170  
hypothetical protein ORF9 - Melanoplus sanguinipes entomopoxvirus (strain Tuscon)  
C;Species: Melanoplus sanguinipes entomopoxvirus  
A;Variety: strain Tuscon  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T28170  
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.  
J. Virol. 73, 533-552, 1999  
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.  
A;Reference number: 220484; MUID:99102612; PMID:9847359  
A;Accession: T28170  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-254 <AFO>  
A;Cross-references: UNIPROT:Q9YW83; UNIPARC:UPI00000F390B; EMBL:AF063866; NID:G4049647;  
A;Experimental source: strain tuscon  
C;Genetics:  
A;Note: MSV009  
Query Match 82.4%; Score 28; DB 2; Length 254;  
Best Local Similarity 83.3%; Pred. No. 74;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPFF 6  
||:||||  
DB 94 KKLVPFF 99  
||:||||  
RESULT 47  
B82243  
hypothetical protein VC1074 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: B82243

R;Heidelberg, J.P.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardonson, D.; Esmolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: B82243  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-276 <HEI>  
A;Cross-references: UNIPROT:Q9KT31; UNIPARC:UPI00000C2E83; GB:AE004189; GB:AE003852; N1  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC1074  
A;Map position: 1  
Query Match 82.4%; Score 28; DB 2; Length 276;  
Best Local Similarity 85.7%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KKLVPFF 7  
||:||||  
DB 119 KKLVPFF 125  
||:||||  
RESULT 48  
D69355  
hypothetical protein AF0844 - *Archaeoglobus fulgidus*  
C;Species: *Archaeoglobus fulgidus*  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: D69355  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: D69355  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-293 <KLE>  
A;Cross-references: UNIPROT:Q29414; UNIPARC:UPI0000056F64; GB:AE001046; GB:AE000782; N1  
Query Match 82.4%; Score 28; DB 2; Length 293;  
Best Local Similarity 71.4%; Pred. No. 84;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPFF 7  
||:||||  
DB 139 KKLVPFF 145  
||:||||  
RESULT 49  
H90318  
glycerol kinase (glpK-1) [imported] - *Sulfolobus solfataricus*  
C;Species: *Sulfolobus solfataricus*  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: H90318  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan, J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: *Sulfolobus solfataricus* complete genome.  
A;Reference number: A99139  
A;Accession: H90318  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-294 <KUR>  
A;Cross-references: UNIPROT:Q97XW2; UNIPARC:UPI00000644E6; GB:AE006641; NID:G13814829;  
C;Genetics:  
A;Gene: glpK-1

```
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: A95039
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: A95039
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <KUR>
A:Cross-references: UNIPROT:Q97SK3; UNIPARC:UPI00000C9C8D; GB:AE005672; PIDN:AAK74506.1,
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0330

Query Match      82.4%; Score 28; DB 2; Length 333;
Best Local Similarity 83.3%; Pred. NO. 94;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFF 6
      ||:|||
DB      143 KKMVFF 148

RESULT 53
B97909
transcription regulator, member of GalR family regR [imported] - Streptococcus pneumoniae
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B97909
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blazczak, L.; Burgett, S.; Dehoff, B.S.; El
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; E
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B97909
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <KUR>
A:Cross-references: UNIPROT:Q8DR72; UNIPARC:UPI00000E3406; GB:AE007317; PIDN:AAK99102.1,
C:Genetics:
A:Gene: regR

Query Match      82.4%; Score 28; DB 2; Length 355;
Best Local Similarity 83.3%; Pred. NO. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFF 6
      ||:|||
DB      165 KKMVFF 170

RESULT 54
AF1893
hydrogenase expression/formation protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF1893
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF1893
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <KUR>
```

---

```
Query Match      82.4%; Score 28; DB 2; Length 294;
Best Local Similarity 71.4%; Pred. NO. 84;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFF 7
      ||:|||
DB      183 KKMVFFA 189

RESULT 50
A70313
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuoM - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: A70313
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: A70313
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-315 <AQF>
A:Cross-references: UNIPROT:O66532; UNIPARC:UPI000005628F; GB:AE000675; NID:g2982863; PI
A:Experimental source: strain VF5
C:Genetics:
A:Gene: nuoM
C:Keywords: NAD; oxidoreductase

Query Match      82.4%; Score 28; DB 2; Length 315;
Best Local Similarity 71.4%; Pred. NO. 89;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFF 7
      ||:|||
DB      241 KKLVEFFA 247

RESULT 51
H71729
hypothetical protein RP189 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: H71729
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: H71729
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-321 <AND>
A:Cross-references: UNIPROT:Q9ZDK5; UNIPARC:UPI0000139421; GB:AJ235270; GB:AJ235269; NID
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: RP189
C:Superfamily: Rickettsia prowazekii hypothetical protein RP189

Query Match      82.4%; Score 28; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. NO. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 KKLVEFF 7
      ||:|||
DB      178 KLIFFA 183

RESULT 52
A95039
sugar binding transcription regulator RegR [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
```



A;Cross-references: UNIPROT:Q8YYZ5; UNIPARC:UPI00000CDE2C; GB:BA000019; PIDN:BA072653.1;  
A;Experimental source: strain FCC 7120  
C;Genetics:  
A;Gene: hupD  
C;Superfamily: [NiFe]-hydrogenase maturation factor, HypD type

Query Match 82.4%; Score 28; DB 2; Length 383;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7  
|:|||||  
Db 134 KKLVFFA 140

## RESULT 55

T50330  
hypothetical protein SPBC1718.02 [imported] - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe  
C;Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
C;Accession: T50330

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.  
submitted to the EMBL Data Library, February 2000

A;Reference number: 225062

A;Accession: T50330

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-528 <LYN>

A;Cross-references: UNIPROT:Q9PTP2; UNIPARC:UPI000006C7BE; EMBL:AL157874; PIDN:CAB75992.  
A;Experimental source: strain 972h(-); cosmid c1718

C;Genetics:

A;Gene: SPDB:SPBC1718.02

A;Map position: 2

A;Introns: 32/2; 81/3; 138/1; 218/2; 348/3; 424/1

Query Match 82.4%; Score 28; DB 2; Length 528;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7  
|:|||||  
Db 18 KKLVFFA 24

## RESULT 56

T33750  
hypothetical protein R11E3.7 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T33750

R;Langston, Z.; Wohldmann, P.

submitted to the EMBL Data Library, October 1998

A;Description: The sequence of C. elegans cosmid R11E3.

A;Reference number: 221397

A;Accession: T33750

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-605 <LAN>

A;Cross-references: UNIPROT:Q9TYX2; UNIPARC:UPI00000782CB; EMBL:AF100669; PIDN:AAC68992.  
A;Experimental source: strain Bristol N2; clone R11E3

C;Genetics:

A;Gene: CBSP:R11E3.7

A;Map position: 4

A;Introns: 272/3; 283/3; 404/2; 450/3; 489/3

Query Match 82.4%; Score 28; DB 2; Length 605;  
Best Local Similarity 71.4%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7  
|:|||||  
Db 156 KKLVFFA 162

## RESULT 57

JQ0498

genome polyprotein - watermelon mosaic virus 2 (fragment)

N;Contains: 49K protease; coat protein; nuclear inclusion protein NIB

C;Species: watermelon mosaic virus 2, WMV2

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C;Accession: JQ0498

R;Slightom, J.L.

submitted to JIPID, April 1990

A;Description: Watermelon mosaic virus II and zucchini yellow mosaic virus: cloning of

A;Reference number: JQ0498

A;Accession: JQ0498

A;Molecule type: Genomic RNA

A;Residues: 1-1016 <QUE>

A;Cross-references: UNIPROT:P18478; UNIPARC:UPI0000131E80

A;Note: readthrough of the terminator codon TGA occurs between residues 267-Ala and 268

C;Superfamily: tobacco etch virus genome polyprotein

C;Keywords: polyprotein

F;1-219/Product: 49K proteinase (fragment) #status predicted <PRT>

F;220-736/Product: nuclear inclusion protein Nib #status predicted <NIB>

F;737-1016/Product: coat protein #status predicted <COP>

Query Match 82.4%; Score 28; DB 2; Length 1016;

Best Local Similarity 71.4%; Pred. No. 2.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7  
|:|||||  
Db 561 RRLVFFA 567

## RESULT 58

T30302

P-type ATPase - Tetrahymena thermophila

C;Species: Tetrahymena thermophila

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T30302

R;Wang, S.; Takeyasu, K.

submitted to the EMBL Data Library, November 1995

A;Description: The starvation-induced P-type ATPase in Tetrahymena thermophila.

A;Reference number: Z20815

A;Accession: T30302

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1133 <WAN>

A;Cross-references: UNIPROT:Q95050; UNIPARC:UPI0000126641; EMBL:U41063; NID:GI545827;

C;Genetics:

A;Genetic code: SGC5

A;Note: TPA9

Query Match 82.4%; Score 28; DB 2; Length 1133;

Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFF 6  
|:|||||  
Db 39 KKLVFF 44

## RESULT 59

T07329

hypothetical protein 41e - Chlorella vulgaris chloroplast

C;Species: chloroplast Chlorella vulgaris

C;Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 21-Jul-2000

C;Accession: T07329

R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; S.; Taudruki, J.; Naka

Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997

A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chl

A;Reference number: Z15985; MUID:97303241; PMID:9159184

A;Accession: T07329

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA



```
A;Residues: 1-41 <WAK>
A;Cross-references: UNIPARC:UPI000011E487; EMBL:AB0011E487; NID:g2224352; PIDN:BAA57977.1;
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match          79.4%; Score 27; DB 2; Length 41;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 6
        ||::||
Db       17 KKMIFV 22

RESULT 60
H97796
RP534 protein homolog RC0776 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97796
R;Gata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:2142074; PMID:11557893
A;Accession: H97796
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <KUR>
A;Cross-references: UNIPROT:Q92HJ5; UNIPARC:UPI00000CBCEB; GB:AE006914; PIDN:AAL03314.1;
C;Genetics:
A;Gene: RC0776

Query Match          79.4%; Score 27; DB 2; Length 91;
Best Local Similarity 83.3%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 6
        ||::||
Db       18 KKLVFY 23

RESULT 61
AI0493
probable membrane protein YPO4063 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AI0493
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AI0493
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <KUR>
A;Cross-references: UNIPROT:Q8Z9X4; UNIPARC:UPI00000DC790; GB:AL590842; PIDN:CAC93517.1;
C;Genetics:
A;Gene: YPO4063

Query Match          79.4%; Score 27; DB 2; Length 110;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 6
        ||::||
Db       18 KKIIFV 23

RESULT 62
T24057
```

```
hypothetical protein R08H2.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24057
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19835
A;Accession: T24057
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-147 <WIL>
A;Cross-references: UNIPARC:UPI000007A733; EMBL:Z81575; PIDN:CAB04637.1; GSPDB:GN000023;
A;Experimental source: clone R08H2
C;Genetics:
A;Gene: CESP:R08H2.12
A;Map position: 5
A;Introns: 31/2; 130/1

Query Match          79.4%; Score 27; DB 2; Length 147;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 6
        ||::||
Db       127 KRLVPFF 132

RESULT 63
D70134
flagellar biosynthesis protein (fliz) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: D70134
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: D70134
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-208 <KLE>
A;Cross-references: UNIPROT:Q44904; UNIPARC:UPI00000573FD; GB:AE001137; GB:AE000783; NID
A;Experimental source: strain B31

Query Match          79.4%; Score 27; DB 2; Length 208;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
        ||::||
Db       84 KKLAFYS 90

RESULT 64
JC4540
transcription initiation factor IID p30 beta chain - human
N;Alternate names: transcription factor TFIID chain TAFII28
C;Species: Homo sapiens (man)
C;Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: JC4540; PC4125; S54780
R;Kuzuhara, T.; Horikoshi, M.
Biol. Pharm. Bull. 19, 122-126, 1996
A;Title: Isolation and characterization of a cDNA encoding a human TFIID subunit contain
A;Reference number: JC4540; MUID:96418138; PMID:8820923
A;Accession: JC4540
A;Molecule type: mRNA
A;Residues: 1-211 <KUZ>
A;Cross-references: UNIPROT:Q15544; UNIPARC:UPI000000106D; DBJ:D63705; NID:g2645174; PI
A;Accession: PC4125
A;Molecule type: protein
```

A;Residues: 145-211 <KUR>  
A;Cross-references: UNIPARC:UPI0000178C8D  
A;Experimental source: brain  
R;Mungus, G.; May, M.; Jacq, X.; Staub, A.; Tora, L.; Chambon, P.; Davidson, I.  
EMBO J. 14, 1520-1531, 1995  
A;Title: Cloning and characterization of hTAF(II)20 and hTAF(II)28: three su  
A;Reference number: S54780; MUID:95246745; PMID:7729427  
A;Accession: S54780  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-211 <MEN>  
A;Cross-references: UNIPARC:UPI00000106D; EMBL:X83928; NID:g791056; PIDN:CRA58780.1; PI  
C;Superfamily: transcription initiation factor IID beta chain  
C;Keywords: brain; phosphoprotein; transcription initiation  
F;82-85/Region: nuclear location signal  
F;108-137,160-194/Region: repeats  
F;121-180/Region: histone H4 similarity  
F;9,112,114/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status  
F;31,33,40,67,68/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status  
Query Match 79.4%; Score 27; DB 2; Length 211;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPF 6  
||:||||  
Db 206 KKIIF 211  
RESULT 65  
S74602  
hypothetical protein slr1095 - Synechocystis sp. (strain PCC 6803)  
C;Species: Synechocystis sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S74602  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O, K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
8.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S74602  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-215 <KAN>  
A;Cross-references: UNIPROT:P72739; UNIPARC:UPI00000C0BF5; EMBL:D90900; GB:AB001339; NID  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Superfamily: Synechocystis hypothetical protein slr1461  
Query Match 79.4%; Score 27; DB 2; Length 215;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPF 6  
||:||||  
Db 111 KKLVPF 116  
RESULT 66  
C64703  
hypothetical protein HP1467 - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: C64703  
R;Tombs, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khairak, H.G.; Glodek, A.; McKen  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.  
Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: C64703

A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-231 <TOM>  
A;Cross-references: UNIPROT:O26003; UNIPARC:UPI00000C0934; GB:AE000647; GB:AE000511; NI  
Query Match 79.4%; Score 27; DB 2; Length 231;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPF 6  
||:||||  
Db 3 KKIIF 8  
RESULT 67  
G97198  
HAD superfamily hydrolase [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: G97198  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: G97198  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-263 <KUR>  
A;Cross-references: UNIPROT:O97GB4; UNIPARC:UPI00000CA500; GB:AE001437; PIDN:AAK80378.1  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC2423  
Query Match 79.4%; Score 27; DB 2; Length 263;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPF 6  
||:||||  
Db 3 KKIIF 8  
RESULT 68  
F97176  
HAD superfamily hydrolases, YKRA B. subtilis ortholog [imported] - Clostridium acetobut  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: F97176  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: F97176  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-266 <KUR>  
A;Cross-references: UNIPROT:Q97GX1; UNIPARC:UPI00000CA472; GB:AE001437; PIDN:AAK80201.1  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC2244  
Query Match 79.4%; Score 27; DB 2; Length 266;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPF 6  
||:||||  
Db 3 KKIIF 8  
RESULT 69

```
T26245
hypothetical protein W06G6.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26245
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20180
A:Accession: T26245
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-300 <WIL>
A:Cross-references: UNIPROT:Q9XUG1; UNIPARC:UPI0000061208; EMBL:Z83129; PIDN:CAB05641.1;
A:Experimental source: clone W06G6
C:Genetics:
A:Gene: CESP:W06G6.6
A:Map position: 5
A:Introns: 1/1/2; 204/2

Query Match      79.4%; Score 27; DB 2; Length 300;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 KLVFFA 7
DB      281 KMVFFA 286
      |||||

RESULT 70
T25850
hypothetical protein T01B11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25850
R:Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z20099
A:Accession: T25850
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-313 <GEI>
A:Cross-references: UNIPROT:P91410; UNIPARC:UPI0000081DDA; EMBL:U80931; PIDN:AAB38001.1;
A:Experimental source: strain Bristol N2; clone T01B11
C:Genetics:
A:Gene: CESP:T01B11.4
A:Map position: 4
A:Introns: 4/1; 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match      79.4%; Score 27; DB 2; Length 313;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVFPA 7
DB      223 KKLNFPA 229
      |||||

RESULT 71
T23207
hypothetical protein K01H12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23207
R:McMurray, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19707
A:Accession: T23207
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-313 <WIL>
A:Cross-references: UNIPROT:Q21103; UNIPARC:UPI0000080D88; EMBL:Z68218; PIDN:CAA92472.1;
```

```
A:Experimental source: clone K01H12
C:Genetics:
A:Gene: CESP:K01H12.2
A:Map position: 4
A:Introns: 4/1; 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match      79.4%; Score 27; DB 2; Length 313;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVFPA 7
DB      223 KKLNFPA 229
      |||||

RESULT 72
T28942
hypothetical protein F07C4.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28942
R:Miller, N.; Stellyes, L.
submitted to the EMBL Data Library, January 1997
A:Description: The sequence of C. elegans cosmid F07C4.
A:Reference number: Z20546
A:Accession: T28942
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-315 <MIL>
A:Cross-references: UNIPROT:P91211; UNIPARC:UPI000007D6C2; EMBL:U80023; PIDN:AAC48017.1;
A:Experimental source: strain Bristol N2; clone F07C4
C:Genetics:
A:Gene: CESP:F07C4.8
A:Map position: 5
A:Introns: 60/2; 221/3

Query Match      79.4%; Score 27; DB 2; Length 315;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVFPA 7
DB      121 KKLVFPA 127
      |||||

RESULT 73
S76400
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76400
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76400
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-326 <KAN>
A:Cross-references: UNIPROT:P74429; UNIPARC:UPI00000C1025; EMBL:DS0915; GB:AB001339; NIT
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      79.4%; Score 27; DB 2; Length 326;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVFPA 7
DB      103 KKFVFS 109
      |||||
```

## RESULT 74

D88109  
protein T24E12.6 (imported) - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C;Accession: D88109  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/projects/C\_elegans/  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999  
A;Accession: D88109  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-329 <STO>  
A;Cross-references: UNIPARC:UPI000017A58E; GB:chr\_II; PIDN:AB95046.1; PID:g2746893; GSPT24E12.6  
C;Genetics:  
A;Gene: T24E12.6  
A;Map position: 2

Query Match 79.4%; Score 27; DB 2; Length 329;  
Best Local Similarity 85.7%; Pred. NO. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
|||  
Db 292 KKNVFFA 298

## RESULT 75

S51490  
chaperone (cpn60) - Pyrenomonas salina  
C;Species: Pyrenomonas salina  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C;Accession: S51490  
R;Maier, U.G.; Rensing, S.A.; Igloi, G.L.; Maerz, M.  
Mol. Gen. Genet. 246, 128-131, 1995  
A;Title: Twintrons are not unique to the Euglena chloroplast genome: structure and evolution  
A;Reference number: S51490; MUID:95124294; PMID:7823908  
A;Accession: S51490  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-331 <MAI>  
A;Cross-references: UNIPARC:UPI000017AED6

Query Match 79.4%; Score 27; DB 2; Length 331;  
Best Local Similarity 83.3%; Pred. NO. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6  
|||  
Db 197 KKLVPF 202

Search completed: December 29, 2005, 17:49:06  
Job time : 19.129 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.83871 Seconds  
(without alignments)  
13.656 Million cell updates/sec

Title: US-10-009-122-2

Perfect score: 34

Sequence: 1 KKLFFFA 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pep.\*

2: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.\*

3: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pep.\*

4: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.\*

5: /cgn2\_6/ptodata/2/pubaa/US03\_NEW\_PUB.pep.\*

6: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pep.\*

7: /cgn2\_6/ptodata/2/pubaa/US11\_NEW\_PUB.pep.\*

8: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	88.2	19	6	US-10-923-605-5
2	30	88.2	19	6	US-10-934-818-5
3	30	88.2	40	7	US-11-016-706-36
4	30	88.2	40	7	US-11-098-674-12
5	30	88.2	42	6	US-10-923-605-1
6	30	88.2	42	6	US-10-934-818-1
7	30	88.2	42	7	US-11-016-706-37
8	30	88.2	43	6	US-10-934-818-6
9	30	88.2	43	6	US-10-250-581-1
10	30	88.2	43	6	US-10-250-581-1
11	30	88.2	770	6	US-10-982-545-15
12	30	88.2	770	6	US-10-783-273-38
13	27	79.4	50	6	US-10-467-657-7892
14	27	79.4	558	7	US-11-078-189-19
15	27	79.4	708	7	US-11-174-150-25
16	27	79.4	710	7	US-11-078-189-18
17	27	79.4	736	7	US-11-174-150-26
18	27	79.4	736	7	US-11-078-189-9
19	27	79.4	739	7	US-11-078-189-12
20	26	76.5	1070	7	US-11-186-284-132
21	26	76.5	1070	7	US-11-147-047-49
22	25	73.5	5	7	US-11-098-674-1
23	25	73.5	47	6	US-10-467-657-5436
24	25	73.5	207	6	US-10-858-730-196
25	25	73.5	443	6	US-10-793-626-1860

26	73.5	528	6	US-10-793-626-1930	Sequence 1330, Ap
27	73.5	660	7	US-11-186-284-125	Sequence 125, App
28	73.5	708	6	US-10-821-234-917	Sequence 917, App
29	70.6	134	6	US-10-793-626-2374	Sequence 2374, Ap
30	70.6	148	6	US-10-467-657-2934	Sequence 2934, Ap
31	70.6	167	6	US-10-967-457-79	Sequence 79, Appl
32	70.6	182	6	US-10-793-626-2836	Sequence 2836, Ap
33	70.6	194	7	US-11-044-899-26	Sequence 26, Appl
34	70.6	196	6	US-10-793-626-630	Sequence 630, App
35	70.6	211	6	US-10-467-657-6932	Sequence 6932, Ap
36	70.6	215	6	US-10-131-826A-4	Sequence 4, Appli
37	70.6	228	6	US-10-467-657-568	Sequence 568, App
38	70.6	228	6	US-10-467-657-4838	Sequence 4838, Ap
39	70.6	233	6	US-10-821-234-1322	Sequence 1322, Ap
40	70.6	249	7	US-11-113-424-30	Sequence 30, Appl
41	70.6	259	6	US-10-512-184-34	Sequence 34, Appl
42	70.6	338	6	US-10-878-556A-19	Sequence 19, Appl
43	70.6	344	6	US-10-131-826A-376	Sequence 376, App
44	70.6	371	6	US-10-512-184-71	Sequence 71, Appl
45	70.6	374	7	US-11-080-991-16	Sequence 16, Appl
46	70.6	396	6	US-10-995-561-1005	Sequence 1005, Ap
47	70.6	453	7	US-11-082-389-198	Sequence 198, App
48	70.6	476	7	US-11-069-642-19	Sequence 19, Appl
49	70.6	481	6	US-10-995-561-959	Sequence 959, App
50	70.6	482	6	US-10-793-626-24	Sequence 24, Appl
51	70.6	598	6	US-10-719-311-16	Sequence 16, Appl
52	70.6	626	6	US-10-512-184-49	Sequence 49, Appl
53	70.6	725	7	US-11-078-189-15	Sequence 15, Appl
54	70.6	734	6	US-10-719-311-4	Sequence 4, Appli
55	70.6	858	6	US-10-613-744-6	Sequence 6, Appli
56	70.6	899	6	US-10-821-234-975	Sequence 975, App
57	70.6	1113	7	US-11-067-811-4	Sequence 4, Appli
58	67.6	21	7	US-11-040-159-20	Sequence 20, Appl
59	67.6	186	6	US-10-467-657-3918	Sequence 3918, Ap
60	67.6	187	6	US-10-980-388-65	Sequence 65, Appl
61	67.6	216	6	US-10-467-657-8102	Sequence 8102, Ap
62	67.6	221	6	US-10-467-657-290	Sequence 290, App
63	67.6	221	6	US-10-467-657-5750	Sequence 5750, Ap
64	67.6	224	6	US-10-793-626-1430	Sequence 1430, Ap
65	67.6	269	6	US-10-467-657-330	Sequence 330, App
66	67.6	271	6	US-10-821-234-1419	Sequence 1419, Ap
67	67.6	272	6	US-10-632-150-46	Sequence 46, Appl
68	67.6	272	7	US-11-073-457-46	Sequence 46, Appl
69	67.6	272	7	US-11-073-460-46	Sequence 46, Appl
70	67.6	337	6	US-10-485-517-234	Sequence 234, App
71	67.6	346	6	US-10-770-726-55	Sequence 55, Appl
72	67.6	370	6	US-10-821-234-1105	Sequence 1105, Ap
73	67.6	400	6	US-10-793-626-1056	Sequence 1056, Ap
74	67.6	402	6	US-10-467-657-9070	Sequence 9070, Ap
75	67.6	433	6	US-10-467-657-6352	Sequence 6352, Ap
76	67.6	463	6	US-10-467-657-7604	Sequence 7604, Ap
77	67.6	522	6	US-10-995-561-1030	Sequence 1030, Ap
78	67.6	600	6	US-10-131-826A-462	Sequence 462, App
79	67.6	615	6	US-10-995-561-940	Sequence 940, App
80	67.6	662	6	US-10-995-561-943	Sequence 943, App
81	67.6	702	6	US-10-995-561-942	Sequence 942, App
82	67.6	745	7	US-11-147-109-2	Sequence 2, Appli
83	67.6	754	6	US-10-995-561-941	Sequence 941, App
84	67.6	104	6	US-10-467-657-6866	Sequence 6866, Ap
85	64.7	113	6	US-10-793-626-1950	Sequence 1950, Ap
86	64.7	134	6	US-10-467-657-8520	Sequence 8520, Ap
87	64.7	153	7	US-11-098-765-2	Sequence 2, Appli
88	64.7	155	6	US-10-467-657-2420	Sequence 2420, Ap
89	64.7	182	6	US-10-980-388-89	Sequence 89, Appl
90	64.7	194	6	US-10-878-556A-130	Sequence 130, App
91	64.7	195	7	US-11-019-955-24	Sequence 24, Appl
92	64.7	200	6	US-10-524-198-2	Sequence 2, Appli
93	64.7	204	6	US-10-980-388-102	Sequence 102, App
94	64.7	209	6	US-10-793-626-304	Sequence 304, App
95	64.7	210	6	US-10-467-657-6318	Sequence 6318, Ap
96	64.7	211	6	US-10-821-234-1372	Sequence 1372, Ap
97	64.7	229	6	US-10-131-826A-410	Sequence 410, App
98	64.7	239	6	US-10-467-657-8743	Sequence 8743, Ap

99	22	64.7	241	7	US-11-019-955-27	Sequence 27, Appl	172	21	61.8	179	6	US-10-467-657-306	Sequence 306, Appl
100	22	64.7	268	7	US-11-019-955-28	Sequence 28, Appl	173	21	61.8	179	6	US-10-467-657-6422	Sequence 6422, Ap
101	22	64.7	276	6	US-10-793-626-1156	Sequence 1156, Ap	174	21	61.8	190	6	US-10-467-657-3436	Sequence 3436, Ap
102	22	64.7	271	6	US-10-873-528-134	Sequence 134, App	175	21	61.8	194	7	US-11-103-957-57	Sequence 57, Appl
103	22	64.7	310	7	US-11-102-240-140	Sequence 140, App	176	21	61.8	198	6	US-10-131-826A-550	Sequence 550, App
104	22	64.7	327	6	US-10-793-626-1104	Sequence 1104, Ap	177	21	61.8	198	7	US-11-069-642-25	Sequence 25, Appl
105	22	64.7	347	6	US-10-467-657-2014	Sequence 2014, Ap	178	21	61.8	205	6	US-10-873-528-52	Sequence 52, Appl
106	22	64.7	409	6	US-10-821-234-1425	Sequence 1425, Ap	179	21	61.8	216	6	US-10-467-657-5376	Sequence 5376, Ap
107	22	64.7	412	7	US-11-074-176-24	Sequence 24, Appl	180	21	61.8	233	6	US-10-467-657-2300	Sequence 2300, Ap
108	22	64.7	426	6	US-10-467-657-2120	Sequence 2120, Ap	181	21	61.8	241	6	US-10-878-556A-35	Sequence 35, Appl
109	22	64.7	433	6	US-10-652-893-4	Sequence 4, Appl	182	21	61.8	243	6	US-10-512-109-23	Sequence 23, Appl
110	22	64.7	433	6	US-10-821-234-1429	Sequence 1429, Ap	183	21	61.8	243	6	US-10-512-109-48	Sequence 48, Appl
111	22	64.7	445	6	US-10-873-528-30	Sequence 30, Appl	184	21	61.8	248	6	US-10-793-626-3218	Sequence 3218, Ap
112	22	64.7	452	6	US-10-878-556A-151	Sequence 151, App	185	21	61.8	258	6	US-10-793-626-2360	Sequence 2360, Ap
113	22	64.7	461	7	US-10-131-826A-454	Sequence 454, App	186	21	61.8	259	6	US-10-467-657-3410	Sequence 3410, Ap
114	22	64.7	475	7	US-11-174-150-45	Sequence 45, Appl	187	21	61.8	267	6	US-10-467-657-5556	Sequence 5556, Ap
115	22	64.7	524	6	US-10-689-742-13	Sequence 13, Appl	188	21	61.8	298	6	US-10-793-626-1298	Sequence 1298, Ap
116	22	64.7	529	7	US-11-174-150-46	Sequence 46, Appl	189	21	61.8	311	6	US-10-793-626-2450	Sequence 2450, Ap
117	22	64.7	585	6	US-10-967-457-18	Sequence 18, Appl	190	21	61.8	311	7	US-11-179-411-18	Sequence 18, Appl
118	22	64.7	585	6	US-10-939-890-500	Sequence 500, App	191	21	61.8	311	7	US-11-175-766-18	Sequence 18, Appl
119	22	64.7	585	7	US-11-078-663-18	Sequence 18, Appl	192	21	61.8	323	6	US-10-467-657-556	Sequence 556, App
120	22	64.7	585	7	US-11-078-914-18	Sequence 18, Appl	193	21	61.8	346	6	US-10-878-556A-121	Sequence 121, App
121	22	64.7	592	6	US-10-467-657-4888	Sequence 4888, Ap	194	21	61.8	346	7	US-11-069-642-109	Sequence 109, App
122	22	64.7	657	7	US-11-080-991-48	Sequence 48, Appl	195	21	61.8	377	7	US-11-152-892-8	Sequence 8, Appl
123	22	64.7	674	6	US-10-507-275-9	Sequence 9, Appl	196	21	61.8	393	7	US-11-077-712-4	Sequence 4, Appl
124	22	64.7	677	6	US-10-131-826A-230	Sequence 230, App	197	21	61.8	395	6	US-10-793-626-664	Sequence 664, App
125	22	64.7	690	6	US-10-939-890-501	Sequence 501, App	198	21	61.8	413	6	US-10-821-234-989	Sequence 989, App
126	22	64.7	779	7	US-11-128-420-12	Sequence 12, Appl	199	21	61.8	419	6	US-10-821-234-1360	Sequence 1360, Ap
127	22	64.7	856	6	US-10-467-657-8534	Sequence 8534, Ap	200	21	61.8	431	7	US-11-069-642-1	Sequence 1, Appl
128	22	64.7	862	7	US-11-077-550-173	Sequence 173, App	201	21	61.8	437	7	US-11-069-642-92	Sequence 92, Appl
129	22	64.7	1167	6	US-10-601-368-18	Sequence 18, Appl	202	21	61.8	438	7	US-11-069-642-47	Sequence 47, Appl
130	21	61.8	11	6	US-10-914-842A-11	Sequence 11, Appl	203	21	61.8	438	7	US-11-069-642-49	Sequence 49, Appl
131	21	61.8	12	6	US-10-982-891-26	Sequence 26, Appl	204	21	61.8	438	7	US-11-069-642-51	Sequence 51, Appl
132	21	61.8	12	6	US-10-982-891-31	Sequence 31, Appl	205	21	61.8	438	7	US-11-069-642-53	Sequence 53, Appl
133	21	61.8	12	6	US-10-982-891-33	Sequence 33, Appl	206	21	61.8	438	7	US-11-069-642-55	Sequence 55, Appl
134	21	61.8	13	6	US-10-511-559-836	Sequence 836, App	207	21	61.8	438	7	US-11-069-642-59	Sequence 59, Appl
135	21	61.8	13	6	US-10-511-559-837	Sequence 837, App	208	21	61.8	438	7	US-11-069-642-61	Sequence 61, Appl
136	21	61.8	13	6	US-10-511-559-838	Sequence 838, App	209	21	61.8	438	7	US-11-069-642-63	Sequence 63, Appl
137	21	61.8	13	6	US-10-511-559-839	Sequence 839, App	210	21	61.8	446	6	US-10-467-657-930	Sequence 930, App
138	21	61.8	13	6	US-10-511-559-840	Sequence 840, App	211	21	61.8	447	7	US-11-109-156-30	Sequence 30, Appl
139	21	61.8	13	6	US-10-511-559-841	Sequence 841, App	212	21	61.8	448	6	US-10-467-657-1096	Sequence 1096, Ap
140	21	61.8	28	6	US-10-250-581-14	Sequence 14, Appl	213	21	61.8	448	7	US-11-112-882-24	Sequence 24, Appl
141	21	61.8	28	6	US-10-250-581-17	Sequence 17, Appl	214	21	61.8	448	7	US-11-112-882-64	Sequence 64, Appl
142	21	61.8	28	6	US-10-250-581-14	Sequence 14, Appl	215	21	61.8	448	7	US-11-112-882-65	Sequence 65, Appl
143	21	61.8	28	6	US-10-250-581-17	Sequence 17, Appl	216	21	61.8	448	7	US-11-112-882-66	Sequence 66, Appl
144	21	61.8	33	6	US-10-467-657-7026	Sequence 7026, Ap	217	21	61.8	448	7	US-11-112-882-67	Sequence 67, Appl
145	21	61.8	40	6	US-10-250-581-15	Sequence 15, Appl	218	21	61.8	449	6	US-10-467-657-678	Sequence 678, App
146	21	61.8	40	6	US-10-250-581-15	Sequence 15, Appl	219	21	61.8	468	6	US-10-793-626-2242	Sequence 2242, Ap
147	21	61.8	40	6	US-10-250-581-15	Sequence 15, Appl	220	21	61.8	490	6	US-10-793-626-872	Sequence 872, App
148	21	61.8	40	6	US-10-250-581-15	Sequence 15, Appl	221	21	61.8	491	6	US-10-793-626-2770	Sequence 2770, Ap
149	21	61.8	42	6	US-10-250-581-16	Sequence 16, Appl	222	21	61.8	500	6	US-10-957-569-18	Sequence 18, Appl
150	21	61.8	42	6	US-10-250-581-19	Sequence 19, Appl	223	21	61.8	522	7	US-11-080-991-104	Sequence 104, App
151	21	61.8	42	6	US-10-250-581-16	Sequence 16, Appl	224	21	61.8	525	7	US-11-082-389-350	Sequence 350, App
152	21	61.8	42	6	US-10-250-581-19	Sequence 19, Appl	225	21	61.8	525	7	US-11-112-882-27	Sequence 27, Appl
153	21	61.8	48	7	US-11-000-463-388	Sequence 388, App	226	21	61.8	533	6	US-10-467-657-2868	Sequence 2868, Ap
154	21	61.8	48	7	US-11-000-463-860	Sequence 860, App	227	21	61.8	551	7	US-11-109-156-36	Sequence 36, Appl
155	21	61.8	57	6	US-10-467-657-5448	Sequence 5448, Ap	228	21	61.8	553	7	US-11-090-439-18	Sequence 18, Appl
156	21	61.8	57	6	US-10-467-657-6902	Sequence 6902, Ap	229	21	61.8	582	7	US-11-090-439-58	Sequence 58, Appl
157	21	61.8	57	6	US-10-467-657-7888	Sequence 7888, Ap	230	21	61.8	592	6	US-10-623-155-169	Sequence 169, App
158	21	61.8	58	7	US-11-000-463-7885	Sequence 7885, App	231	21	61.8	601	6	US-10-467-657-7120	Sequence 7120, Ap
159	21	61.8	62	7	US-11-000-463-773	Sequence 773, App	232	21	61.8	626	6	US-10-467-657-1196	Sequence 1196, Ap
160	21	61.8	76	6	US-10-467-657-5690	Sequence 5690, App	233	21	61.8	702	6	US-10-467-657-7230	Sequence 7230, Ap
161	21	61.8	79	6	US-10-467-657-2026	Sequence 2026, Ap	234	21	61.8	738	7	US-11-147-047-48	Sequence 48, Appl
162	21	61.8	84	6	US-10-986-501-186	Sequence 186, App	235	21	61.8	757	7	US-11-053-100-47	Sequence 47, Appl
163	21	61.8	98	6	US-10-467-657-4746	Sequence 4746, Ap	236	21	61.8	777	6	US-10-658-986-4	Sequence 4, Appl
164	21	61.8	104	6	US-10-793-626-2512	Sequence 2512, Ap	237	21	61.8	791	6	US-10-623-155-170	Sequence 170, App
165	21	61.8	106	7	US-11-064-174-50	Sequence 50, Appl	238	21	61.8	801	6	US-10-467-657-6470	Sequence 6470, Ap
166	21	61.8	112	6	US-10-467-657-5514	Sequence 5514, Ap	239	21	61.8	881	6	US-10-623-155-430	Sequence 430, App
167	21	61.8	126	6	US-10-467-657-606	Sequence 606, App	240	21	61.8	920	6	US-10-623-155-357	Sequence 357, App
168	21	61.8	133	7	US-11-069-834-2	Sequence 2, Appl	241	21	61.8	921	7	US-11-183-624-2	Sequence 2, Appl
169	21	61.8	138	6	US-10-793-626-1254	Sequence 1254, Ap	242	21	61.8	943	6	US-10-623-155-161	Sequence 161, App
170	21	61.8	155	7	US-11-069-642-97	Sequence 97, Appl	243	21	61.8	949	6	US-11-077-550-68	Sequence 68, Appl
171	21	61.8	160	6	US-10-793-626-750	Sequence 750, App	244	21	61.8	1016	7	US-11-103-957-41	Sequence 41, Appl

Sequence 1, Appli  
Sequence 9, Appli  
Sequence 2, Appli  
Sequence 594, App  
Sequence 595, App  
Sequence 596, App  
Sequence 28, Appl  
Sequence 28, Appl  
Sequence 334, App  
Sequence 110, App  
Sequence 73, Appl  
Sequence 1, Appli  
Sequence 873, App  
Sequence 6, Appli  
Sequence 606, App  
Sequence 13, Appl  
Sequence 11, Appl  
Sequence 608, App  
Sequence 593, App  
Sequence 35, Appl  
Sequence 37, App  
Sequence 29, Appl  
Sequence 8712, Ap  
Sequence 347, App  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 9144, Ap  
Sequence 6120, Ap  
Sequence 4978, Ap  
Sequence 8560, Ap  
Sequence 1050, Ap  
Sequence 5386, Ap  
Sequence 387, App  
Sequence 859, App  
Sequence 765, App  
Sequence 912, App  
Sequence 143, App  
Sequence 431, App  
Sequence 89, Appl  
Sequence 114, App  
Sequence 33, Appl  
Sequence 2378, Ap  
Sequence 2834, Ap  
Sequence 412, App  
Sequence 9209, Ap  
Sequence 12, Appl  
Sequence 4, Appli  
Sequence 377, App  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 15, Appl

21 61.8 1042 7 US-11-067-811-1  
21 61.8 1124 7 US-11-195-197-9  
21 61.8 1170 6 US-10-831-997-2  
21 61.8 1170 6 US-10-995-561-594  
21 61.8 1170 6 US-10-995-561-595  
21 61.8 1170 6 US-10-995-561-596  
21 61.8 1170 7 US-11-046-456-28  
21 61.8 1170 7 US-11-046-444-28  
21 61.8 1389 6 US-10-467-657-334  
21 61.8 1420 7 US-11-077-550-110  
21 61.8 1438 6 US-10-511-559-73  
21 61.8 1467 6 US-10-507-956-1  
21 61.8 1474 6 US-10-995-561-873  
21 61.8 1734 7 US-11-192-967-6  
21 61.8 1734 7 US-11-193-715-6  
21 61.8 2096 6 US-10-995-561-606  
21 61.8 2333 7 US-11-096-281-13  
21 61.8 2339 7 US-11-096-281-11  
21 61.8 2351 6 US-10-995-561-608  
21 61.8 3623 6 US-10-995-561-593  
20.5 60.3 399 7 US-11-147-047-35  
20 58.8 11 7 US-11-074-176-37  
20 58.8 12 6 US-10-982-891-29  
20 58.8 19 6 US-10-467-657-8712  
20 58.8 27 6 US-10-986-501-347  
20 58.8 28 6 US-10-250-581-2  
20 58.8 28 6 US-10-250-581-2  
20 58.8 40 6 US-10-250-581-3  
20 58.8 40 6 US-10-250-581-4  
20 58.8 42 6 US-10-250-581-4  
20 58.8 50 6 US-10-467-657-9144  
20 58.8 53 6 US-10-467-657-6120  
20 58.8 54 6 US-10-467-657-4978  
20 58.8 56 6 US-10-467-657-8560  
20 58.8 56 6 US-10-467-657-1050  
20 58.8 69 7 US-11-000-463-387  
20 58.8 69 7 US-11-000-463-859  
20 58.8 71 7 US-11-000-463-765  
20 58.8 72 6 US-10-467-657-912  
20 58.8 75 6 US-10-986-501-143  
20 58.8 78 7 US-11-123-896-431  
20 58.8 80 7 US-11-123-896-89  
20 58.8 83 6 US-10-510-386-114  
20 58.8 90 7 US-11-020-772-33  
20 58.8 92 6 US-10-467-657-2378  
20 58.8 96 6 US-10-467-657-2834  
20 58.8 103 7 US-11-194-246-412  
20 58.8 105 6 US-10-467-657-9209  
20 58.8 105 7 US-11-155-775-12  
20 58.8 106 7 US-11-096-074-4  
20 58.8 107 6 US-10-485-517-377  
20 58.8 107 7 US-11-107-028-13  
20 58.8 107 7 US-11-107-028-14  
20 58.8 107 7 US-11-107-028-15

## ALIGNMENTS

RESULT 1  
US-10-923-605-5  
; Sequence 5, Application US/10923605  
; Publication No. US20050249727A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004740US  
; CURRENT APPLICATION NUMBER: US/10/923,605  
; PRIOR FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: US/09/322,289

; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-10-923-605-5

Query Match 88.2%; Score 30; DB 6; Length 19;  
Best Local Similarity 85.7%; Pred. No. 0.61;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
:|||||  
Db 3 QKLVFFA 9

RESULT 2  
US-10-934-818-5  
; Sequence 5, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-10-934-818-5

Query Match 88.2%; Score 30; DB 6; Length 19;  
Best Local Similarity 85.7%; Pred. No. 0.61;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
:|||||  
Db 3 QKLVFFA 9

RESULT 3  
US-11-016-706-36  
; Sequence 36, Application US/11016706  
; Publication No. US20050244334A1  
; GENERAL INFORMATION:  
; APPLICANT: CASTILLO, GERARDO  
; APPLICANT: LAKE, THOMAS P.



; APPLICANT: NGUYEN, BETH P.  
; APPLICANT: SANDERS, VIRGINIA J.  
; APPLICANT: SNOW, ALAN D.  
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS  
; FILE REFERENCE: PROTEO.P03C13  
; CURRENT APPLICATION NUMBER: US/11/016,706  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 09/962,955  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 36  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-016-706-36

Query Match 88.2%; Score 30; DB 7; Length 40;  
Best Local Similarity 85.7%; Pred. No. 1.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 15 QKLVPFA 21

RESULT 4  
US-11-098-674-12  
; Sequence 12, Application US/11098674  
; Publication No. US20050267029A1  
; GENERAL INFORMATION:  
; APPLICANT: Ancsin, John B.  
; APPLICANT: Elimova, Elena  
; APPLICANT: Kisilevsky, Robert  
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their  
; TITLE OF INVENTION: Identification and Use  
; FILE REFERENCE: PTQ-0066  
; CURRENT APPLICATION NUMBER: US/11/098,674  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 60/559,122  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-098-674-12

Query Match 88.2%; Score 30; DB 7; Length 40;  
Best Local Similarity 85.7%; Pred. No. 1.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 15 QKLVPFA 21

RESULT 5  
US-10-923-605-1  
; Sequence 1, Application US/10923605  
; Publication No. US20050249727A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-004740US  
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: US/09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide  
US-10-923-605-1

Query Match 88.2%; Score 30; DB 6; Length 42;  
Best Local Similarity 85.7%; Pred. No. 1.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 15 QKLVPFA 21

RESULT 6  
US-10-934-818-1  
; Sequence 1, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide  
US-10-934-818-1

Query Match 88.2%; Score 30; DB 6; Length 42;  
Best Local Similarity 85.7%; Pred. No. 1.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 15 QKLVPFA 21

RESULT 7  
US-11-016-706-37  
; Sequence 37, Application US/11016706  
; Publication No. US20050244334A1  
; GENERAL INFORMATION:  
; APPLICANT: CASTILLO, GERARDO  
; APPLICANT: LAKE, THOMAS P.  
; APPLICANT: NGUYEN, BETH P.  
; APPLICANT: SANDERS, VIRGINIA J.  
; APPLICANT: SNOW, ALAN D.  
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS  
; FILE REFERENCE: PROTEO.P03C13  
; CURRENT APPLICATION NUMBER: US/11/016,706  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 09/962,955  
; PRIOR FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 37  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-016-706-37

Query Match 88.2%; Score 30; DB 7; Length 42;  
Best Local Similarity 85.7%; Pred. No. 1.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
Db 15 QKLVPFA 21

## RESULT 8

US-10-934-818-6  
; Sequence 6, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide  
US-10-934-818-6

Query Match 88.2%; Score 30; DB 6; Length 43;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
Db 15 QKLVPFA 21

## RESULT 9

US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 88.2%; Score 30; DB 6; Length 43;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
Db 15 QKLVPFA 21

## RESULT 10

US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 88.2%; Score 30; DB 6; Length 43;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
Db 15 QKLVPFA 21

## RESULT 11

US-10-982-545-15  
; Sequence 15, Application US/10982545  
; Publication No. US20050244890A1  
; GENERAL INFORMATION:  
; APPLICANT: Davies, Huw Alun  
; APPLICANT: McGuire, James  
; APPLICANT: Simonsen, Anja Hviid  
; APPLICANT: Blennow, Kaj  
; APPLICANT: Podust, Vladimir  
; APPLICANT: CIPHERGEN Biosystems, Inc.  
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease  
; FILE REFERENCE: 016866-011550US  
; CURRENT APPLICATION NUMBER: US/10/982,545  
; CURRENT FILING DATE: 2004-11-06  
; PRIOR APPLICATION NUMBER: US 60/518,360  
; PRIOR FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US 60/526,753  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: US 60/546,423  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/547,250  
; PRIOR FILING DATE: 2004-02-23  
; PRIOR APPLICATION NUMBER: US 60/558,896  
; PRIOR FILING DATE: 2004-04-02  
; PRIOR APPLICATION NUMBER: US 60/572,617  
; PRIOR FILING DATE: 2004-05-18  
; PRIOR APPLICATION NUMBER: US 60/586,503  
; PRIOR FILING DATE: 2004-07-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

```
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; OTHER INFORMATION: C31
US-10-982-545-15
```

```
Query Match      88.2%; Score 30; DB 6; Length 770;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KKLVEFFA 7
      :|||||
Db      686 QKLVEFFA 692
```

RESULT 12

```
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-38
```

```
Query Match      88.2%; Score 30; DB 6; Length 770;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KKLVEFFA 7
      :|||||
Db      686 QKLVEFFA 692
```

```
RESULT 13
US-10-467-657-7892
; Sequence 7892, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 7892
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7892
```

```
Query Match      79.4%; Score 27; DB 6; Length 50;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KKLVEFF 6
      :||:|
Db      32 KKLIEFF 37
```

```
RESULT 14
US-11-078-189-19
; Sequence 19, Application US/11078189
; Publication No. US20050277167A1
; GENERAL INFORMATION:
```

; APPLICANT: Bachinger, Hans Peter  
; APPLICANT: Vranka, Janice  
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES  
; FILE REFERENCE: 08062-020001  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: US/11/078,189  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: US 60/552,409  
; PRIOR FILING DATE: 2004-03-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 558  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
US-11-078-189-19

Query Match 79.4%; Score 27; DB 7; Length 558;  
Best Local Similarity 71.4%; Pred. No. 75;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGLVFFA 7  
|:|:|  
Db 277 KELLFFA 283

RESULT 15  
US-11-174-150-25  
; Sequence 25, Application US/11/174150  
; Publication No. US20050260714A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Rizvi, Safia K.  
; APPLICANT: Smith, Randall F.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50022  
; CURRENT APPLICATION NUMBER: US/11/174,150  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US/10/257,174  
; PRIOR FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: PCT/US01/11797  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/196,603  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/199,417  
; PRIOR FILING DATE: 2000-04-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 708  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-174-150-25

Query Match 79.4%; Score 27; DB 7; Length 708;  
Best Local Similarity 71.4%; Pred. No. 95;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGLVFFA 7  
|:|:|  
Db 345 KELLFFA 351

RESULT 16  
US-11-078-189-18  
; Sequence 18, Application US/11/078189  
; Publication No. US20050277167A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachinger, Hans Peter  
; APPLICANT: Vranka, Janice

; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES  
; FILE REFERENCE: 08062-020001  
; CURRENT APPLICATION NUMBER: US/11/078,189  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: US 60/552,409  
; PRIOR FILING DATE: 2004-03-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-11-078-189-18

Query Match 79.4%; Score 27; DB 7; Length 710;  
Best Local Similarity 57.1%; Pred. No. 95;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGLVFFA 7  
|:|:|  
Db 356 KGLIYYA 362

RESULT 17  
US-11-174-150-26  
; Sequence 26, Application US/11/174150  
; Publication No. US20050260714A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Rizvi, Safia K.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Xiang, Zhaoying  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50022  
; CURRENT APPLICATION NUMBER: US/11/174,150  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US/10/257,174  
; PRIOR FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: PCT/US01/11797  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/196,603  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/199,417  
; PRIOR FILING DATE: 2000-04-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 736  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-174-150-26

Query Match 79.4%; Score 27; DB 7; Length 736;  
Best Local Similarity 71.4%; Pred. No. 99;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGLVFFA 7  
|:|:|  
Db 373 KELLFFA 379

RESULT 18  
US-11-078-189-9  
; Sequence 9, Application US/11/078189  
; Publication No. US20050277167A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachinger, Hans Peter  
; APPLICANT: Vranka, Janice  
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES  
; FILE REFERENCE: 08062-020001  
; CURRENT APPLICATION NUMBER: US/11/078,189  
; CURRENT FILING DATE: 2005-03-11

; PRIOR APPLICATION NUMBER: US 60/552,409  
; PRIOR FILING DATE: 2004-03-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 736  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-078-189-9

Query Match 79.4%; Score 27; DB 7; Length 736;  
Best Local Similarity 71.4%; Pred. No. 99;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
|:|:|  
Db 373 KELLFFA 379

RESULT 19  
US-11-078-189-12  
; Sequence 12, Application US/11078189  
; Publication No. US20050277167A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachinger, Hans Peter  
; APPLICANT: Vranka, Janice  
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES  
; FILE REFERENCE: 08062-020001  
; CURRENT APPLICATION NUMBER: US/11/078,189  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: US 60/552,409  
; PRIOR FILING DATE: 2004-03-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 739  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-078-189-12

Query Match 79.4%; Score 27; DB 7; Length 739;  
Best Local Similarity 71.4%; Pred. No. 99;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
|:|:|  
Db 376 KELLFFA 382

RESULT 20  
US-11-186-284-132  
; Sequence 132, Application US/11186284  
; Publication No. US20050266493A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Berger, Allison  
; APPLICANT: Guillemette, Tracy L.  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Thibodeau, Stephen N.  
; APPLICANT: Burgart, Lawrence J.  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE OF INVENTION: THERAPY OF COLON CANCER  
; FILE REFERENCE: MP01-029P2RNM  
; CURRENT APPLICATION NUMBER: US/11/186,284  
; CURRENT FILING DATE: 2005-07-21  
; PRIOR APPLICATION NUMBER: US/10/301,822  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 60/339,971  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/361,978

; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/381,988  
; PRIOR FILING DATE: 2002-05-20  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 132  
; LENGTH: 707  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-186-284-132

Query Match 76.5%; Score 26; DB 7; Length 707;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
|:|:|  
Db 577 KKLFFFS 583

RESULT 21  
US-11-147-047-49  
; Sequence 49, Application US/11147047  
; Publication No. US20050260668A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdock, Paul R.  
; APPLICANT: Rizvi, Safia K.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Xiang, Zhaoying  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GPS0016  
; CURRENT APPLICATION NUMBER: US/11/147,047  
; CURRENT FILING DATE: 2005-06-07  
; PRIOR APPLICATION NUMBER: US/10/221,097  
; PRIOR FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: PCT/US01/07143  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/187,107  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: 60/236,874  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/188,916  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/237,846  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 49  
; LENGTH: 1070  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-147-047-49

Query Match 76.5%; Score 26; DB 7; Length 1070;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6  
|:|:|  
Db 1011 KQLVFF 1016

RESULT 22  
US-11-098-674-1  
; Sequence 1, Application US/11098674  
; Publication No. US20050267029A1  
; GENERAL INFORMATION:  
; APPLICANT: Ancsin, John B.  
; APPLICANT: Elimova, Elena  
; APPLICANT: Kisilevsky, Robert  
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their  
; TITLE OF INVENTION: Identification and Use

```
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match          73.5%; Score 25; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 6
   |||||
Db 1 KLVFF 5

RESULT 23
US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match          73.5%; Score 25; DB 6; Length 47;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFF 6
   :|||
Db 35 KLVFF 40

RESULT 24
US-10-858-730-196
; Sequence 196, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua J.
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
```

```
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Coryne-bacterium glutamicum
US-10-858-730-196

Query Match          73.5%; Score 25; DB 6; Length 207;
Best Local Similarity 71.4%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFF 7
   |||||
Db 122 KLVFF 128

RESULT 25
US-10-793-626-1860
; Sequence 1860, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1860
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1860

Query Match          73.5%; Score 25; DB 6; Length 443;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFF 6
   |||||
Db 167 KLVFF 172

RESULT 26
US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930

Query Match          73.5%; Score 25; DB 6; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVVFF 6
Db 477 KLVVFF 481

RESULT 27
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

Query Match          73.5%; Score 25; DB 7; Length 660;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFF 7
Db 530 EKAVFFA 536

RESULT 28
US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PT_SEQ_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match          73.5%; Score 25; DB 6; Length 708;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFF 7
Db 578 EKAVFFA 584

RESULT 29
US-10-793-626-2374
; Sequence 2374, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2374
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2374

Query Match          70.6%; Score 24; DB 6; Length 134;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6
Db 6 KKIIYF 11

RESULT 30
US-10-467-657-2934
; Sequence 2934, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2934
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
```

## US-10-467-657-2934

Query Match 70.6%; Score 24; DB 6; Length 148;  
Best Local Similarity 83.3%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVPF 6  
Db 21 KKLVPF 26

## RESULT 31

US-10-967-457-79  
; Sequence 79, Application US/10967457  
; Publication No. US20050244931A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF545PCT  
; CURRENT APPLICATION NUMBER: US/10/967,457  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: US/09/833,041  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229,358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256,931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199,384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 79  
; LENGTH: 167  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-967-457-79

Query Match 70.6%; Score 24; DB 6; Length 167;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 5  
Db 106 KKLVPF 110

## RESULT 32

US-10-793-626-2836  
; Sequence 2836, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2836  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2836

Query Match 70.6%; Score 24; DB 6; Length 182;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
Db 13 KKVTFPS 19

## RESULT 33

US-11-044-899-26  
; Sequence 26, Application US/11044899  
; Publication No. US20050260616A1  
; GENERAL INFORMATION:  
; APPLICANT: Schwab, M.  
; APPLICANT: Chen, M.  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED  
; TITLE OF INVENTION: THEREON  
; FILE REFERENCE: 10200-017-999  
; CURRENT APPLICATION NUMBER: US/11/044,899  
; CURRENT FILING DATE: 2005-01-26  
; PRIOR APPLICATION NUMBER: 09/830,972  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: PCT/US99/26160  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: 60/107,446  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: C. elegans  
US-11-044-899-26

Query Match 70.6%; Score 24; DB 7; Length 194;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 5  
Db 101 KKLVPF 105

## RESULT 34

US-10-793-626-630  
; Sequence 630, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 630  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-630

Query Match 70.6%; Score 24; DB 6; Length 196;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVPF 6  
Db 125 KKVTF 130

## RESULT 35



```

US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

```

```

Query Match      70.6%; Score 24; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LVFFA 7
Db      19 LVFFA 23

```

```

RESULT 36
US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17

```

```

; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match      70.6%; Score 24; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LVFFA 7
Db      166 LVFFA 170

```

```

RESULT 37
US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

```

```

Query Match      70.6%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LVFFA 7
Db      156 LVFFA 160

```

```

RESULT 38
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218

```

```
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match          70.6%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LVFFA 7
Db      156 LVFFA 160

RESULT 39
US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match          70.6%; Score 24; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LVFFA 7
Db      166 LVFFA 170

RESULT 40
US-11-113-424-30
; Sequence 30, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli, et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113.424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075

; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-30

Query Match          70.6%; Score 24; DB 7; Length 249;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KKLVPFA 7
Db      3 KKLVPFS 9

RESULT 41
US-10-512-184-34
; Sequence 34, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-34

Query Match          70.6%; Score 24; DB 6; Length 259;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KKLVPFA 7
Db      195 KKLVPFA 201

RESULT 42
US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19
```

Query Match 70.6%; Score 24; DB 6; Length 338;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 6  
||:|  
Db 76 KLIF 80

## RESULT 43

US-10-131-826A-376  
; Sequence 376, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bereasini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 376  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-376

Query Match 70.6%; Score 24; DB 6; Length 344;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 6  
||:|  
Db 279 KLIF 283

## RESULT 44

US-10-512-184-71  
; Sequence 71, Application US/10512184  
; Publication No. US2005024901A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.v.  
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant  
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease  
; TITLE OF INVENTION: resistance against fungi  
; FILE REFERENCE: 3581.01US01  
; CURRENT APPLICATION NUMBER: US/10/512,184  
; CURRENT FILING DATE: 2004-10-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 71  
; LENGTH: 371  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: precursor  
; OTHER INFORMATION: fusion protein comprising ACE - linker -  
; OTHER INFORMATION: scFv PL2.  
US-10-512-184-71

Query Match 70.6%; Score 24; DB 6; Length 371;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7  
||:|  
Db 307 KLLVFFA 313

## RESULT 45

US-11-080-991-16  
; Sequence 16, Application US/11080991  
; Publication No. US20050266437A1  
; GENERAL INFORMATION:  
; APPLICANT: Veiby, Petter Ole  
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST  
; TITLE OF INVENTION: AND OVARIAN CANCER  
; FILE REFERENCE: MRI-039  
; CURRENT APPLICATION NUMBER: US/11/080,991  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: US/10/176,847  
; PRIOR FILING DATE: 2002-06-21  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-080-991-16

Query Match 70.6%; Score 24; DB 7; Length 374;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7  
||:|  
Db 343 KPLIEFA 349

## RESULT 46

US-10-995-561-1005  
; Sequence 1005, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1005  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-1005

Query Match 70.6%; Score 24; DB 6; Length 396;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
|||  
Db 78 KKLVPFA 84

RESULT 47

US-11-082-389-198  
; Sequence 198, Application US/11082389  
; Publication No. US20050244935A1

; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus

; APPLICANT: Kroeger, Burkhard  
; APPLICANT: Schroder, Hartwig

; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberkauer, Gregor

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; TITLE OF INVENTION: TRANSPORT

; FILE REFERENCE: BGI-131CPCN  
; CURRENT APPLICATION NUMBER: US/11/082,389  
; CURRENT FILING DATE: 2005-03-16

; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27

; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446

; SEQ ID NO 198  
; LENGTH: 453  
; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum  
US-11-082-389-198

Query Match 70.6%; Score 24; DB 7; Length 453;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVFFFA 7  
|||||  
Db 401 LVFFFA 405

RESULT 48

US-11-069-642-19  
; Sequence 19, Application US/11069642  
; Publication No. US20050260626A1

; GENERAL INFORMATION:  
; APPLICANT: LORENS, JAMES B.

; APPLICANT: PRAY, TODD R.  
; APPLICANT: KINSELLA, TODD M.

; APPLICANT: BENNETT, MARK K.  
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR

; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION  
; FILE REFERENCE: RIGI-022CIP3  
; CURRENT APPLICATION NUMBER: US/11/069,642

; CURRENT FILING DATE: 2005-02-28  
; PRIOR APPLICATION NUMBER: 10/232,758

; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: 10/422,536

; PRIOR FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: 09/800,770

; PRIOR FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: 60/187,130

; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 168

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 476

; TYPE: PRT  
; ORGANISM: Pyrococcus horikoshii OT3  
US-11-069-642-19

Query Match 70.6%; Score 24; DB 7; Length 476;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVPF 6  
|||  
Db 346 KKLVPF 351

RESULT 49

US-10-995-561-959  
; Sequence 959, Application US/10995561  
; Publication No. US20050272034A1

; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 959  
; LENGTH: 481

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-959

Query Match 70.6%; Score 24; DB 6; Length 481;  
Best Local Similarity 66.7%; Pred. No. 2.8e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KLVFFFA 7  
|||  
Db 275 KLVFFFA 280

RESULT 50

US-10-793-626-24  
; Sequence 24, Application US/10793626  
; Publication No. US20050255478A1

```
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-24

Query Match          70.6%; Score 24; DB 6; Length 482;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
        ||::||
DB      387 KKVILFA 393

RESULT 51
US-10-719-311-16
; Sequence 16, Application US/10719311
; Publication No. US20040086490A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John A.
;          Kotin, Robert M.
;          Safir, Brian
; TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Needle & Rosenberg
; STREET: 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/719,311
; FILING DATE: 20-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,747
; FILING DATE: 26-Nov-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Selby, Elizabeth
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 14014.0252
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 598 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: protein
; FEATURE:
; OTHER INFORMATION: AAV4 capsid protein VP2
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-719-311-16
```

```
Query Match          70.6%; Score 24; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVP 5
        |||||
DB      32 KKLVP 36

RESULT 52
US-10-512-184-49
; Sequence 49, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase- linker
; OTHER INFORMATION: - scFv PL2 - cmcy/His6.
US-10-512-184-49
```

```
Query Match          70.6%; Score 24; DB 6; Length 626;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
        ||::||
DB      536 KLLVFA 542
```

```
RESULT 53
US-11-078-189-15
; Sequence 15, Application US/11078189
; Publication No. US2005027167A1
; GENERAL INFORMATION:
; APPLICANT: Bachinger, Hans Peter
; APPLICANT: Vranka, Janice
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES
; FILE REFERENCE: 08062-020001
; CURRENT APPLICATION NUMBER: US/11/078,189
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,409
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 725
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-078-189-15
```

```
Query Match          70.6%; Score 24; DB 7; Length 725;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
        ||::||
DB      366 KELLVFA 372
```

RESULT 54

```

US-10-719-311-4
; Sequence 4, Application US/10719311
; Publication No. US20040086490A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John A.
;          Kotin, Robert M.
;          Safar, Brian
; TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg
; STREET: 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/719,311
; FILING DATE: 20-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,747
; FILING DATE: 26-Nov-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Selby, Elizabeth
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 14014.0252
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 734 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: protein
; FEATURE:
; OTHER INFORMATION: AAV4 capsid protein VP1
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-719-311-4
Query Match      70.6%; Score 24; DB 6; Length 734;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVF 5
Db      168 KKLVF 172

RESULT 55
US-10-613-744-6
; Sequence 6, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307

US-10-719-311-4
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-6
Query Match      70.6%; Score 24; DB 6; Length 858;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LVFFFA 7
Db      348 LVFFFA 352

RESULT 56
US-10-821-234-975
; Sequence 975, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 975
; LENGTH: 989
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-975
Query Match      70.6%; Score 24; DB 6; Length 989;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVFFA 7
Db      311 KESVFFA 317

RESULT 57
US-11-067-811-4
; Sequence 4, Application US/11067811
; Publication No. US20050260688A1
; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A
; APPLICANT: Enshell-Schjffers, David
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HAIR GROWTH
; FILE REFERENCE: 10287-083001
; CURRENT APPLICATION NUMBER: US/11/067,811
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/548,272
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-11-067-811-4
Query Match      70.6%; Score 24; DB 7; Length 1113;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

US-10-719-311-4
; Sequence 4, Application US/10719311
; Publication No. US20040086490A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John A.
;          Kotin, Robert M.
;          Safar, Brian
; TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg
; STREET: 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/719,311
; FILING DATE: 20-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,747
; FILING DATE: 26-Nov-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Selby, Elizabeth
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 14014.0252
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 734 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: protein
; FEATURE:
; OTHER INFORMATION: AAV4 capsid protein VP1
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-719-311-4
Query Match      70.6%; Score 24; DB 6; Length 734;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVF 5
Db      168 KKLVF 172

RESULT 55
US-10-613-744-6
; Sequence 6, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307

```

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
|:|:|  
Db 572 KYLMFFA 578

## RESULT 58

US-11-040-159-20  
; Sequence 20, Application US/11040159  
; Publication No. US2005025552A1  
; GENERAL INFORMATION:  
; APPLICANT: Flynn, Peter  
; APPLICANT: Luehrsen, Kenneth  
; APPLICANT: Balint, Robert F.  
; APPLICANT: Her, Jeng-Hong  
; APPLICANT: Bebbington, Christopher R.  
; APPLICANT: Yarranton, Geoffrey I.  
; APPLICANT: Kalobios, Inc.  
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential  
; FILE REFERENCE: 021167-001730US  
; CURRENT APPLICATION NUMBER: US/11/040,159  
; CURRENT FILING DATE: 2005-01-20  
; PRIOR APPLICATION NUMBER: US 60/537,364  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/546,216  
; PRIOR FILING DATE: 2004-02-23  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence:non-natural  
; OTHER INFORMATION: synthetic secretion signal peptide designated SP2  
US-11-040-159-20

Query Match 67.6%; Score 23; DB 7; Length 21;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
|:|:|  
Db 4 KQLVVEA 10

## RESULT 59

US-10-467-657-3918  
; Sequence 3918, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 3918  
; LENGTH: 186  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3918

Query Match 67.6%; Score 23; DB 6; Length 186;

Best Local Similarity 57.1%; Pred. No. 1.8e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
|:|:|  
Db 2 KKLIFAA 8

## RESULT 60

US-10-980-388-65  
; Sequence 65, Application US/10980388  
; Publication No. US20050255490A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Hiebsch, Ronald R.  
; APPLICANT: Lind, Peter  
; APPLICANT: Kaytes, Paul S.  
; APPLICANT: Ruff, Valerie  
; APPLICANT: Huff, Rita M.  
; APPLICANT: Wood, Linda S.  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl  
; FILE REFERENCE: 00325.US1  
; CURRENT APPLICATION NUMBER: US/10/980,388  
; CURRENT FILING DATE: 2004-11-02  
; PRIOR APPLICATION NUMBER: US/09/791,932  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/184,305  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,304  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,303  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,397  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,247  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/188,880  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/217,369  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/217,370  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/218,492  
; PRIOR FILING DATE: 2000-07-20  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 65  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-980-388-65

Query Match 67.6%; Score 23; DB 6; Length 187;  
Best Local Similarity 57.1%; Pred. No. 1.8e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
|:|:|  
Db 178 KRYVYFA 184

## RESULT 61

US-10-467-657-8102  
; Sequence 8102, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8102  
; LENGTH: 216  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8102

Query Match 67.6%; Score 23; DB 6; Length 216;  
Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVFFPA 7  
|:|:|  
Db 18 LIPFA 22

RESULT 62  
US-10-467-657-290  
; Sequence 290, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 290  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-290

Query Match 67.6%; Score 23; DB 6; Length 221;  
Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVFFPA 7  
|:|:|  
Db 41 LIPFA 45

RESULT 63  
US-10-467-657-5750  
; Sequence 5750, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 5750  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-5750

Query Match 67.6%; Score 23; DB 6; Length 221;  
Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVFFPA 7  
|:|:|  
Db 41 LIPFA 45

RESULT 64  
US-10-793-626-1430  
; Sequence 1430, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; FILE REFERENCE: PUB3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1430  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1430

Query Match 67.6%; Score 23; DB 6; Length 224;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLFFPA 7  
|:|:|  
Db 107 KRLIFVA 113

RESULT 65  
US-10-467-657-330  
; Sequence 330, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 330  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-330

Query Match 67.6%; Score 23; DB 6; Length 269;



Best Local Similarity 80.0%; Pred. No. 2.6e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 2 KLVFF 6  
|:|:|  
Db 11 KLVFF 15

RESULT 66  
US-10-821-234-1419  
; Sequence 1419, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pc\_seq\_genes Version 1.0  
; SEQ ID NO 1419  
; LENGTH: 271  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1419

Query Match 67.6%; Score 23; DB 6; Length 271;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFF 6  
|:|:|  
Db 109 KLVFF 114

RESULT 67  
US-10-632-150-46  
; Sequence 46, Application US/10632150  
; Publication No. US20050251871A1  
; GENERAL INFORMATION:  
; APPLICANT: Chiaux, D.  
; APPLICANT: Pagano, M.  
; APPLICANT: Latres, E.  
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS  
; FILE REFERENCE: 5914-081  
; CURRENT APPLICATION NUMBER: US/10/632,150  
; CURRENT FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US/09/385,219  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/098,355  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 60/118,568  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: 60/124,449  
; PRIOR FILING DATE: 1999-03-15  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 272  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-632-150-46

Query Match 67.6%; Score 23; DB 6; Length 272;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 7

Db 211 KLVFF 216  
|:|:|

RESULT 68  
US-11-073-457-46  
; Sequence 46, Application US/11073457  
; Publication No. US20050260556A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, M.  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS  
; FILE REFERENCE: 5914-090-999  
; CURRENT APPLICATION NUMBER: US/11/073,457  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR APPLICATION NUMBER: 10/042,417  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 60/260,179  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 272  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-073-457-46

Query Match 67.6%; Score 23; DB 7; Length 272;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 7  
|:|:|  
Db 211 KLVFF 216

RESULT 69  
US-11-073-460-46  
; Sequence 46, Application US/11073460  
; Publication No. US20050272066A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, M.  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS  
; FILE REFERENCE: 5914-090-999  
; CURRENT APPLICATION NUMBER: US/11/073,460  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR APPLICATION NUMBER: 10/042,417  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 60/260,179  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 272  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-073-460-46

Query Match 67.6%; Score 23; DB 7; Length 272;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 7  
|:|:|  
Db 211 KLVFF 216

RESULT 70  
US-10-485-517-234  
; Sequence 234, Application US/10485517  
; Publication No. US20050256299A1  
; GENERAL INFORMATION:

```
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-234

Query Match      67.6%; Score 23; DB 6; Length 337;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVPF 6
DB      174 KKVAFP 179

RESULT 71
US-10-770-726-55
; Sequence 55, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Eugene
; APPLICANT: Lib, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-55

Query Match      67.6%; Score 23; DB 6; Length 346;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPF 5
DB      342 KKLIF 346

RESULT 72
US-10-821-234-1105
; Sequence 1105, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Lebat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Suban
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt_SEQ_genes Version 1.0
; SEQ ID NO 1105
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1105

Query Match      67.6%; Score 23; DB 6; Length 370;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 KLVFFA 7
DB      115 RLFFFA 120

RESULT 73
US-10-793-626-1056
; Sequence 1056, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: F03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1056

Query Match      67.6%; Score 23; DB 6; Length 400;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 KLVFF 6
DB      7 KIVFF 11

RESULT 74
US-10-467-657-9070
; Sequence 9070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 9070
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9070
```

Query Match 67.6%; Score 23; DB 6; Length 402;  
 Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVFPA 7  
 Db 262 RHIVFFA 268

RESULT 75  
 US-10-467-657-6352  
 ; Sequence 6352, Application US/10467657  
 ; Publication No. US20050260581A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SPA  
 ; APPLICANT: FONTANA Maria Rita  
 ; APPLICANT: PIZZA Mariagrazia  
 ; APPLICANT: MASIGNANI Vega  
 ; APPLICANT: MONACI Elisabetta  
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/467,657  
 ; CURRENT FILING DATE: 2003-08-11  
 ; PRIOR APPLICATION NUMBER: GB-0103424.8  
 ; PRIOR FILING DATE: 2001-02-12  
 ; NUMBER OF SEQ ID NOS: 9218  
 ; SOFTWARE: SeqWin99, version 1.04  
 ; SEQ ID NO 6352  
 ; LENGTH: 463  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria gonorrhoeae  
 US-10-467-657-6352

Query Match 67.6%; Score 23; DB 6; Length 463;  
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVVFFA 7  
 Db 369 LIFFA 373

Search completed: December 29, 2005, 18:50:14  
 Job time : 4.83871 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 95.4032 Seconds  
(without alignments)  
32.238 Million cell updates/sec

Title: US-10-009-122-2

Perfect score: 34

Sequence: 1 KKLVPFA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	100.0	7	4	AAB48475
2	34	100.0	7	4	AAB82624
3	34	100.0	7	5	AAU96812
4	34	100.0	7	5	AAU11649
5	34	100.0	7	6	AAE35439
6	34	100.0	7	8	ADQ37314
7	34	100.0	7	8	ADQ37263
8	34	100.0	7	9	ADY37922
9	34	100.0	9	6	ABU79063
10	34	100.0	9	7	ABW00197
11	31	91.2	277	7	ADK82706
12	30	88.2	7	2	AAW02312
13	30	88.2	7	2	AAW89376
14	30	88.2	7	5	ABG71007
15	30	88.2	7	5	ABW05155
16	30	88.2	7	8	ADJ64058
17	30	88.2	7	8	ADQ37351
18	30	88.2	7	9	ADZ08903
19	30	88.2	8	2	AAW02310
20	30	88.2	8	2	AAW89374
21	30	88.2	8	5	ABG71005
22	30	88.2	8	5	ABW05153
23	30	88.2	8	8	ADJ64056
24	30	88.2	8	8	ADQ37349

25	30	88.2	9	2	AAR45239	Aar45239	Mutant am
26	30	88.2	9	4	AAB48493	Aab48493	Antifibri
27	30	88.2	9	5	AAU11667	Aau11667	Peptide #
28	30	88.2	9	6	ABP57517	Abp57517	Different
29	30	88.2	9	6	ABU79053	Abu79053	Aggregati
30	30	88.2	9	6	AAE35436	Aae35436	Abeta pep
31	30	88.2	9	7	ABW00187	Abw00187	Peptide #
32	30	88.2	9	8	ADI35874	Adi35874	Amyloid b
33	30	88.2	9	8	ADQ37260	Adq37260	Vaccine a
34	30	88.2	9	8	ADQ37332	Adq37332	Antifibri
35	30	88.2	10	4	AAB46226	Aab46226	Human APP
36	30	88.2	10	4	AAB46225	Aab46225	Human APP
37	30	88.2	10	4	AAB46224	Aab46224	Human APP
38	30	88.2	10	4	AAB46227	Aab46227	Human APP
39	30	88.2	10	4	AAB82641	Aab82641	All-D pep
40	30	88.2	10	5	AAU96829	Aau96829	Amyloid t
41	30	88.2	10	6	ABP57511	Abp57511	Different
42	30	88.2	10	6	AAE35455	Aae35455	Abeta pep
43	30	88.2	10	8	ADQ37280	Adq37280	Vaccine a
44	30	88.2	10	8	ADQ37371	Adq37371	Amyloid-b
45	30	88.2	10	8	ADQ37374	Adq37374	Amyloid-b
46	30	88.2	10	9	ADY37939	Ady37939	Amyloid-c
47	30	88.2	11	2	AAW32560	Aaw32560	Anti-amyl
48	30	88.2	11	5	AAU99431	Aau99431	Human amy
49	30	88.2	11	5	AAE29504	Aae29504	Amyloid b
50	30	88.2	11	6	ABU79013	Abu79013	Amyloidog
51	30	88.2	11	7	ABR84683	AbR84683	Aggregati
52	30	88.2	11	7	ABW00147	Abw00147	Amyloid-b
53	30	88.2	12	6	AAE35464	Aae35464	Abeta pep
54	30	88.2	12	6	AAE35435	Aae35435	Abeta pep
55	30	88.2	12	6	AAE35466	Aae35466	Abeta pep
56	30	88.2	12	7	ADD20745	Add20745	Human bet
57	30	88.2	12	7	ADZ020744	Adz020744	Human bet
58	30	88.2	12	8	ADJ71476	Adj71476	N-termina
59	30	88.2	12	8	ADQ37407	Adq37407	Amyloid-b
60	30	88.2	12	8	ADQ37289	Adq37289	Vaccine a
61	30	88.2	12	8	ADQ37259	Adq37259	Vaccine a
62	30	88.2	12	9	ADZ08890	Adz08890	Human bet
63	30	88.2	13	6	ADA37467	Ada37467	Human amy
64	30	88.2	13	8	ADJ71477	Adj71477	N-termina
65	30	88.2	13	8	ADJ71464	Adj71464	N-termina
66	30	88.2	14	6	ADA89887	Ada89887	Beta-A4 s
67	30	88.2	14	8	ADJ71452	Adj71452	N-termina
68	30	88.2	14	8	ADJ71465	Adj71465	N-termina
69	30	88.2	14	8	ADJ71478	Adj71478	N-termina
70	30	88.2	14	9	ADZ08889	Adz08889	Human bet
71	30	88.2	15	2	AAW89358	Aaw89358	Beta-amyl
72	30	88.2	15	6	ABU79064	Abu79064	Aggregati
73	30	88.2	15	6	ABU79059	Abu79059	Aggregati
74	30	88.2	15	6	ABU79060	Abu79060	Aggregati
75	30	88.2	15	6	ABU79055	Abu79055	Aggregati
76	30	88.2	15	6	ABU79056	Abu79056	Aggregati
77	30	88.2	15	7	ABU79062	Abu79062	Aggregati
78	30	88.2	15	7	ABW00190	Abw00190	Peptide #
79	30	88.2	15	7	ABW00198	Abw00198	Peptide #
80	30	88.2	15	7	ABW00189	Abw00189	Peptide #
81	30	88.2	15	7	ABW00193	Abw00193	Peptide #
82	30	88.2	15	7	ABW00196	Abw00196	Peptide #
83	30	88.2	15	7	ABW00194	Abw00194	Peptide #
84	30	88.2	15	8	ADJ71466	Adj71466	N-termina
85	30	88.2	15	8	ADJ71453	Adj71453	N-termina
86	30	88.2	15	8	ADJ71479	Adj71479	N-termina
87	30	88.2	15	8	ADJ71440	Adj71440	N-termina
88	30	88.2	16	5	AAE26330	Aae26330	Human bet
89	30	88.2	16	8	ADJ71454	Adj71454	N-termina
90	30	88.2	16	8	ADJ71480	Adj71480	N-termina
91	30	88.2	16	8	ADJ71441	Adj71441	N-termina
92	30	88.2	16	8	ADJ71467	Adj71467	N-termina
93	30	88.2	16	8	ADJ71428	Adj71428	N-termina
94	30	88.2	17	2	AAW54703	Aaw54703	Beta-amyl
95	30	88.2	17	2	AAW18880	Aaw18880	Beta-amyl
96	30	88.2	17	4	AAB91774	Aab91774	Amyloid b
97	30	88.2	17	4	AAB91807	Aab91807	Amyloid b

98	30	88.2	17	4	AAB48346	Aab48346 Beta-amyl	171	30	88.2	28	4	AAB91800	Aab91800 Amyloid b
99	30	88.2	17	5	AB804911	Ab804911 Human amy	172	30	88.2	28	4	AAB49396	Aab49396 Human amy
100	30	88.2	17	6	AA35468	Abeta pep	173	30	88.2	28	5	AAE21439	Abeta pep
101	30	88.2	17	6	AB99611	Peptide d	174	30	88.2	28	5	AB76030	Beta amyl
102	30	88.2	17	8	ADG93165	Novel exp	175	30	88.2	28	5	AAO18476	Human bet
103	30	88.2	17	8	ADG65843	Amyloid B	176	30	88.2	28	5	AAU76484	Amino aci
104	30	88.2	17	8	ADN02827	Mammalian	177	30	88.2	28	5	AB804910	Human amy
105	30	88.2	17	8	ADQ37291	Vaccine a	178	30	88.2	28	5	AAE26081	Beta amyl
106	30	88.2	17	8	ADQ37291	Vaccine a	179	30	88.2	28	5	AAE26081	Beta amyl
107	30	88.2	18	3	AA310963	Beta-amyl	180	30	88.2	28	5	AB77991	Fragment
108	30	88.2	18	3	AAW18882	AEDANS-be	181	30	88.2	28	5	AB77991	Fragment
109	30	88.2	19	2	AAW18882	Trp-Beta-	182	30	88.2	28	6	AAE35672	Human bet
110	30	88.2	19	3	AAW18882	Trp-Beta-	183	30	88.2	28	6	AAE35672	Human bet
111	30	88.2	19	3	AAW18882	Trp-Beta-	184	30	88.2	28	6	AAE35672	Human bet
112	30	88.2	19	3	AAW18882	Trp-Beta-	185	30	88.2	28	6	AAE35672	Human bet
113	30	88.2	19	4	AA346201	Human APP	186	30	88.2	28	6	ABG72234	Wild-type
114	30	88.2	19	4	AA346201	Human APP	187	30	88.2	28	6	ABG72234	Wild-type
115	30	88.2	19	4	AA346201	Human APP	188	30	88.2	28	6	ABG72234	Wild-type
116	30	88.2	19	4	AA346201	Human APP	189	30	88.2	28	6	ABG72234	Wild-type
117	30	88.2	19	4	AA346201	Human APP	190	30	88.2	28	6	ABG72234	Wild-type
118	30	88.2	19	4	AA346201	Human APP	191	30	88.2	28	6	ABG72234	Wild-type
119	30	88.2	19	4	AA346201	Human APP	192	30	88.2	28	6	ABG72234	Wild-type
120	30	88.2	19	4	AA346201	Human APP	193	30	88.2	28	6	ABG72234	Wild-type
121	30	88.2	19	4	AA346201	Human APP	194	30	88.2	28	6	ABG72234	Wild-type
122	30	88.2	19	4	AA346201	Human APP	195	30	88.2	28	6	ABG72234	Wild-type
123	30	88.2	19	4	AA346201	Human APP	196	30	88.2	28	6	ABG72234	Wild-type
124	30	88.2	19	4	AA346201	Human APP	197	30	88.2	28	6	ABG72234	Wild-type
125	30	88.2	19	4	AA346201	Human APP	198	30	88.2	28	6	ABG72234	Wild-type
126	30	88.2	19	4	AA346201	Human APP	199	30	88.2	28	6	ABG72234	Wild-type
127	30	88.2	19	4	AA346201	Human APP	200	30	88.2	28	6	ABG72234	Wild-type
128	30	88.2	19	4	AA346201	Human APP	201	30	88.2	28	6	ABG72234	Wild-type
129	30	88.2	19	4	AA346201	Human APP	202	30	88.2	28	6	ABG72234	Wild-type
130	30	88.2	19	4	AA346201	Human APP	203	30	88.2	28	6	ABG72234	Wild-type
131	30	88.2	19	4	AA346201	Human APP	204	30	88.2	28	6	ABG72234	Wild-type
132	30	88.2	19	4	AA346201	Human APP	205	30	88.2	28	6	ABG72234	Wild-type
133	30	88.2	19	4	AA346201	Human APP	206	30	88.2	28	6	ABG72234	Wild-type
134	30	88.2	19	4	AA346201	Human APP	207	30	88.2	28	6	ABG72234	Wild-type
135	30	88.2	19	4	AA346201	Human APP	208	30	88.2	28	6	ABG72234	Wild-type
136	30	88.2	19	4	AA346201	Human APP	209	30	88.2	28	6	ABG72234	Wild-type
137	30	88.2	19	4	AA346201	Human APP	210	30	88.2	28	6	ABG72234	Wild-type
138	30	88.2	19	4	AA346201	Human APP	211	30	88.2	28	6	ABG72234	Wild-type
139	30	88.2	19	4	AA346201	Human APP	212	30	88.2	28	6	ABG72234	Wild-type
140	30	88.2	19	4	AA346201	Human APP	213	30	88.2	28	6	ABG72234	Wild-type
141	30	88.2	19	4	AA346201	Human APP	214	30	88.2	28	6	ABG72234	Wild-type
142	30	88.2	19	4	AA346201	Human APP	215	30	88.2	28	6	ABG72234	Wild-type
143	30	88.2	19	4	AA346201	Human APP	216	30	88.2	28	6	ABG72234	Wild-type
144	30	88.2	19	4	AA346201	Human APP	217	30	88.2	28	6	ABG72234	Wild-type
145	30	88.2	19	4	AA346201	Human APP	218	30	88.2	28	6	ABG72234	Wild-type
146	30	88.2	19	4	AA346201	Human APP	219	30	88.2	28	6	ABG72234	Wild-type
147	30	88.2	19	4	AA346201	Human APP	220	30	88.2	28	6	ABG72234	Wild-type
148	30	88.2	19	4	AA346201	Human APP	221	30	88.2	28	6	ABG72234	Wild-type
149	30	88.2	19	4	AA346201	Human APP	222	30	88.2	28	6	ABG72234	Wild-type
150	30	88.2	19	4	AA346201	Human APP	223	30	88.2	28	6	ABG72234	Wild-type
151	30	88.2	19	4	AA346201	Human APP	224	30	88.2	28	6	ABG72234	Wild-type
152	30	88.2	19	4	AA346201	Human APP	225	30	88.2	28	6	ABG72234	Wild-type
153	30	88.2	19	4	AA346201	Human APP	226	30	88.2	28	6	ABG72234	Wild-type
154	30	88.2	19	4	AA346201	Human APP	227	30	88.2	28	6	ABG72234	Wild-type
155	30	88.2	19	4	AA346201	Human APP	228	30	88.2	28	6	ABG72234	Wild-type
156	30	88.2	19	4	AA346201	Human APP	229	30	88.2	28	6	ABG72234	Wild-type
157	30	88.2	19	4	AA346201	Human APP	230	30	88.2	28	6	ABG72234	Wild-type
158	30	88.2	19	4	AA346201	Human APP	231	30	88.2	28	6	ABG72234	Wild-type
159	30	88.2	19	4	AA346201	Human APP	232	30	88.2	28	6	ABG72234	Wild-type
160	30	88.2	19	4	AA346201	Human APP	233	30	88.2	28	6	ABG72234	Wild-type
161	30	88.2	19	4	AA346201	Human APP	234	30	88.2	28	6	ABG72234	Wild-type
162	30	88.2	19	4	AA346201	Human APP	235	30	88.2	28	6	ABG72234	Wild-type
163	30	88.2	19	4	AA346201	Human APP	236	30	88.2	28	6	ABG72234	Wild-type
164	30	88.2	19	4	AA346201	Human APP	237	30	88.2	28	6	ABG72234	Wild-type
165	30	88.2	19	4	AA346201	Human APP	238	30	88.2	28	6	ABG72234	Wild-type
166	30	88.2	19	4	AA346201	Human APP	239	30	88.2	28	6	ABG72234	Wild-type
167	30	88.2	19	4	AA346201	Human APP	240	30	88.2	28	6	ABG72234	Wild-type
168	30	88.2	19	4	AA346201	Human APP	241	30	88.2	28	6	ABG72234	Wild-type
169	30	88.2	19	4	AA346201	Human APP	242	30	88.2	28	6	ABG72234	Wild-type
170	30	88.2	19	4	AA346201	Human APP	243	30	88.2	28	6	ABG72234	Wild-type



XX Chalfour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 XX  
 XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 XX which elicits production of antibodies to prevent fibrillogenesis and  
 XX associated cellular toxicity.  
 XX  
 XX Disclosure; Page 10; 31pp; English.  
 XX  
 XX The present sequence is that of an all-D peptide suitable for use for  
 XX preparing vaccines for preventing or treating Alzheimer's disease and  
 XX other amyloid related disorders in humans. It is based on a portion of  
 XX amyloid-beta peptide (see AAB82622), and may be modified by removing or  
 XX inserting 1 or more amino acid residues, or by substituting 1 or more  
 XX amino acid residues with other amino acid residues or non-amino acid  
 XX fragments. Vaccines of the invention are produced using 'non-self',  
 XX peptides synthesised from the unnatural D-configuration amino acids to  
 XX avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 XX aggregated to be operative or immunogenic. They preferably interact with  
 XX at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 XX CAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 XX fragments, protein conjugates, immunogenic derivative peptides and  
 XX immunogenic peptidomimetics. Examples include all-D peptides  
 XX corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 XX 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 XX in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 XX related diseases may be localised amyloidosis, e.g. diabetes type II,  
 XX neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 XX Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 XX prion protein related disorders, or systemic amyloidosis associated with  
 XX chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 XX rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 XX amyloidosis found in long-term haemodialysis patients  
 XX  
 XX Sequence 7 AA;  
 XX  
 XX Query Match 100.0%; Score 34; DB 4; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 KKLVPFFA 7  
 XX |||||  
 XX Db 1 KKLVPFFA 7  
 XX  
 XX RESULT 3  
 XX AAU96812  
 XX ID AAU96812 standard; peptide; 7 AA.  
 XX AC AAU96812;  
 XX  
 XX 30-JUL-2002 (first entry)  
 XX  
 XX Amyloid targeting peptide #2.  
 XX  
 XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 XX transmissible cerebral amyloidosis; transmissible virus dementia;  
 XX scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 XX bovine spongiform encephalopathy; inflammation associated amyloid;  
 XX primary amyloidosis; feline spongiform encephalopathy;  
 XX Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 XX dialysis-related amyloidosis; light chain-related amyloidosis;  
 XX cerebral amyloid angiopathy.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX Misc-difference 1..7 /note= "Preferably D-form residue"  
 XX FT

XX WO200207781-A2.  
 XX 31-JAN-2002.  
 XX  
 XX 25-JUL-2001; 2001WO-CA001071.  
 XX  
 XX 25-JUL-2000; 2000US-0220808P.  
 XX  
 XX 24-JUL-2001; 2001US-00915092.  
 XX  
 XX (NEUR-) NEUROCHEM INC.  
 XX  
 XX Gervais F, Kong X, Chalfour R, Migneault D;  
 XX WPI; 2002-371447/40.  
 XX  
 XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 XX plaques and/or for the treatment of amyloidosis disorders.  
 XX  
 XX Claim 49; Page 21; 57pp; English.  
 XX  
 XX The invention relates to an amyloid-targeting imaging agent comprising an  
 XX amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 XX agent is of general formula A\_t-(A\_l)\_n\_k-z-A\_l\_a\_b (I) where z = 0 - 1;  
 XX A\_t = an amyloid targeting moiety; A\_l\_n\_k = a linker moiety; and A\_l\_a\_b  
 XX = a labelling moiety. Also included are imaging amyloid deposition or  
 XX diagnosing an amyloid-related condition in a patient involving  
 XX administering (I) to the patient, and ultrasound imaging (I) in the  
 XX patient to determine the presence of amyloid or amyloid-related condition  
 XX ; and a kit for preparing a radiopharmaceutical preparation comprising  
 XX (I), a reducing agent, a buffering agent, a transchelating agent, and  
 XX instructions for the preparation and use of the radiopharmaceutical in  
 XX the imaging of amyloid or an amyloid-related condition. The agents are  
 XX used for imaging amyloid deposition and for diagnosing an amyloid related  
 XX condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible  
 XX cerebral amyloidosis (transmissible virus dementia), familial CJD,  
 XX scrapie, transmissible mink encephalopathy, bovine spongiform  
 XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 XX primary amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 XX cerebral amyloidosis, light chain-related amyloidosis, cerebral  
 XX dialysis-related amyloidosis, the agents are capable of crossing the blood-brain  
 XX amyloid angiopathy. The agents are capable of binding specifically to amyloid plaques. The  
 XX barrier and are capable of binding specifically to amyloid plaques. The  
 XX present sequence is a peptide forming the amyloid targeting moiety of the  
 XX agent of the invention  
 XX  
 XX Sequence 7 AA;  
 XX  
 XX Query Match 100.0%; Score 34; DB 5; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 KKLVPFFA 7  
 XX |||||  
 XX Db 1 KKLVPFFA 7  
 XX  
 XX RESULT 4  
 XX AAU11649  
 XX ID AAU11649 standard; peptide; 7 AA.  
 XX AC AAU11649;  
 XX  
 XX 09-APR-2002 (first entry)  
 XX  
 XX Peptide #2, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 XX  
 XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 XX CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.  
 XX  
 XX Synthetic.  
 XX OS





XX	15-JUL-2004.	XX	ADQ37263;	XX
PD		AC		
XX		XX	07-OCT-2004 (first entry)	
PF		DT		
XX		XX		
PR	24-DEC-2003; 2003WO-CA002021.	DE	Vaccine antigen amyloid-beta related amino acid sequence.	
XX		XX		
PR	24-DEC-2002; 2002US-0436379P.	KW	amyloid-beta; amyloid-beta related disease;	
PR	23-JUN-2003; 2003US-0482214P.	KW	amyloid-beta fibril formation; immune response; neurotropic;	
XX		KW	neuroprotective; cerebroprotective; haemostatic; ophthalmological;	
XX		KW	antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;	
XX		KW	anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;	
PA	(NEUR-) NEUROCHEM INT LTD.	KW	cardiant; antidepressant; endocrine; hypnotic;	
XX		KW	amyloid-beta fibril formation modulator; immune system modulator;	
XX	Gervais F, Bellini F;	KW	Alzheimer's disease; mild cognitive impairment;	
XX	WPI; 2004-543342/52.	KW	mild-to-moderate cognitive impairment; vascular dementia;	
XX		KW	cerebral amyloid angiopathy; hereditary cerebral haemorrhage;	
PT	Composition for treating e.g. Alzheimer's disease comprises first agent	KW	senile dementia; Down's syndrome; inclusion body myositis;	
PT	that prevents or treats amyloid-beta related disease and second agent	KW	age-related macular degeneration; hypothyroidism;	
PT	that is either a peptide or peptidomimetic or an immune system modulator.	KW	cerebrovascular disease; cardiovascular disease; memory loss; anxiety;	
XX		KW	behavioural dysfunction; neurological condition; psychological condition;	
PS	Disclosure; Page 69; 143pp; English.	KW	vaccine antigen.	
XX		OS	Synthetic.	
CC	The present invention describes compositions (C) comprising: (a) a first	XX		
CC	agent (a1) that prevents or treats amyloid-beta related disease; and (b)	XX		
CC	a second agent (a2) that is: (i) a peptide or peptidomimetic that	XX		
CC	modulates amyloid-beta fibril formation or induces a prophylactic or	OS		
CC	therapeutic immune response against amyloid-beta fibril formation; or	XX		
CC	(ii) an immune system modulator that prevents or inhibits amyloid-beta	PH		
CC	fibril formation. Also described is a kit comprising (C). (C) have	FT		
CC	neurotropic, neuroprotective, cerebroprotective, haemostatic,	FT		
CC	ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,	XX		
CC	uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,	XX		
CC	neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,	XX		
CC	and can be used as amyloid-beta fibril formation modulators, and as	XX		
CC	immune system modulators. (C) can be used for preventing or treating an	XX		
CC	amyloid-beta related disease e.g. Alzheimer's disease (including sporadic	PD		
CC	(non-hereditary) or familial (hereditary)), mild cognitive impairment,	XX		
CC	mild-to-moderate cognitive impairment, vascular dementia, cerebral	XX		
CC	amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,	XX		
CC	Down's syndrome, inclusion body myositis, age-related macular	XX		
CC	degeneration, or a condition associated with Alzheimer's disease	XX		
CC	(including hypothyroidism, cerebrovascular disease, cardiovascular	XX		
CC	disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,	XX		
CC	aggression, or incontinence), a neurological condition (e.g. Huntington's	XX		
CC	disease, amyotrophic lateral sclerosis, acquired immunodeficiency,	XX		
CC	Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia	XX		
CC	with Lewy bodies, altered muscle tone, seizures, sensory loss, visual	XX		
CC	field deficits, incoordination, gait disturbance, transient ischaemic	XX		
CC	attack or stroke, transient alertness, attention deficit, frequent falls,	XX		
CC	syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural	XX		
CC	haematoma, brain tumour, posttraumatic brain injury, or posthypoxic	XX		
CC	damage), or a psychological condition (e.g. depression, delusions,	XX		
CC	illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep	XX		
CC	disturbance, insomnia, behavioural disinhibition, poor insight, suicidal	XX		
CC	ideation, depressed mood, irritability, anhedonia, social withdrawal, or	XX		
CC	excessive guilt)) in a subject e.g. human having a genomic mutation in an	XX		
CC	amyloid precursor protein gene, an ApoE gene, or a presenilin gene;	XX		
CC	having amyloid-beta deposits. The present sequence represents a peptide	XX		
CC	that can be used as an antifebrile amyloidosis inhibiting peptide	XX		
CC	in the exemplification of the present invention.	XX		
XX		XX		
SQ	Sequence 7 AA;	XX		
	Query Match 100.0%; Score 34; DB 8; Length 7;	XX		
	Best Local Similarity 100.0%; Pred. No. 2e+06;	XX		
	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX		
QY	1 KKLVPFA 7	XX		
DB	1 KKLVPFA 7	XX		
RESULT 7		XX		
ADQ37263		XX		
ID	ADQ37263 standard; peptide; 7 AA.	XX		

CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as a vaccine antigen in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7  
 Db 1 KKLVFPA 7

RESULT 8  
 ADY37922  
 ID ADY37922 standard; peptide; 7 AA.  
 XX  
 AC ADY37922;  
 XX  
 DT 19-MAY-2005 (first entry)  
 XX  
 DE Amyloid-targeting peptide, SEQ ID NO:2, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 KW transmissible spongiform encephalopathy; scrapie; BSE;  
 KW Alzheimer's disease; neurological disease; amyloidosis;  
 KW non-insulin dependent diabetes; metabolic disorder.  
 XX  
 OS Synthetic.

XX US2005048000-A1.  
 XX  
 XX 03-MAR-2005.  
 XX  
 XX 03-DEC-2003; 2003US-00728028.  
 XX  
 XX 25-JUL-2000; 2000US-0220808P.  
 XX  
 XX 24-JUL-2001; 2001US-00915092.  
 XX  
 XX 29-JAN-2003; 2003US-0443291P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX  
 XX Gervais F, Kong X, Chalifour R, Migneault D;  
 XX  
 XX WPI; 2005-212201/22.  
 XX

XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform  
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.

XX Disclosure; SEQ ID NO 2; 34pp; English.

XX The invention relates to an amyloid-targeting imaging agent. The imaging  
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 CC a labeling moiety via a linking moiety, and is preferably able to cross  
 CC the blood-brain barrier. The invention also relates to a kit for  
 CC preparing a radiopharmaceutical preparation from the imaging agent of the  
 CC invention, a method for imaging amyloid deposition in a patient and a  
 CC method for diagnosing an amyloid-related condition in a patient. The

CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,  
 CC transmissible cerebral amyloidoses (also known as transmissible virus  
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 CC mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7  
 Db 1 KKLVFPA 7

RESULT 9  
 ABU79063  
 ID ABU79063 standard; peptide; 9 AA.  
 XX  
 AC ABU79063;  
 XX  
 DT 17-JUN-2003 (first entry)  
 XX  
 DE Aggregation blocking peptide #15.

XX Amyloid formation; amyloid-like deposit; Alzheimer's disease;  
 KW pathological beta-sheet rich conformation; Down's syndrome;  
 KW amyloidosis disorder; human prion disease; Kuru; CJD;  
 KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;  
 KW prion associated human neurodegenerative disease; animal prion disease;  
 KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;  
 KW chronic wasting disease.

XX Unidentified.  
 XX  
 XX US6462171-B1.  
 XX  
 XX 08-OCT-2002.  
 XX  
 XX 12-DEC-1996; 96US-00766596.  
 XX  
 XX 07-JUN-1995; 95US-00478326.  
 XX  
 XX 10-APR-1996; 96US-00630645.  
 XX  
 XX (UNY ) UNIV NEW YORK STATE.  
 XX  
 XX Soto-Jara C, Baumann MH, Frangione B;  
 XX  
 XX WPI; 2003-379012/36.

XX Novel inhibitory peptides which inhibit and structurally block abnormal  
 PT folding of protein into amyloid or amyloid-like deposit and into  
 PT pathological beta-sheet rich conformation, useful for treating  
 PT Alzheimer's disease.

XX Disclosure; Col 51-52; 51pp; English.

XX The invention describes an isolated inhibitory peptide (I) which  
 CC interacts with a hydrophobic beta-sheet forming cluster of amino acid  
 CC residues on a protein or peptide for amyloid or amyloid-like deposit  
 CC formation, and inhibits or structurally blocks the abnormal folding of

CC proteins and peptides into amyloid or amyloid-like deposits and into  
 CC pathological beta-sheet-rich conformation. (I) is useful for disorders or  
 CC diseases associated with abnormal protein folding into amyloid or amyloid  
 CC -like deposits or into pathological beta-sheet-rich precursors of such  
 CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis  
 CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease  
 CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated  
 CC human neurodegenerative diseases as well as animal prion diseases such as  
 CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and  
 CC chronic wasting disease of mule deer and elk. (I) is also useful for  
 CC detecting and diagnosing the presence or absence of amyloid or amyloid-  
 CC like deposits in vivo and its precursors. This is the amino acid sequence  
 CC of peptide associated with the inhibition of amyloid or amyloid like  
 CC deposits  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 34; DB 6; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7  
 |||||  
 Db 1 KKLVEFFA 7

RESULT 10  
 ABW00197  
 ID ABW00197 standard; peptide; 9 AA.

AC ABW00197;

XX 15-JAN-2004 (first entry)

DE Peptide #15 used in the invention.

XX Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;  
 KW Alzheimer's disease.

XX Unidentified.

XX US2003087407-A1.

XX 08-MAY-2003.

XX 06-SEP-2002; 2002US-00235483.

XX 07-JUN-1995; 95US-00478326.

XX 10-APR-1996; 96US-00630645.

XX 12-DEC-1996; 96US-00766596.

XX (UYNV ) UNIV NEW YORK STATE.

XX Soto-Jara C, Baumann MH, Frangione B;

XX WPI; 2003-616149/58.

XX New inhibitory peptide, useful for preparing a composition for  
 PT diagnosing, preventing or treating disorders associated with amyloid-like  
 PT fibril deposits, e.g. Alzheimer's disease, or prion related  
 PT encephalopathies.

XX Claim 1; Page 28; 52pp; English.

XX The invention relates to inhibitory peptide comprising a portion of at  
 CC least three amino acid residues and a sequence predicted not to adopt a  
 CC beta-sheet structure that associates with a hydrophobic beta-sheet  
 CC cluster on a protein or peptide involved in the abnormal folding of the  
 CC beta-sheet structure, to structurally block the abnormal folding of the  
 CC protein or peptide. The inhibitory peptide is useful for preparing a  
 CC composition for preventing, treating or detecting disorders or diseases  
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and  
 CC prion related encephalopathies. The invention is also useful in gene

CC therapy. The present sequence is a peptide used in the invention  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 34; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7  
 |||||  
 Db 1 KKLVEFFA 7

RESULT 11  
 ADK82706  
 ID ADK82706 standard; protein; 277 AA.

XX ADK82706;

XX 06-MAY-2004 (first entry)

XX Beta-amyloid peptide antibody sequence #2.

XX fusion antibody; senile dementia; beta-amyloid peptide; fibre;  
 KW immunocell.

XX Unidentified.

XX CN1396183-A.

XX 12-FEB-2003.

XX 13-JUL-2001; 2001CN-00120278.

XX 13-JUL-2001; 2001CN-00120278.

XX (ZHAN/) ZHANG X.

XX Zhang X, Zhang J;

XX WPI; 2003-442233/42.

XX Human fusion antibody for reducing cerebral amyloid fibers associated  
 PT with senile dementia.

XX Disclosure; Page 8; 26pp; Chinese.

XX The invention relates to a human fusion antibody for preventing and  
 CC treating senile dementia. The antibody recognises and binds the beta-  
 CC amyloid peptide and the fibres generated by it. The human antibody Pc  
 CC segment recognized by human immunocells are sequentially contained by its  
 CC terminals from N to C. The fusion gene coding for the antibody is also  
 CC disclosed. This sequence represents the sequence of a anti-beta-amyloid  
 CC peptide antibody.

XX Sequence 277 AA;

Query Match 91.2%; Score 31; DB 7; Length 277;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7  
 :|||  
 Db 32 RKLVEFFA 38

RESULT 12  
 AAW02312  
 ID AAW02312 standard; peptide; 7 AA.

XX AAW02312;

XX 02-MAY-1997 (first entry)

XX DE Beta-amyloid modulator peptide #3.

XX KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis; cerebral blood vessel; Alzheimer's disease; amyloidogenic protein; familial amyloid polynuropathy; familial amyloid cardiomyopathy; isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma; bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria; adult-onset diabetes; familial Mediterranean fever; therapy; deafness; scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.

XX OS Synthetic.

XX PN WO9628471-A1.

XX PD 19-SEP-1996.

XX PF 14-MAR-1996; 96WO-US003492.

XX PR 14-MAR-1995; 95US-00404831.

XX PR 07-JUN-1995; 95US-00475579.

XX PR 27-OCT-1995; 95US-00548998.

XX PA (PHAR-) PHARM PEPTIDES INC.

XX PI Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A; Kaaman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S; Kubasek W, Chin J, Lee J, Kelley M;

XX PI WPI; 1996-433762/43.

XX DR Modulators of amyloid aggregation - comprising, e.g. amyloidogenic protein coupled (indirectly) to at least 1 modifying gp., useful in treatment of Alzheimer's disease.

XX PT Claim 16; Page 91; 106pp; English.

XX CC AAW02310-W02332 represent the peptide portions of the beta-amyloid modulator compounds of the invention. Beta-amyloid peptide is a 4 kilodalton peptide that is the major protein component of amyloid plaques. Amyloid plaques are present both in the brain lesions, and in the walls of cerebral blood vessels in Alzheimer's disease patients. The amyloid modulators of the invention comprise an amyloidogenic protein or peptide (such as this sequence) coupled directly or indirectly to at least one modifying group. The modifying group is preferably a cyclic, heterocyclic, or polycyclic group, such as declain, a cholanyl group, a biotin containing group, or a fluorescein containing group. These compounds then modulate the aggregation of these sequences to natural amyloid proteins or peptides when contacted with the natural amyloidogenic proteins or peptides. The modulator compounds can be used in the treatment of disorders associated with amyloidosis, such as familial amyloid polynuropathy, familial amyloid cardiomyopathy, isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie, bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset diabetes, insulinoma, familial Mediterranean fever, familial amyloid nephropathy with urticaria and deafness, hereditary cerebral haemorrhage and other types of amyloidosis. The modulators are also useful for the treatment of disorders associated with beta-amyloidosis, especially Alzheimer's disease

XX SQ Sequence 7 AA;

Query Match 88.2%; Score 30; DB 2; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||

Db 1 QKLVPFA 7

RESULT 13  
AAW89376

ID AAW89376 standard; peptide; 7 AA.

XX AC AAW89376;

XX DT 02-MAR-1999 (first entry)

XX DE Beta-amyloid peptide derivative A-beta-15-21.

XX KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein; aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy; familial amyloid polynuropathy; bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; bAP.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN US5854204-A.

XX PD 29-DEC-1998.

XX PF 14-MAR-1996; 96US-00612785.

XX PR 14-MAR-1995; 95US-00404831.

XX PR 07-JUN-1995; 95US-00475579.

XX PR 27-OCT-1995; 95US-00548998.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PI Hundal A, Geffer ML, Kaaman L, Musso G, Molineaux S, Benjamin H; Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J; Garnick MB, Kubasek W, Signer ER;

XX PI WPI; 1999-094964/08.

XX DR New peptide(s) derived from beta-amyloid peptide that inhibit amyloid aggregation - and neurotoxicity, specifically for treatment and prevention of Alzheimer's disease.

XX PT Example 12; Col 64; 52pp; English.

XX CC The present invention describes beta-amyloid peptide (bAP) derivatives. The bAP derivatives inhibit aggregation of amyloidogenic proteins and peptides, specifically bAP, and their neurotoxicity, so are useful for treating and preventing any disease involving amyloidosis, specifically Alzheimer's disease but also Down's syndrome, familial amyloid polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose these diseases in vitro or in vivo, by detecting binding of bAP to labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation even when bAP is present in molar excess. The present sequence represents a bAP derivative

XX SQ Sequence 7 AA;

Query Match 88.2%; Score 30; DB 2; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||

Db 1 QKLVPFA 7

RESULT 14  
ABG71007

ID ABG71007 standard; peptide; 7 AA.

XX AC ABG71007;

XX DT 05-DEC-2002 (first entry)

XX DE Long form beta-amyloid protein fragment #4.

KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;  
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;  
 KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;  
 KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;  
 KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;  
 KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;  
 KW macroglobulinemia-associated amyloidosis; reactive amyloidosis;  
 KW primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;  
 KW hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;  
 KW hereditary non-neuropathic systemic amyloidosis;  
 KW familial Mediterranean Fever.

XX Homo sapiens.

XX US2002098173-A1.

XX 25-JUL-2002.

XX 04-OCT-2001; 2001US-00972475.

XX 14-MAR-1995; 95US-00404831.

XX 07-JUN-1995; 95US-00475579.

XX 27-OCT-1995; 95US-00548998.

XX 14-MAR-1996; 96US-00617267.

XX (PRAE-) PRAECIS PHARM INC.

XX Findeis MA, Benjamin H, Garnick MB, Geftter ML, Hundal A;

XX Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;

XX WPI; 2002-697709/75.

XX Amyloid modulator useful for treating a disorder associated with

XX amyloidosis, comprise an amyloidogenic protein and/or a peptide fragment

XX coupled to a modifying group.

XX Example 12; Page 35; 41pp; English.

XX The invention describes an amyloid modulator comprising an amyloidogenic  
 CC protein and/or peptide fragment coupled to a modifying group so that the  
 CC compound modulates the aggregation of natural amyloid proteins or  
 CC peptides. The modulator is used for treating a disorder associated with  
 CC amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese  
 CC and Swedish types), familial amyloid cardiomyopathy (Danish type),  
 CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine  
 CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset  
 CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated  
 CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or  
 CC macroglobulinemia-associated amyloidosis, primary localised cutaneous  
 CC nodular amyloidosis associated with Sjogren's syndrome, reactive  
 CC (secondary) amyloidosis, familial Mediterranean Fever and familial  
 CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),  
 CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,  
 CC amyloidosis associated with long term haemodialysis, hereditary non-  
 CC neuropathic systemic amyloidosis (familial amyloid polyneuropathy I/II),  
 CC familial amyloidosis of Finnish type, amyloidosis associated with  
 CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary  
 CC renal amyloidosis and lysozyme-associated hereditary systemic  
 CC amyloidosis. The compound is capable of altering and inhibiting beta-  
 CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins  
 CC or peptides when contacted with a molar excess amount of natural beta-APs  
 CC relative to the modulator. This sequence represents a fragment of the  
 CC long form of beta-amyloid used in the creation of an amyloid modulator

XX Sequence 7 AA;

Query Match 88.2%; Score 30; DB 5; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

DB 1 QKLVPFA 7

RESULT 15

ABB05155

ID ABB05155 standard; peptide; 7 AA.

XX ABB05155;

DT 02-APR-2002 (first entry)

DE Beta amyloid peptide (15-21) SEQ ID NO: 7.

Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;  
 APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;  
 KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;  
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;  
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;  
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;  
 KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.

XX Homo sapiens.

XX Synthetic.

XX US6319498-B1.

XX 20-NOV-2001.

XX 14-MAR-1996; 96US-00617267.

XX 14-MAR-1995; 95US-00404831.

XX 07-JUN-1995; 95US-00475579.

XX 27-OCT-1995; 95US-00548998.

XX (PRAE-) PRAECIS PHARM INC.

XX Findeis MA, Benjamin H, Garnick MB, Geftter ML, Hundal A;

XX Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;

XX WPI; 2002-146668/19.

XX Amyloid modulator compound useful for treatment of an amyloidogenic

XX disease such as Alzheimer's disease comprises an aggregation core domain

XX and a modifying group attached to it.

XX Disclosure; Col 19; 54pp; English.

XX The present invention describes an amyloid modulator compound (I)  
 CC comprising an aggregation core domain and a modifying group attached to  
 CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,  
 CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic  
 CC and auditory activities, and can be used as a natural amyloid aggregation  
 CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide  
 CC (beta-AP). (I) are used in the manufacture of a medicament for the  
 CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's  
 CC disease and other clinical occurrences of beta amyloid deposition such as  
 CC Down's syndrome individuals and in patients with hereditary cerebral  
 CC haemorrhage with amyloidosis, and for treating a disorder associated with  
 CC amyloidosis such as familial amyloid polyneuropathy. (I) reduces the  
 CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)  
 CC not only reduces the formation of neurotoxic aggregates but also have the  
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The  
 CC present sequence represents a beta-AP peptide, which is used in the  
 CC exemplification of the present invention

XX Sequence 7 AA;

Query Match 88.2%; Score 30; DB 5; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

DB 1 QKLVPFA 7

Best Local Similarity 85.7%; Pred. No. 2e+06; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;

ADJ64058 standard; peptide; 7 AA.

ADJ64058;

06-MAY-2004 (first entry)

Human beta-amyloid long form peptide fragment #4.

Amlyoidogenic protein; therapy; amyloidosis; familial amyloid polyneuropathy; cardiomyopathy; systemic senile amyloidosis; bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; diabetes; inulinoma; myeloma; Sjogren's syndrome; familial mediterranean fever; urticaria; deafness; hereditary cerebral haemorrhage; haemodialysis; thyroid; renal amyloidosis; lysozyme-associated hereditary systemic amyloidosis; beta-amyloid peptide; human.

Homo sapiens.

US2004005307-A1.

08-JAN-2004.

17-JUN-2003; 2003US-00463729.

14-MAR-1995; 95US-00404831.

07-JUN-1995; 95US-00475579.

27-OCT-1995; 95US-00548998.

14-MAR-1996; 96US-00617267.

04-OCT-2001; 2001US-00972475.

(PRAE-) PRACIS PHARM INC.

Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A; Kaaman L, Musso G, Sagner ER, Wakefield J, Reed MJ; WPI; 2004-131767/13.

New amyloidogenic protein aggregation modulators useful for treating disorder associated with amyloidosis e.g. familial amyloid polyneuropathy, Creutzfeldt-Jakob disease and adult onset diabetes.

Example 12; SEQ ID NO 7; 52pp; English.

The invention relates to amyloidogenic proteins or peptide fragments aggregation modulators. The invention is used for treating disorder associated with amyloidosis, particularly familial amyloid polyneuropathy (Portuguese, Japanese and Swedish types), familial amyloid cardiomyopathy (Danish type), isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, adult onset diabetes, inulinoma, isolated atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or macroglobulinemia-associated amyloidosis, primary localized cutaneous nodular amyloidosis associated with Sjogren's syndrome, reactive (secondary) amyloidosis, familial Mediterranean Fever and familial amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome), hereditary cerebral haemorrhage with amyloidosis of Icelandic type, amyloidosis associated with long term haemodialysis, hereditary non-neuropathic systemic amyloidosis (familial amyloid polyneuropathy III), familial amyloidosis of Finnish type, amyloidosis associated with medullary carcinoma of the thyroid, fibrinogen associated hereditary renal amyloidosis and lysozyme-associated hereditary systemic amyloidosis. The present sequence is beta-amyloid peptide fragment used in the exemplification of the invention.

Sequence 7 AA;

Query Match 88.2%; Score 30; DB 8; Length 7;

Best Local Similarity 85.7%; Pred. No. 2e+06; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7  
:|||||

DB 1 QKLVEFFA 7

RESULT 17  
ADQ37351  
ID ADQ37351 standard; peptide; 7 AA.  
XX  
AC ADQ37351;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Beta-amyloid modulator peptide.  
XX  
KW amyloid-beta; amyloid-beta related disease;  
KW amyloid-beta fibril formation; immune response; nootropic;  
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
KW antithyroid; vasotropic; cardiovascular; tranquilizer; uropathic;  
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
KW cardiant; antidepressant; endocrine; hypnotic;  
KW amyloid-beta fibril formation modulator; immune system modulator;  
KW Alzheimer's disease; mild cognitive impairment;  
KW mild-to-moderate cognitive impairment; vascular dementia;  
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
KW senile dementia; Down's syndrome; inclusion body myositis;  
KW age-related macular degeneration; hypothyroidism;  
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
KW behavioural dysfunction; neurological condition; psychological condition;  
KW vaccine antigen.  
XX  
OS Synthetic.  
XX  
XX WO2004058239-A1.  
XX  
XX 15-JUL-2004.  
XX  
XX 24-DEC-2003; 2003WO-CA002021.  
XX  
XX 24-DEC-2002; 2002US-0436379P.  
XX  
XX 23-JUN-2003; 2003US-0482214P.  
XX  
XX (NEUR-) NEUROCHEM INT LTD.  
XX  
XX Gervais F, Bellini F;  
XX  
XX WPI; 2004-543342/52.  
XX  
XX Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.  
XX  
XX Disclosure; Page 87; 143pp; English.  
XX  
XX The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilizer, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral

CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a beta-  
 CC amyloid modulator peptide which is used in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 88.2%; Score 30; DB 8; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 :|||||  
 Db 1 QKLVPFA 7

## RESULT 18

ADZ08903  
 ID ADZ08903 standard; peptide; 7 AA.

AC ADZ08903;

DT 16-JUN-2005 (first entry)

DE Human beta-amyloid peptide (SEQ ID No:128) probed with anti-amyloid IgG.

XX amyloid; antibody engineering; antibody production;  
 KW amyloid-associated disorder; Alzheimers disease; cancer; allergy;  
 KW autoimmune disease; Parkinsons disease;  
 KW acquired immune deficiency syndrome; multiple sclerosis; migraine;  
 KW dementia; infection; nootropic; neuroprotective; cytostatic;  
 KW antiallergic; immunosuppressive; antiparkinsonian; antimigraine;  
 KW antimicrobial; anti-HIV; beta-amyloid.

OS Homo sapiens.

XX WO2005028511-A2.

PD 31-MAR-2005.

XX 26-MAR-2004; 2004WO-US009522.

XX 28-MAR-2003; 2003US-0458469P.

PR 28-MAR-2003; 2003US-0458474P.

PR 28-MAR-2003; 2003US-0458509P.

PR 28-MAR-2003; 2003US-0458510P.

XX (CENZ ) CENTOCOR INC.

PA (MERC/) MERCKEN M.

PA (BENS/) BENSON J M.

XX Mercken M, Benson JM;

XX WPI; 2005-242565/25.

PT  
 PT  
 PT  
 PT  
 XX  
 PS  
 XX

New isolated mammalian anti-amyloid antibodies useful for treating  
 amyloid-associated disorders, such as Alzheimer's disease, cancer,  
 allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,  
 migraine and dementia.

Example 4; SEQ ID NO 128; 306pp; English.

The invention relates to at least one isolated mammalian amyloid antibody  
 comprising at least one variable region comprising at least one heavy  
 chain and at least one light chain, of a fully defined sequence of SEQ ID  
 NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:  
 (i) at least one isolated mammalian amyloid antibody that binds to the  
 same region of an amyloid polypeptide as an antibody comprising at least  
 one heavy chain or light chain complementarity determining region (CDR)  
 having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)  
 at least one isolated mammalian amyloid antibody, comprising at least one  
 human CDR, where the antibody specifically binds at least one epitope  
 selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined  
 sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic  
 acid encoding at least one of any of the isolated mammalian amyloid  
 antibodies mentioned and having at least one human CDR of a fully defined  
 sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an  
 isolated nucleic acid vector comprising an isolated nucleic acid encoding  
 an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising  
 an isolated nucleic acid encoding an amyloid antibody, (vi) a method of  
 producing at least one amyloid antibody, (vii) a composition comprising  
 at least one of any of the isolated mammalian amyloid antibodies  
 mentioned, and at least one pharmaceutical carrier or diluent, (viii) an  
 anti-idiotypic antibody or fragment that specifically binds at least one  
 of the amyloid antibodies mentioned, (ix) a method of diagnosing or  
 treating an amyloid related condition in a cell, tissue, organ or animal,  
 comprising contacting or administering a composition comprising at least  
 one of the antibodies mentioned, with, or to, the cell, tissue, organ or  
 animal, (x) a medical device comprising at least one amyloid antibody  
 mentioned, where the device is suitable for contacting or administering  
 at least one amyloid antibody, (xi) an article of manufacture for human  
 pharmaceutical or diagnostic use, comprising packaging material and a  
 container comprising a solution or a lyophilized form of at least one of  
 the amyloid antibodies mentioned, and (xii) a method of producing at  
 least one of the isolated mammalian amyloid antibodies, comprising  
 providing a host cell or transgenic animal or transgenic plant or plant  
 cell capable of expressing the antibody in recoverable amounts. The  
 methods and compositions of the present invention are useful for  
 producing therapeutic compositions and devices for treating amyloid-  
 associated disorders, such as Alzheimer's disease, cancer, allergies,  
 autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,  
 migraine, dementia and infections. This sequence represents a peptide  
 from human beta-amyloid probed with anti-beta-amyloid IgG antibodies.

Sequence 7 AA;

Query Match 88.2%; Score 30; DB 9; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 :|||||  
 Db 1 QKLVPFA 7

## RESULT 19

AAW02310

ID AAW02310 standard; peptide; 8 AA.

XX AAW02310;

XX 02-MAY-1997 (first entry)

XX Beta-amyloid modulator peptide #1.

Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;  
 cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;  
 familial amyloid polyneuropathy; familial amyloid cardiomyopathy;



KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;  
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;  
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;  
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.  
 XX Synthetic.  
 OS

FN W09628471-A1.  
 XX  
 XX 19-SEP-1996.  
 XX  
 XX 14-MAR-1996; 96WO-US003492.  
 XX  
 XX 14-MAR-1995; 95US-00404831.  
 PR 07-JUN-1995; 95US-00475579.  
 PR 27-OCT-1995; 95US-00548998.  
 XX  
 XX (PHAR-) PHARM PEPTIDES INC.  
 XX  
 XX Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;  
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S;  
 PI Kubasek W, Chin J, Lee J, Kelley M;  
 XX WPI; 1996-433762/43.  
 DR

XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic  
 PT protein coupled (in)directly to at least 1 modifying gp., useful in  
 PT treatment of Alzheimer's disease.  
 XX  
 XX Claim 16; Page 90; 106pp; English.  
 PS

XX AAW02310-W02332 represent the peptide portions of the beta-amyloid  
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4  
 CC kilodalton peptide that is the major protein component of amyloid  
 CC plaques. Amyloid plaques are present both in the brain lesions, and in  
 CC the walls of cerebral blood vessels in Alzheimer's disease patients. The  
 CC amyloid modulators of the invention comprise an amyloidogenic protein or  
 CC peptide (such as this sequence) coupled directly or indirectly to at  
 CC least one modifying group. The modifying group is preferably a cyclic,  
 CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a  
 CC biotin containing group, or a fluorescein containing group. These  
 CC compounds then modulate the aggregation of these sequences to natural  
 CC amyloid proteins or peptides when contacted with the natural  
 CC amyloidogenic proteins or peptides. The modulator compounds can be used  
 CC in the treatment of disorders associated with amyloidosis, such as  
 CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,  
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,  
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset  
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid  
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage  
 CC and other types of amyloidosis. The modulators are also useful for the  
 CC treatment of disorders associated with beta-amyloidosis, especially  
 CC Alzheimer's disease  
 CC  
 XX Sequence 8 AA;

Query Match 88.2%; Score 30; DB 2; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7  
 :|||||  
 Db 2 QKLVFPA 8

RESULT 20  
 AAW89374  
 ID AAW89374 standard; peptide; 8 AA.  
 XX  
 AC AAW89374;  
 XX  
 XX 02-MAR-1999 (first entry)  
 DT  
 XX

DE Beta-amyloid peptide derivative A-beta-14-21.

XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;  
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;  
 KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;  
 KW Creutzfeldt-Jakob disease; BAP.  
 XX

OS Homo sapiens.  
 OS Synthetic.

XX US5854204-A.

XX 29-DEC-1998.

XX 14-MAR-1996; 96US-00612785.

XX 14-MAR-1995; 95US-00404831.

PR 07-JUN-1995; 95US-00475579.

PR 27-OCT-1995; 95US-00548998.

XX (PRAE-) PRACIS PHARM INC.

XX Hundal A, Gefter ML, Kasman L, Musso G, Molineaux S, Benjamin H;  
 PI Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;  
 PI Garnick MB, Kubasek W, Signer ER;  
 XX WPI; 1999-094964/08.

XX New peptide(s) derived from beta-amyloid peptide that inhibit amyloid

PT aggregation - and neurotoxicity, specifically for treatment and  
 PT prevention of Alzheimer's disease.  
 XX

XX Example 12; Col 64; 52pp; English.

XX The present invention describes beta-amyloid peptide (BAP) derivatives.  
 CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and  
 CC peptides, specifically BAP, and their neurotoxicity, so are useful for  
 CC treating and preventing any disease involving amyloidosis, specifically  
 CC Alzheimer's disease but also Down's syndrome, familial amyloid  
 CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and  
 CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose  
 CC these diseases, in vitro or in vivo, by detecting binding of BAP to  
 CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation  
 CC even when BAP is present in molar excess. The present sequence represents  
 CC a BAP derivative  
 XX

XX Sequence 8 AA;

Query Match 88.2%; Score 30; DB 2; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7  
 :|||||  
 Db 2 QKLVFPA 8

RESULT 21  
 ABG71005  
 ID ABG71005 standard; peptide; 8 AA.

XX ABG71005;

XX 05-DEC-2002 (first entry)

XX Long form beta-amyloid protein fragment #2.

XX Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;  
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;  
 KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;  
 KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;  
 KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;  
 KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;



KW macroglobulinaemia-associated amyloidosis; reactive amyloidosis;  
 KW primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;  
 KW hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;  
 KW hereditary non-neuropathic systemic amyloidosis;  
 KW familial Mediterranean Fever.

XX Homo sapiens.

XX US2002098173-A1.

XX 25-JUL-2002.

XX 04-OCT-2001; 2001US-00972475.

XX 14-MAR-1995; 95US-00404831.

XX 07-JUN-1995; 95US-00475579.

XX 27-OCT-1995; 95US-00548998.

XX 14-MAR-1996; 96US-00617267.

XX (PRAE-) PRAECIS PHARM INC.

XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;  
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;

XX WPI; 2002-697709/75.

PT Amyloid modulator useful for treating a disorder associated with  
 PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment  
 PT coupled to a modifying group.

PS Example 12; Page 35; 41pp; English.

XX The invention describes an amyloid modulator comprising an amyloidogenic  
 CC protein and/or peptide fragment coupled to a modifying group so that the  
 CC compound modulates the aggregation of natural amyloid proteins or  
 CC peptides. The modulator is used for treating a disorder associated with  
 CC amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese  
 CC and Swedish types), familial amyloid cardiomyopathy (Danish type),  
 CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine  
 CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset  
 CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated  
 CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or  
 CC macroglobulinaemia-associated amyloidosis, primary localised cutaneous  
 CC (secondary) amyloidosis associated with Sjogren's syndrome, reactive  
 CC familial amyloidosis, familial Mediterranean Fever and familial  
 CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),  
 CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,  
 CC amyloidosis associated with long term haemodialysis, hereditary non-  
 CC neuropathic systemic amyloidosis (familial amyloid polyneuropathy III),  
 CC familial amyloidosis of Finnish type, amyloidosis associated with  
 CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary  
 CC renal amyloidosis and lysozyme-associated hereditary systemic  
 CC amyloidosis. The compound is capable of altering and inhibiting beta-  
 CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins  
 CC or peptides when contacted with a molar excess amount of natural beta-APs  
 CC relative to the modulator. This sequence represents a fragment of the  
 CC long form of beta-amyloid used in the creation of an amyloid modulator

XX Sequence 8 AA;

Query Match 88.2%; Score 30; DB 5; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

DB 2 QKLVPFA 8

RESULT 22

ABB05153

ID ABB05153 standard; peptide; 8 AA.

XX

AC ABB05153;

XX 02-APR-2002 (first entry)

XX Beta amyloid peptide (14-21) SEQ ID NO:5.

XX Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;  
 KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;  
 KW nontropic; neuroprotective; immunosuppressive; antimicrobial; auditory;  
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;  
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;  
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;  
 KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.

XX Homo sapiens.

OS Synthetic.

XX US6319498-B1.

XX 20-NOV-2001.

XX 14-MAR-1996; 96US-00617267.

XX 14-MAR-1995; 95US-00404831.

XX 07-JUN-1995; 95US-00475579.

XX 27-OCT-1995; 95US-00548998.

XX (PRAE-) PRAECIS PHARM INC.

XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;  
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;

XX WPI; 2002-146668/19.

PT Amyloid modulator compound useful for treatment of an amyloidogenic  
 PT disease such as Alzheimer's disease comprises an aggregation core domain  
 PT and a modifying group attached to it.

XX Disclosure; Col 18; 54pp; English.

XX The present invention describes an amyloid modulator compound (I)  
 CC comprising an aggregation core domain and a modifying group attached to  
 CC it. (I) has nontropic, neuroprotective, immunosuppressive, antimicrobial,  
 CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic  
 CC and auditory activities, and can be used as a natural amyloid aggregation  
 CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide  
 CC (beta-AP). (I) are used in the manufacture of a medicament for the  
 CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's  
 CC disease and other clinical occurrences of beta amyloid deposition such as  
 CC Down's syndrome individuals and in patients with hereditary cerebral  
 CC haemorrhage with amyloidosis, and for treating a disorder associated with  
 CC amyloidosis such as familial amyloid polyneuropathy. (I) reduces the  
 CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)  
 CC not only reduces the formation of neurotoxic aggregates but also have the  
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The  
 CC present sequence represents a beta-AP peptide, which is used in the  
 CC exemplification of the present invention

XX Sequence 8 AA;

Query Match 88.2%; Score 30; DB 5; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

DB 2 QKLVPFA 8

RESULT 23

ADJ64056

ID ADJ64056 standard; peptide; 8 AA.

XX

AC ADJ64056;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human beta-amyloid long form peptide fragment #2.  
 XX  
 KW Amyloidogenic protein; therapy; amyloidosis;  
 KW familial amyloid polyneuropathy; cardiomyopathy;  
 KW systemic senile amyloidosis; bovine spongiform encephalopathy;  
 KW Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker syndrome;  
 KW diabetes; insulinoma; myeloma; Sjogren's syndrome;  
 KW familial mediterranean fever; urticaria; deafness;  
 KW hereditary cerebral haemorrhage; haemodialysis; thyroid;  
 KW renal amyloidosis; lysosome-associated hereditary systemic amyloidosis;  
 KW beta-amyloid peptide; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004005307-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 17-JUN-2003; 2003US-00463729.  
 XX  
 PR 14-MAR-1995; 95US-00404831.  
 PR 07-JUN-1995; 95US-00475579.  
 PR 27-OCT-1995; 95US-00548998.  
 PR 14-MAR-1996; 96US-00617267.  
 PR 04-OCT-2001; 2001US-00972475.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA  
 PI Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;  
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;  
 XX  
 XX WPI; 2004-131767/13.  
 DR  
 XX  
 PT New amyloidogenic protein aggregation modulators useful for treating  
 PT disorder associated with amyloidosis e.g. familial amyloid  
 PT polyneuropathy, Creutzfeldt-Jakob disease and adult onset diabetes.  
 XX  
 XX Example 12; SEQ ID NO 5; 52pp; English.  
 PS  
 XX  
 CC The invention relates to amyloidogenic proteins or peptide fragments  
 CC aggregation modulators. The invention is used for treating disorder  
 CC associated with amyloidosis, particularly familial amyloid polyneuropathy  
 CC (Portuguese, Japanese and Swedish types), familial amyloid cardiomyopathy  
 CC (Danish type), isolated cardiac amyloid, systemic senile amyloidosis,  
 CC scrapie, bovine spongiform encephalopathy, Creutzfeldt-Jakob disease,  
 CC Gerstmann-Straussler-Scheinker syndrome, adult onset diabetes,  
 CC insulinoma, isolated atrial amyloidosis, idiopathic (primary)  
 CC amyloidosis, myeloma or macroglobulinemia-associated amyloidosis, primary  
 CC localized cutaneous nodular amyloidosis associated with Sjogren's  
 CC syndrome, reactive (secondary) amyloidosis, familial Mediterranean Fever  
 CC and familial amyloid nephropathy with urticaria and deafness (Muckle-  
 CC Wells syndrome), hereditary cerebral haemorrhage with amyloidosis of  
 CC Icelandic type, amyloidosis associated with long term haemodialysis, of  
 CC hereditary non-neuropathic systemic amyloidosis (familial amyloid  
 CC polyneuropathy III), familial amyloidosis of Finnish type, amyloidosis  
 CC associated with medullary carcinoma of the thyroid, fibrinogen associated  
 CC hereditary renal amyloidosis and lysosome-associated hereditary systemic  
 CC amyloidosis. The present sequence is beta-amyloid peptide fragment used  
 CC in the exemplification of the invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 88.2%; Score 30; DB 8; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KGLVFFA 7  
 :|||||  
 Db 2 QKLVFFA 8

RESULT 24  
 ADQ37349  
 ID ADQ37349 standard; peptide; 8 AA.  
 XX  
 AC ADQ37349;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Beta-amyloid modulator peptide.  
 XX  
 KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; nootropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment; vascular dementia;  
 KW mild-to-moderate cognitive impairment; hereditary cerebral haemorrhage;  
 KW cerebral amyloid angiopathy; Down's syndrome; inclusion body myositis;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004058239-A1.  
 XX  
 PD 15-JUL-2004.  
 XX  
 PF 24-DEC-2003; 2003WO-CA002021.  
 XX  
 PR 24-DEC-2002; 2002US-0436379P.  
 PR 23-JUN-2003; 2003US-0482214P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 PA  
 XX Gervais F, Bellini P;  
 PI  
 DR WPI; 2004-543342/52.  
 XX  
 CC Composition for treating e.g. Alzheimer's disease comprises first agent  
 CC that prevents or treats amyloid-beta related disease and second agent  
 CC that is either a peptide or peptidomimetic or an immune system modulator.  
 XX  
 PS Disclosure; Page 87; 143pp; English.  
 XX  
 CC The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, and as  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's

CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a beta-  
 CC amyloid modulator peptide which is used in the exemplification of the  
 CC present invention.

XX Sequence 8 AA;

Query Match 88.2%; Score 30; DB 8; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 :|||||  
 Db 2 QKLVPFA 8

RESULT 25

AA45239  
 ID AAR45239 standard; peptide; 9 AA.

AC AAR45239;

XX 20-JUN-1994 (first entry)

DE Mutant amyloid precursor protein fragment.

XX Amyloid precursor protein; APP; beta amyloid protein; BAP; detection;  
 KW Alzheimer's disease; Down's syndrome.

XX Homo sapiens.

PN AU9338358-A.

PD 04-NOV-1993.

PF 03-MAY-1993; 93AU-00038358.

PR 01-MAY-1992; 92US-00877675.

PA (AMCV ) AMERICAN CYANAMID CO.

PI Vitek MP, Jacobsen JS;

XX WPI; 1993-406194/51.

DR N-PSDB; AAQ54267.

XX New mutant forms of amyloid precursor protein - for detecting cpds. that  
 PT modify activity of enzymes involved in precursor cleavage, also new  
 FT nucleic acid encoding them.

XX Disclosure; Page 35; 66pp; English.

XX Recombinant polypeptides produced using the coding sequences of mutant  
 CC forms of amyloid precursor proteins comprising from the 5' to the 3' end  
 CC a sequence encoding a marker and either (1) a sequence encoding the N-  
 CC terminus of an amyloid precursor protein (APP) up to, but not including,  
 CC the nucleotides encoding the beta amyloid protein (BAP) domain or (2) the  
 CC BAP domain; or the two ligated together, can be used to detect drugs or  
 CC compounds that inhibit/augment the activity of proteolytic enzymes which  
 CC cleave APP to generate BAP fragments (deposition of which occurs in  
 CC patients with Alzheimers disease and Down's syndrome). This is a fragment

CC of amyloid precursor protein containing a mutation which is associated  
 CC with diseases involving BAP deposition

SQ Sequence 9 AA;

Query Match 88.2%; Score 30; DB 2; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 :|||||

Db 1 QKLVPFA 7

RESULT 26

AA48493  
 ID AAB48493 standard; peptide; 9 AA.

AC AAB48493;

XX 02-MAR-2001 (first entry)

DE Antifibrillogenic peptide #20.

XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.

XX Homo sapiens.

FT Key Location/Qualifiers

FT Modified-site 9 /note= "C-terminal amide"

XX WO200068263-A2.

XX 16-NOV-2000.

XX 04-MAY-2000; 2000WO-CA000515.

PR 05-MAY-1999; 99US-0132592P.

XX (NEUR-) NEUROCHEM INC.

PI Chalifour R, Gervais F, Gupta A;

XX WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein

SQ Sequence 9 AA;

Query Match 88.2%; Score 30; DB 4; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 :|||||

Db 3 QKLVPFA 9

RESULT 27  
AAU11667  
ID AAU11667 standard; peptide; 9 AA.  
XX  
XX AC AAU11667;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Peptide #20, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.  
XX  
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 9 /note= "C-terminal amide"  
FT  
XX WO200185093-A2.  
XX  
XX 15-NOV-2001.  
XX  
XX 22-DEC-2000; 2000WO-IB002078.  
XX  
XX 23-DEC-1999; 99US-0171877P.  
XX  
XX (NEUR-) NEUROCHEM INC.  
XX  
XX Green AM, Gervais F;  
XX  
XX WPI; 2002-075222/10.  
XX  
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
PT disease comprises contacting blood vessel wall cell with amyloid-beta 40  
PT inhibitor.  
XX  
XX Disclosure; Page 10; 68pp; English.  
XX  
XX The present invention relates to a new method of inhibiting cerebral  
CC amyloid angiopathy. The new method of the invention involves contacting a  
CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
CC can be used for treating disease states characterised by cerebral amyloid  
CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
CC The present sequence represents one of a group of peptides (AAU11648-  
CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
CC was used in the invention to treat a disease state characterised by  
CC cerebral amyloid angiopathy (CAA)  
XX  
SQ Sequence 9 AA;  
Query Match 88.2%; Score 30; DB 5; Length 9;  
Best Local Similarity 85.7%; Pred. No. 2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KKLVPFA 7  
Db :|||||  
3 QKLVPFA 9  
RESULT 28  
ABP57517  
ID ABP57517 standard; peptide; 9 AA.  
XX  
XX AC ABP57517;  
XX  
XX 28-APR-2003 (first entry)  
XX  
XX Differentially isotopically labelled (DiMas) peptide #10.  
DE  
XX

KW Mass spectrometry; polymer; analysis; cleavage; substrate specificity;  
KW isotope; protease.  
XX  
XX Synthetic.  
XX  
XX WO2003001206-A1.  
XX  
XX 03-JAN-2003.  
XX  
XX 25-JUN-2002; 2002WO-GB002921.  
XX  
XX 26-JUN-2001; 2001GB-00015581.  
XX  
XX (GLAX ) GLAXO GROUP LTD.  
XX  
XX Mckeown SC;  
XX  
XX WPI; 2003-184066/18.  
XX  
XX Analyzing cleavage of polymer, by providing polymer sample, incubating  
PT the sample with labeled isotope for cleavage at potential cleavage site,  
PT and analyzing the masses of any uncleaved fragments by mass spectrometry.  
XX  
XX Example 3; Page 26; 73pp; English.  
XX  
XX The present invention describes a method (M1) for analysing cleavage of a  
CC polymer. M1 comprises: (a) providing a sample of the polymer, a portion  
CC of the polymer molecules having been labeled at a position on one side of  
CC the potential cleavage site with a first isotopic label and a portion of  
CC the polymer molecules having been labeled at a position on the opposite  
CC side of the potential cleavage site with a second isotopic label; (b)  
CC incubating the sample under conditions suitable for cleavage at the  
CC potential cleavage site; and (c) analysing the mass(es) of any cleaved  
CC fragments by mass spectrometry and thereby determining whether and/or  
CC where cleavage has taken place. M1 is useful for analysing cleavage of a  
CC polymer, where the polymer is a linear polymer, and comprises a peptide  
CC or protein. Methods from the present invention can be used in discovering  
CC new or improved synthetic substrates for both known and unknown enzymes,  
CC e.g. enzymes identified from the human genome. The methods are also  
CC useful to identify the sequence origin, and in screening methods to  
CC identify new substrates for enzymes, in positional peptide scanning  
CC libraries, in *in vivo/ex vivo* in vitro peptide, and in assaying methods  
CC for oligonucleotide or peptide sequencing and in measuring differential  
CC protein expression. The methods are useful for monitoring the cleavage of  
CC polypeptides or polynucleotides, and for determining optimal polymer  
CC substrates. ABP57505 to ABP57605 represent peptides used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 9 AA;  
Query Match 88.2%; Score 30; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KKLVPFA 7  
Db :|||||  
3 QKLVPFA 9  
RESULT 29  
ABU79053  
ID ABU79053 standard; peptide; 9 AA.  
XX  
XX AC ABU79053;  
XX  
XX 17-JUN-2003 (first entry)  
XX  
XX Aggregation blocking peptide #5.  
XX  
XX Amyloid formation; amyloid-like deposit; Alzheimer's disease;  
KW pathological beta-sheet-rich conformation; Down's syndrome;  
KW amyloidosis disorder; human prion disease; kuru; CJD;  
KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;  
KW

KW prion associated human neurodegenerative disease; animal prion disease;  
 KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;  
 KW chronic wasting disease.

XX Unidentified.

XX US6462171-B1.

XX 08-OCT-2002.

XX 12-DEC-1996; 96US-00766596.

XX 07-JUN-1995; 95US-00478326.

XX 10-APR-1996; 96US-00630645.

XX (UUNY ) UNIV NEW YORK STATE.

XX Soto-Jara C, Baumann MH, Frangione B;

XX WPI; 2003-379012/36.

XX Novel inhibitory peptides which inhibit and structurally block abnormal  
 PT folding of protein into amyloid or amyloid-like deposit and into  
 PT pathological beta-sheet rich conformation, useful for treating  
 PT Alzheimer's disease.

XX Disclosure; Col 47-48; 51pp; English.

CC The invention describes an isolated inhibitory peptide (I) which  
 CC interacts with a hydrophobic beta-sheet forming cluster of amino acid  
 CC residues on a protein or peptide for amyloid or amyloid-like deposit  
 CC formation, and inhibits or structurally blocks the abnormal folding of  
 CC proteins and peptides into amyloid or amyloid-like deposits and into  
 CC pathological beta-sheet rich conformation. (I) is useful for disorders or  
 CC diseases associated with abnormal protein folding into amyloid or amyloid  
 CC -like deposits or into pathological beta-sheet-rich precursors of such  
 CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis  
 CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease  
 CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated  
 CC human neurodegenerative diseases as well as animal prion diseases such as  
 CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and  
 CC chronic wasting disease of mule deer and elk. (I) is also useful for  
 CC detecting and diagnosing the presence or absence of amyloid or amyloid-  
 CC like deposits in vivo and its precursors. This is the amino acid sequence  
 CC of peptide associated with the inhibition of amyloid or amyloid like  
 CC deposits

XX Sequence 9 AA;

Query Match 88.2%; Score 30; DB 6; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFF 6

Db 1 KKLVEFF 6

RESULT 30

AAE35436

ID AAE35436 standard; peptide; 9 AA.

XX AAE35436;

XX 17-JUN-2003 (first entry)

XX Abeta peptide #7.

XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;

KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.  
 XX Unidentified.  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..9  
 FT /note= "D-form residues"

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.

XX Prevention and/or treatment of an amyloid-related disease e.g.

XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.

XX Claim 1; Page 58; 44pp; English.

CC The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention

XX Sequence 9 AA;

Query Match 88.2%; Score 30; DB 6; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFF 7

Db 3 QKLVEFF 9

RESULT 31

ABW00187

ID ABW00187 standard; peptide; 9 AA.

XX ABW00187;

XX 15-JAN-2004 (first entry)

XX Peptide #5 used in the invention.

XX Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;  
 KW Alzheimer's disease.  
 XX Unidentified.

XX PN US2003087407-A1.  
 XX PD 08-MAY-2003.  
 XX PF 06-SEP-2002; 2002US-00235483.  
 XX PR 07-JUN-1995; 95US-00478326.  
 XX PR 10-APR-1996; 96US-00630645.  
 XX PR 12-DEC-1996; 96US-00766596.  
 XX PA (UJNY ) UNIV NEW YORK STATE.  
 XX PI Soto-Jara C, Baumann MH, Frangione B;  
 XX DR WPI; 2003-616149/58.  
 XX PT New inhibitory peptide, useful for preparing a composition for  
 PT diagnosing, preventing or treating disorders associated with amyloid-like  
 PT fibril deposits, e.g. Alzheimer's disease, or prion related  
 PT encephalopathies.  
 XX PS Claim 1; Page 25; 52pp; English.  
 XX CC The invention relates to inhibitory peptide comprising a portion of at  
 CC least three amino acid residues and a sequence predicted not to adopt a  
 CC beta-sheet structure that associates with a hydrophobic beta-sheet  
 CC cluster on a protein or peptide involved in the abnormal folding into a  
 CC beta-sheet structure, to structurally block the abnormal folding of the  
 CC protein or peptide. The inhibitory peptide is useful for preparing a  
 CC composition for preventing, treating or detecting disorders or disease  
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and  
 CC prion related encephalopathies. The invention is also useful in gene  
 CC therapy. The present sequence is a peptide used in the invention  
 XX SQ Sequence 9 AA;  
 Query Match 88.2%; Score 30; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPF 6  
 DB 1 KKLVPF 6  
 RESULT 32  
 ADI35874  
 ID ADI35874 standard; peptide; 9 AA.  
 AC ADI35874;  
 XX DT 22-APR-2004 (first entry)  
 XX DE Amyloid beta peptide SEQ ID NO:28.  
 XX KW amyloid beta peptide; vaccine; immunisation; neuroprotective;  
 KW Alzheimer's disease.  
 XX OS Synthetic.  
 XX PN WO2004006861-A2.  
 XX PD 22-JAN-2004.  
 XX PF 16-JUL-2003; 2003WO-US022280.  
 XX PR 17-JUL-2002; 2002US-0396245P.  
 XX PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.  
 XX PI Chain DG, Fitzer-Attas C;  
 XX

DR WPI; 2004-122759/12.  
 XX PT New amyloid beta peptide, useful for preparing a composition for  
 PT preventing the formation or progression of amyloid plaques for preventing  
 PT or treating Alzheimer's disease.  
 XX PS Example 2; SEQ ID NO 28; 69pp; English.  
 XX CC The present invention describes an isolated amyloid beta peptide or its  
 CC homologue which is selected by a method comprising: (a) determining the  
 CC binding value of each amino acid of a subsequence of amyloid beta peptide  
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)  
 CC determining the resulting score of all amino acids of the subsequence,  
 CC based on the binding value of each amino acid obtained in step (1); and  
 CC (c) comparing the resulting score to a preselected value. Also described:  
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier  
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;  
 CC (3) predicting the reaction of an individual to a vaccine; (4) matching a  
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,  
 CC for immunisation of an individual based on the HLA haplotype of the  
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta  
 CC peptide to an individual based on the HLA haplotype of the individual;  
 CC and (6) preventing the formation or progression of amyloid plaques. The  
 CC amyloid beta peptide has neuroprotective activity, and can be used in  
 CC vaccines. The amyloid beta peptide is useful for preparing a composition  
 CC for preventing the formation or progression of amyloid plaques for  
 CC preventing or treating Alzheimer's disease. The present sequence  
 CC represents an amyloid beta (Abeta) peptide, which is used in an example  
 CC from the present invention.  
 XX SQ Sequence 9 AA;  
 Query Match 88.2%; Score 30; DB 8; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 DB 3 QKLVPFA 9  
 RESULT 33  
 ADQ37260  
 ID ADQ37260 standard; peptide; 9 AA.  
 XX AC ADQ37260;  
 XX DT 07-OCT-2004 (first entry)  
 XX DE Vaccine antigen amyloid-beta related amino acid sequence.  
 XX KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX OS Synthetic.  
 XX PF Key Location/Qualifiers  
 XX FT Misc-difference 1...9 /note= "D-form residues"  
 XX FT

PN	WO2004058239-A1.	ID	ADQ37332 standard; peptide; 9 AA.
XX		XX	
PD	15-JUL-2004.	AC	ADQ37332;
XX		XX	
PF	24-DEC-2003; 2003WO-CA002021.	DT	07-OCT-2004 (first entry)
XX		XX	
PR	24-DEC-2002; 2002US-0436379P.	DE	Antifibrillogenic amyloidosis inhibiting peptide.
PR	23-JUN-2003; 2003US-0482214P.	XX	
XX		XX	
PA	(NEUR-) NEUROCHEM INT LTD.	KW	amyloid-beta; amyloid-beta related disease;
XX		KW	amyloid-beta fibril formation; immune response; nootropic;
PI	Gervais F, Bellini F;	KW	neuroprotective; cerebroprotective; haemostatic; ophthalmological;
XX		KW	antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;
XX		KW	anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
XX		KW	cardiant; antidepressant; endocrine; hypnotic;
XX		KW	amyloid-beta fibril formation modulator; immune system modulator;
XX		KW	Alzheimer's disease; mild cognitive impairment; dementia;
XX		KW	mild-to-moderate cognitive impairment; vascular dementia;
PT	Composition for treating e.g. Alzheimer's disease comprises first agent	KW	cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
PT	that prevents or treats amyloid-beta related disease and second agent	KW	senile dementia; Down's syndrome; inclusion body myositis;
PT	that is either a peptide or peptidomimetic or an immune system modulator.	KW	age-related macular degeneration; hypothyroidism;
XX		KW	cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
PS	Disclosure; Page 67; 143pp; English.	KW	behavioural dysfunction; neurological condition; psychological condition;
XX		XX	vaccine antigen.
XX		OS	Synthetic.
CC	The present invention describes compositions (C) comprising: (a) a first	XX	
CC	agent (a1) that prevents or treats amyloid-beta related disease; and (b)	XX	
CC	a second agent (a2) that is: (i) a peptide or peptidomimetic that	XX	
CC	modulates amyloid-beta fibril formation or induces a prophylactic or	XX	
CC	therapeutic immune response against amyloid-beta fibril formation; or	XX	
CC	(ii) an immune system modulator that prevents or inhibits amyloid-beta	XX	
CC	fibril formation. Also described is a kit comprising (C). (C) have	XX	
CC	nootropic, neuroprotective, cerebroprotective, haemostatic,	XX	
CC	ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,	XX	
CC	uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,	XX	
CC	neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,	XX	
CC	and can be used as amyloid-beta fibril formation modulators, and as	XX	
CC	immune system modulators. (C) can be used for preventing or treating an	XX	
CC	amyloid-beta related disease e.g. Alzheimer's disease (including sporadic	XX	
CC	(non-hereditary) or familial (hereditary)), mild cognitive impairment,	XX	
CC	mild-to-moderate cognitive impairment, vascular dementia, cerebral	XX	
CC	amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,	XX	
CC	Down's syndrome, inclusion body myositis, age-related macular	XX	
CC	degeneration, or a condition associated with Alzheimer's disease	XX	
CC	(including hypothyroidism, cerebrovascular disease, cardiovascular	XX	
CC	disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,	XX	
CC	aggression, or incontinence), a neurological condition (e.g. Huntington's	XX	
CC	disease, amyotrophic lateral sclerosis, acquired immunodeficiency,	XX	
CC	Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia	XX	
CC	with Lewy bodies, altered muscle tone, seizures, sensory loss, visual	XX	
CC	field deficits, incoordination, gait disturbance, transient ischaemic	XX	
CC	attack or stroke, transient alertness, attention deficit, frequent falls,	XX	
CC	syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural	XX	
CC	haematoma, brain tumour, posttraumatic brain injury, or posthypoxic	XX	
CC	damage), or a psychological condition (e.g. depression, delusions,	XX	
CC	illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep	XX	
CC	disturbance, insomnia, behavioural disinhibition, poor insight, suicidal	XX	
CC	ideation, depressed mood, irritability, anhedonia, social withdrawal, or	XX	
CC	excessive guilt) in a subject e.g. human having a genomic mutation in an	XX	
CC	amyloid precursor protein gene, an ApoE gene, or a presenilin gene;	XX	
CC	having amyloid-beta deposits. The present sequence represents a peptide	XX	
CC	that can be used as a vaccine antigen in the exemplification of the	XX	
CC	present invention.	XX	
XX		XX	
SQ	Sequence 9 AA;	XX	
	Query Match 88.2%; Score 30; DB 8; Length 9;	XX	
	Best Local Similarity 85.7%; Pred. No. 2e+06;	XX	
	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	XX	
QY	1 KKLVPFA 7	XX	
	:	XX	
Db	3 QKLVPFA 9	XX	
		XX	
RESULT 34		XX	
ADQ37332		XX	



CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or postrhypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 88.2%; Score 30; DB 8; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 2e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 DB 3 QKLVPFA 9

RESULT 35

AAB46226  
 ID AAB46226 standard; peptide; 10 AA.

XX AC AAB46226;

XX DT 04-APR-2001 (first entry)

XX DE Human APP derived immunogenic peptide #22.

XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US014810.

XX PR 28-MAY-1999; 99US-00322289.

XX PA (NEUR-) NEURALAB LTD.

PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX WPI; 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid specific  
 PT antibody.

XX PS Disclosure; Fig 19; 143pp; English.

XX CC This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 88.2%; Score 30; DB 4; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 DB 2 QKLVPFA 8

RESULT 36

AAB46225  
 ID AAB46225 standard; peptide; 10 AA.

XX AC AAB46225;

XX DT 04-APR-2001 (first entry)

XX DE Human APP derived immunogenic peptide #21.

XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US014810.

XX PR 28-MAY-1999; 99US-00322289.

XX PA (NEUR-) NEURALAB LTD.

PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX WPI; 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid specific  
 PT antibody.

XX PS Disclosure; Fig 19; 143pp; English.

XX CC This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have neurotropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 88.2%; Score 30; DB 4; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7



```

Db      :|||||
        3 QKLVFFA 9

RESULT 37
AAB46224
ID AAB46224 standard; peptide; 10 AA.
XX AC AAB46224;
XX DT 04-APR-2001 (first entry)
XX DE Human APP derived immunogenic peptide #20.
XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
XX KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
XX KW amyloid precursor protein; Alzheimer's disease.
XX OS Homo sapiens.
XX PN WO200072880-A2.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 2000WO-US014810.
XX PR 28-MAY-1999; 99US-00322289.
XX PA (NEUR-) NEURALAB LTD.
XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX PI WPI; 2001-032104/04.
XX PD Preventing or treating a disease associated with amyloid deposits,
XX PT especially Alzheimer's disease, comprises administering amyloid specific
XX PT antibody.
XX PS Disclosure; Fig 19; 143pp; English.
XX CC This invention describes a novel method of preventing or treating a
XX CC disease associated with amyloid deposits of amyloid precursor protein
XX CC (APP) Abeta fragments in the brain of a patient, which comprises
XX CC administering to the patient: (a) an antibody that binds to Abeta, the
XX CC antibody binds to an amyloid deposit and induces a clearing response (Fc
XX CC receptor mediated phagocytosis) against it (b) a polypeptide containing
XX CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
XX CC that induces an immunogenic response against residues 1-3 to 7-11 of
XX CC Abeta. The products of the invention have neurotropic and neuroprotective
XX CC activity. The method is also useful for monitoring a course of treatment
XX CC being administered to a patient e.g. active and passive immunization. The
XX CC methods are useful for prophylactic and therapeutic treatment of
XX CC Alzheimer's disease
XX SQ Sequence 10 AA;
      Query Match      88.2%; Score 30; DB 4; Length 10;
      Best Local Similarity 85.7%; Pred. No. 13;
      Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVFFA 7
      :|||||
Db      1 QKLVFFA 7

RESULT 39
AAB82641
ID AAB82641 standard; peptide; 10 AA.
XX AC AAB82641;
XX DT 02-OCT-2001 (first entry)
XX DE All-D peptide used in Alzheimer's disease vaccine.
XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
XX KW therapy; antigen.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..10
XX FT /note= "all D-form residues"
XX PN WO200139796-A2.

```

XX 07-JUN-2001.  
 XX 29-NOV-2000; 2000WO-CA001413.  
 XX 29-NOV-1999; 99US-0168594P.  
 PR 28-NOV-2000; 2000US-00724842.  
 XX (NEUR-) NEUROCHEM INC.  
 XX  
 XX Chalifour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 XX  
 XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT which elicits production of antibodies to prevent fibrillogenesis and  
 PT associated cellular toxicity.  
 XX  
 PS Disclosure; Page 11; 31pp; English.  
 XX  
 CC The present sequence is that of an all-D peptide suitable for use in  
 CC preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see AA882622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in AA882623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 10 AA;  
 SQ  
 Query Match 88.2%; Score 30; DB 4; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
 :|||||  
 Db 3 QKLVPFA 9

RESULT 40  
 AAU96829  
 ID AAU96829 standard; peptide; 10 AA.  
 XX  
 AC AAU96829;  
 XX  
 XX 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #19.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;

KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..10  
 FT /note= "Preferably D-form residue"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid

XX plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 22; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A-t-(A<sub>1</sub>-n-K)-z-A<sub>1</sub>-a-b (I) where z = 0-1;  
 CC A<sub>1</sub> = an amyloid targeting moiety; A<sub>1</sub>-n-K = a linker moiety; and A<sub>1</sub>-a-b  
 CC = a labelling moiety. Also included are imaging amyloid deposition or  
 CC diagnosing an amyloid-related condition in a patient involving  
 CC administering (I) to the patient, and ultrasound imaging (I) in the  
 CC patient to determine the presence of amyloid or amyloid-related condition  
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising  
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and  
 CC instructions for the preparation and use of the radiopharmaceutical in  
 CC the imaging of amyloid or an amyloid-related condition. The agents are  
 CC used for imaging amyloid deposition and for diagnosing an amyloid related  
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible  
 CC cerebral amyloidosis (transmissible virus dementias), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention

XX Sequence 10 AA;

Query Match 88.2%; Score 30; DB 5; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
 :|||||  
 Db 3 QKLVPFA 9

RESULT 41  
 ABP57511  
 ID ABP57511 standard; peptide; 10 AA.  
 XX  
 XX ABP57511;  
 XX  
 DT 28-APR-2003 (first entry)

XX Differentially isotopically labelled (DiMas) peptide #4.  
 XX Mass spectrometry; polymer; analysis; cleavage; substrate specificity;  
 KW isotope; protease.  
 XX Synthetic.  
 OS  
 XX WO2003001206-A1.  
 XX  
 XX 03-JAN-2003.  
 XX  
 XX 25-JUN-2002; 2002WO-GB002921.  
 XX  
 XX 26-JUN-2001; 2001GB-00015581.  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX  
 XX Mckesown SC;  
 XX  
 XX WPI; 2003-184066/18.  
 XX  
 XX Analyzing cleavage of polymer, by providing polymer sample, incubating  
 PT the sample with labeled isotope for cleavage at potential cleavage site,  
 PT and analyzing the masses of any uncleaved fragments by mass spectrometry.  
 XX  
 PS Example 3; Page 22; 73pp; English.  
 XX  
 CC The present invention describes a method (M1) for analysing cleavage of a  
 CC polymer. M1 comprises: (a) providing a sample of the polymer, a portion  
 CC of the polymer molecules having been labeled at a position on one side of  
 CC the potential cleavage site with a first isotopic label and a portion of  
 CC the polymer molecules having been labeled at a position on the opposite  
 CC side of the potential cleavage site with a second isotopic label; (b)  
 CC incubating the sample under conditions suitable for cleavage at the  
 CC potential cleavage site; and (c) analysing the mass(es) of any cleaved  
 CC fragments by mass spectrometry and thereby determining whether and/or  
 CC where cleavage has taken place. M1 is useful for analysing cleavage of a  
 CC polymer, where the polymer is a linear polymer, and comprises a peptide  
 CC or protein. Methods from the present invention can be used in discovering  
 CC new or improved synthetic substrates for both known and unknown enzymes,  
 CC e.g. enzymes identified from the human genome. The methods are also  
 CC useful to identify the sequence origin, and in screening methods to  
 CC identify new substrates for enzymes, in positional peptide scanning  
 CC libraries, in *in vivo/ex vivo*/in vitro peptide, and in assaying methods  
 CC for oligonucleotide or peptide sequencing and in measuring differential  
 CC protein expression. The methods are useful for monitoring the cleavage of  
 CC polypeptides or polynucleotides, and for determining optimal polymer  
 CC substrates. ABP57505 to ABP57605 represent peptides used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 10 AA;  
 Query Match 88.2%; Score 30; DB 6; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db 3 QKLVPFA 9  
 RESULT 42  
 ID AAE35455  
 XX AAE35455 standard; peptide; 10 AA.  
 AC AAE35455;  
 XX  
 XX 17-JUN-2003 (first entry)  
 DT  
 XX Abeta peptide #26.  
 DE  
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW

KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.  
 XX  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..10  
 FT /note= "D-form residues"  
 FT  
 XX WO200296937-A2.  
 XX  
 XX 05-DEC-2002.  
 XX  
 XX 29-MAY-2002; 2002WO-CA000763.  
 XX  
 XX 29-MAY-2001; 2001US-00867847.  
 XX (NEUR-) NEUROCHEM INC.  
 XX  
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;  
 PI WPI; 2003-201269/19.  
 XX  
 XX Prevention and/or treatment of an amyloid-related disease e.g.  
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 XX  
 PS Claim 1; Page 59; 44pp; English.  
 XX  
 CC The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention  
 XX  
 SQ Sequence 10 AA;  
 Query Match 88.2%; Score 30; DB 6; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db 3 QKLVPFA 9  
 RESULT 43  
 ID ADQ37280  
 XX ADQ37280 standard; peptide; 10 AA.  
 AC ADQ37280;  
 XX  
 XX 07-OCT-2004 (first entry)  
 DT  
 XX Vaccine antigen amyloid-beta related amino acid sequence.  
 DE  
 XX

KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX  
 OS Synthetic.  
 XX  
 XX  
 PH Key Location/Qualifiers  
 FT Misc-difference 1. 10  
 FT /note= "D-form residues"  
 XX  
 XX WO2004058239-A1.  
 XX  
 XX 15-JUL-2004.  
 XX  
 XX 24-DEC-2003; 2003WO-CA002021.  
 XX  
 XX 24-DEC-2002; 2002US-0436379P.  
 XX  
 XX 23-JUN-2003; 2003US-0482214P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX  
 XX Gervais F, Bellini F;  
 XX WPI; 2004-543342/52.  
 XX  
 XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 XX that prevents or treats amyloid-beta related disease and second agent  
 XX that is either a peptide or peptidomimetic or an immune system modulator.  
 XX  
 XX Disclosure; Page 67; 143pp; English.  
 XX  
 XX The present invention describes compositions (C) comprising: (a) a first  
 XX agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 XX a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 XX modulates amyloid-beta fibril formation or induces a prophylactic or  
 XX therapeutic immune response against amyloid-beta fibril formation; or  
 XX (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 XX fibril formation. Also described is a kit comprising (C). (C) have  
 XX neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 XX ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 XX uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 XX neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 XX and can be used as amyloid-beta fibril formation modulators, and as  
 XX immune system modulators. (C) can be used for preventing or treating an  
 XX amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 XX (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 XX mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 XX amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 XX Down's syndrome, inclusion body myositis, age-related macular  
 XX degeneration, or a condition associated with Alzheimer's disease  
 XX (including hypothyroidism, cerebrovascular disease, cardiovascular  
 XX disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 XX aggression, or incontinence), a neurological condition (e.g. Huntington's  
 XX disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 XX Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 XX with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 XX field deficits, incoordination, gait disturbance, transient ischaemic  
 XX attack or stroke, transient alertness, attention deficit, frequent falls,  
 XX syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 XX haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 XX damage), or a psychological condition (e.g. depression, delusions,

CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as a vaccine antigen in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 10 AA;

Query Match 88.2%; Score 30; DB 8; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 Db 3 QKLVPFA 9  
 :|||||

RESULT 44  
 ADQ37371  
 ID ADQ37371 standard; peptide; 10 AA.  
 XX  
 AC ADQ37371;

DT 07-OCT-2004 (first entry)

DE Amyloid-beta polymerisation peptide.

XX amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.

OS Synthetic.

PN WO2004058239-A1.

PD 15-JUL-2004.

PF 24-DEC-2003; 2003WO-CA002021.

PR 24-DEC-2002; 2002US-0436379P.

PR 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

PI Gervais F, Bellini F;

DR WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 XX that prevents or treats amyloid-beta related disease and second agent  
 XX that is either a peptide or peptidomimetic or an immune system modulator.  
 XX

PS Disclosure; Page 95; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
 XX agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 XX a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 XX modulates amyloid-beta fibril formation or induces a prophylactic or

therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

CC nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, disturbance, hallucination, sexual disorder, weight loss, psychosis, a sleep ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; having amyloid-beta deposits. The present sequence represents an amyloid-beta polymerisation peptide which is used in the exemplification of the present invention.

XX Sequence 10 AA;

Query Match 88.2%; Score 30; DB 8; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 :|||||  
 Db 3 QKLVPFA 9

RESULT 45

ADQ37374  
 ID ADQ37374 standard; peptide; 10 AA.

XX AC ADQ37374;

XX DT 07-OCT-2004 (first entry)

XX DE Amyloid-beta polymerisation peptide.

XX amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; nootropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.

XX Synthetic.

XX WO2004058239-A1.  
 XX 15-JUL-2004.  
 XX 24-DEC-2003; 2003WO-CA002021.  
 XX 23-DEC-2002; 2002US-0436379P.  
 XX 23-JUN-2003; 2003US-0482214P.  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX Gervais F, Bellini F;  
 XX WPI, 2004-543342/52.

Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.  
 Disclosure; Page 95; 143pp; English.

The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C): (C) have nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; having amyloid-beta deposits. The present sequence represents an amyloid-beta polymerisation peptide which is used in the exemplification of the present invention.

XX Sequence 10 AA;

Query Match 88.2%; Score 30; DB 8; Length 10;

Best Local Similarity 85.7%; Pred. No. 13;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

Db 4 QKLVPFA 10

RESULT 46

ADY37939  
 ID ADY37939 standard; peptide; 10 AA.  
 XX AC ADY37939;  
 XX DT 19-MAY-2005 (first entry)  
 XX DE Amyloid-targeting peptide, SEQ ID NO:19, for use in imaging agent.  
 XX  
 KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 KW transmissible spongiform encephalopathy; scrapie; BSE;  
 KW Alzheimer's disease; neurological disease; amyloidosis;  
 KW non-insulin dependent diabetes; metabolic disorder.  
 XX  
 OS Synthetic.  
 XX US2005048000-A1.  
 XX PN 03-MAR-2005.  
 XX PD 03-DEC-2003; 2003US-00728028.  
 XX PF 25-JUL-2000; 2000US-0220808P.  
 XX PR 24-JUL-2001; 2001US-00915092.  
 XX PR 29-JAN-2003; 2003US-0443291P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX Gervais P, Kong X, Chalifour R, Migneault D;  
 XX WPI; 2005-212201/22.  
 XX  
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 PT related condition, e.g. Creutzfeldt-Jakob disease, bovine spongiform  
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.  
 XX  
 PS Disclosure; SEQ ID NO 19; 34pp; English.  
 XX  
 CC The invention relates to an amyloid-targeting imaging agent. The imaging  
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 CC a labeling moiety via a linking moiety, and is preferably able to cross  
 CC the blood-brain barrier. The invention also relates to a kit for  
 CC preparing a radiopharmaceutical preparation from the imaging agent of the  
 CC invention, a method for imaging amyloid deposition in a patient and a  
 CC method for diagnosing an amyloid-related condition in a patient. The  
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 CC related conditions such as Creutzfeldt-Jakob disease (CJD), Kuru,  
 CC transmissible cerebral amyloidosis (also known as transmissible virus  
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 CC mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 88.2%; Score 30; DB 9; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KKLVFPA 7  
 :|||||  
 Db 3 QKLVFPA 9

AAW32560  
 ID AAW32560 standard; peptide; 11 AA.  
 XX AC AAW32560;  
 XX DT 21-JAN-1998 (first entry)  
 XX DE Anti-amyloid peptide Abeta inhibiting abnormal protein folding.  
 XX  
 KW Anti-amyloid peptide; iAbeta; abnormal protein folding inhibitor;  
 KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;  
 KW human prion disease; Kuru; Creutzfeldt-Jakob disease;  
 KW Gerstmann-Strausler-Scheinker Syndrome; animal prion disease;  
 KW prion associated human neurodegenerative disease; scrapie;  
 KW spongiform encephalopathy; transmissible mink encephalopathy;  
 KW chronic wasting disease; mule; deer; elk; human.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO96399834-A1.  
 XX PN 19-DEC-1996.  
 XX PD 06-JUN-1996; 96WO-US010220.  
 XX PF 07-JUN-1995; 95US-00478326.  
 XX PR 10-APR-1996; 96US-00630645.  
 XX  
 XX (UANY ) UNIV NEW YORK STATE.  
 XX  
 XX Soto-Jara C, Baumann MH, Frangione B;  
 XX WPI; 1997-051637/05.  
 XX  
 XX New inhibitors of fibrillogenesis proteins or peptides - used for  
 PT preventing, treating or detecting amyloidosis disorders such as  
 PT Alzheimer's disease.  
 XX  
 XX Example 1; Fig 9; 63pp; English.  
 XX  
 CC A method has been developed for the prevention or treatment of a disorder  
 CC or disease associated with the formation of amyloid or amyloid-like  
 CC deposits, involving the abnormal folding of a protein or peptide. The  
 CC method involves administering an inhibitory peptide which prevents the  
 CC abnormal folding or which dissolves existing amyloid or amyloid-like  
 CC deposits, where the peptide comprises a sequence of 3-15 amino acid  
 CC residues and has a hydrophobic cluster of at least 3 amino acids, where  
 CC at least one of the 3 amino acids is a beta-sheet blocking amino acid  
 CC residue selected from Pro, Gly, Asn and His. The present sequence  
 CC represents an anti-amyloid peptide, Abeta, which inhibits abnormal  
 CC protein folding. The inhibitory peptide is capable of associating with a  
 CC structural determinant on the protein or peptide to structurally block  
 CC and inhibit the abnormal folding into amyloid or amyloid-like deposits.  
 CC The method can be used for preventing, treating or detecting e.g.  
 CC Alzheimer's dementia or disease, Down's syndrome, other amyloidosis  
 CC disorders, human prion diseases such as Kuru, Creutzfeldt-Jakob disease,  
 CC Gerstmann-Strausler-Scheinker Syndrome, prion associated human  
 CC neurodegenerative diseases or animal prion diseases such as scrapie,  
 CC spongiform encephalopathy, transmissible mink encephalopathy and chronic  
 CC wasting disease of mule deer and elk  
 XX  
 SQ Sequence 11 AA;  
 Query Match 88.2%; Score 30; DB 2; Length 11;  
 Best Local Similarity 85.7%; Pred. No. 14;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KKLVFPA 7  
 :|||||  
 Db 1 QKLVFPA 7

```

RESULT 48
AAU99431
ID AAU99431 standard; peptide; 11 AA.
XX
XX AC AAU99431;
XX
XX DT 07-OCT-2002 (first entry)
XX
XX DE Human amyloid beta-peptide (1ba6) helical segment.
XX
XX KW I-helical conformation; discordant helix; amyloid beta-peptide; I-helix;
XX theta-strand structure; amyloidogenic disorder; Abeta; amyloidosis;
XX Alzheimer's disease; prion disease; scrapie; BSE;
XX bovine spongiform encephalopathy; Creutzfeld-Jacob disease; CJD;
XX fibrillation; aggregation; neurotropic; neuroprotective; PDB;
XX protein databank code; 1ba6; human.
XX
XX OS Homo sapiens.
XX
XX PN WO200241002-A2.
XX
XX PD 23-MAY-2002.
XX
XX PF 20-NOV-2001; 2001WO-GB005117.
XX
XX PR 20-NOV-2000; 2000US-0253695P.
XX PR 06-DEC-2000; 2000US-0251662P.
XX
XX PA (ALPH-) ALPHABETA AB.
XX PA (WHIT/) WHITE M P.
XX
XX PI White MF, Johansson J;
XX
XX DR WPI; 2002-519389/55.
XX
XX PT Identifying compounds that stabilize I-helix of discordant helix in
XX polypeptide, by measuring amount of I-helix in sample containing
XX discordant helix-containing polypeptide in presence and absence of
XX compound.
XX
XX PS Example 1; Fig 2A; 55pp; English.
XX
XX CC The present invention relates to a method of identifying a compound that
XX stabilises an I-helical conformation of a discordant helix in a
XX polypeptide, particularly amyloid beta-peptide (Abeta). The method
XX comprises providing a test sample comprising a polypeptide that contains
XX a discordant helix in the form of an I-helix, contacting the test sample
XX with a test compound and determining the rate of decrease in the amount
XX of I-helix or the amount of I-helix present in the test sample. The
XX method is useful for identifying a compound that stabilises an I-helical
XX conformation of a discordant helix in a polypeptide. Such compounds are
XX useful for decreasing the rate of formation of theta-strand structures
XX between at least two discordant helix-containing polypeptides, and for
XX treating amyloidogenic disorders such as amyloidosis in Alzheimer's
XX disease, and prion diseases (e.g. scrapie, bovine spongiform
XX encephalopathy (BSE), Creutzfeld-Jacob disease (CJD)). AAU99426-AAU99446
XX represent >9-residue discordant helical segments from various proteins
XX
XX SQ Sequence 11 AA;
XX
XX Query Match 88.2%; Score 30; DB 5; Length 11;
XX Best Local Similarity 85.7%; Pred. No. 14;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KKLVPFA 7
XX :|||||
XX Db 1 QKLVPFA 7
XX
XX RESULT 49
AAE29504
ID AAE29504 standard; peptide; 11 AA.
XX
XX AC AAE29504;
XX
XX DT 27-JAN-2003 (first entry)
XX
XX DE Amyloid beta-protein related peptide #1.
XX
XX KW Metallopeptide; neurotropic; amyloid beta-protein; Alzheimer's disease; AD;
XX Prion's disease; oxytocin; angiotensin; vasopressin; neuroprotective;
XX therapy; amyloid beta-protein related peptide.
XX
XX OS Unidentified.
XX
XX PN WO200264734-A2.
XX
XX PD 22-AUG-2002.
XX
XX PF 19-DEC-2001; 2001WO-US050075.
XX
XX PR 19-DEC-2000; 2000US-0256842P.
XX PR 11-JUL-2001; 2001US-0304835P.
XX PR 04-OCT-2001; 2001US-0327835P.
XX
XX PA (PALA-) PALATIN TECHNOLOGIES INC.
XX
XX PI Sharma SD, Shi Y;
XX
XX DR WPI; 2002-740699/80.
XX
XX PT Determining secondary structure binding to desired targets within parent
XX polypeptides that bind to targets, by constructing and complexing
XX peptides to metal ions to form metallopeptides and screening the
XX metallopeptides.
XX
XX PS Claim 194; Page 98; 165pp; English.
XX
XX CC The invention relates to a method for identification and determination of
XX target-specific folding sites in peptides and proteins. The invention
XX also relates to a method for determining a secondary structure binding to
XX desired targets within parent polypeptides that bind to targets, by
XX constructing and complexing peptides to metal ions to form
XX metallopeptides and screening the metallopeptides. The method is useful
XX for determining secondary structure binding to desired target within
XX parent polypeptide with primary structure that binds to the target, where
XX the target of interest is a receptor, antibody, toxin, enzyme, hormone,
XX nucleic acid, intracellular protein domain of biological relevance or
XX extracellular protein domain of biological relevance. A library of
XX amyloid beta-protein related peptides is useful for the treatment of
XX Alzheimer's disease (AD). A library of peptides targeting vasopressin,
XX oxytocin or angiotensin receptor is useful for treating Prion's disease.
XX The present sequence is an amyloid beta-protein related peptide
XX
XX SQ Sequence 11 AA;
XX
XX Query Match 88.2%; Score 30; DB 5; Length 11;
XX Best Local Similarity 85.7%; Pred. No. 14;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KKLVPFA 7
XX :|||||
XX Db 2 EKLVPFA 8
XX
XX RESULT 50
ABU79013
ID ABU79013 standard; peptide; 11 AA.
XX
XX AC ABU79013;
XX
XX DT 17-JUN-2003 (first entry)
XX
XX DE Amyloidogenic Amyloid A peptide #3.
XX
XX KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;

```



KW pathological beta-sheet-rich conformation; Down's syndrome;  
 KW amyloidosis disorder; human prion disease; kuru; CJD;  
 KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;  
 KW prion associated human neurodegenerative disease; animal prion disease;  
 KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;  
 KW chronic wasting disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US6462171-B1.  
 XX  
 XX PD 08-OCT-2002.  
 XX  
 XX PF 12-DEC-1996; 96US-00766596.  
 XX  
 XX PR 07-JUN-1995; 95US-00478326.  
 XX PR 10-APR-1996; 96US-00630645.  
 XX  
 XX PA (UTNY ) UNIV NEW YORK STATE.  
 XX  
 XX PI Soto-Jara C, Baumann MH, Frangione B;  
 XX  
 XX DR WPI; 2003-379012/36.  
 XX  
 XX PT Novel inhibitory peptides which inhibit and structurally block abnormal  
 PT folding of protein into amyloid or amyloid-like deposit and into  
 PT pathological beta-sheet rich conformation, useful for treating  
 PT Alzheimer's disease.  
 XX  
 XX PS Disclosure; Fig 9; 5lpp; English.  
 XX  
 CC The invention describes an isolated inhibitory peptide (I) which  
 CC interacts with a hydrophobic beta-sheet forming cluster of amino acid  
 CC residues on a protein or peptide for amyloid or amyloid-like deposit  
 CC formation, and inhibits or structurally blocks the abnormal folding of  
 CC proteins and peptides into amyloid or amyloid-like deposits and into  
 CC pathological beta-sheet-rich conformation. (I) is useful for disorders or  
 CC diseases associated with abnormal protein folding into amyloid or amyloid  
 CC -like deposits or into pathological beta-sheet-rich precursors of such  
 CC disorders, such as Alzheimer's disease, Down's syndrome, other amyloidosis  
 CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease  
 CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated  
 CC human neurodegenerative diseases as well as animal prion diseases such as  
 CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and  
 CC chronic wasting disease of mule deer and elk. (I) is also useful for  
 CC detecting and diagnosing the presence or absence of amyloid or amyloid-  
 CC like deposits in vivo and its precursors. This is the amino acid sequence  
 CC of peptide associated with the inhibition of amyloid or amyloid like  
 CC deposits  
 XX  
 XX SQ Sequence 11 AA;  
 Query Match 88.2%; Score 30; DB 6; Length 11;  
 Best Local Similarity 85.7%; Pred. No. 14;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KKLVPFA 7  
 Db 1 QKLVPFA 7  
 :|||||  
 :|||||  
 RESULT 51  
 ABR84683  
 ID ABR84683 standard; peptide; 11 AA.  
 XX  
 XX AC ABR84683;  
 XX  
 XX DT 18-DEC-2003 (first entry)  
 XX  
 XX DE Aggrecaanase-1 and -2 peptide substrate SEQ ID NO: 33.  
 XX Human; truncated aggrecaanase-1; aggrecaanase-1; aggrecaanase-2;  
 KW metalloprotease; enzyme; substrate.

XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH modified\_site 1  
 FT modified\_site 11 /note= "modified by Aedans"  
 FT modified\_site 11 /note= "modified by (Dabcy1)K-amide"  
 FT  
 XX WO2003062263-A2.  
 XX  
 XX PD 31-JUL-2003.  
 XX  
 XX PF 15-JAN-2003; 2003WO-US001327.  
 XX  
 XX PR 16-JAN-2002; 2002US-00050200.  
 XX  
 XX PA (ORTH-) ORTHO MC NEIL PHARM INC.  
 XX  
 XX PI Fourie A, Karlsson L, Coles P;  
 XX  
 XX DR WPI; 2003-748002/70.  
 XX  
 XX PT New peptides useful as aggrecaanase substrates in assays for aggrecaanase  
 PT inhibitors comprise an aggrecaanase cleavage site between a glutamic acid  
 PT residue and a nonpolar or uncharged residue.  
 XX  
 XX PS Example 2; Page 52; Opp; English.  
 XX  
 XX CC The present invention relates to peptides having an aggrecaanase cleavage  
 CC site between a glutamic acid residue on the N-terminal side and a  
 CC nonpolar or uncharged residue on the C-terminal side, and capable of  
 CC being cleavable by aggrecaanase-1 and/or aggrecaanase-2. The peptides are  
 CC useful as aggrecaanase substrates in high-throughput screening assays for  
 CC aggrecaanase inhibitors as potential therapeutic compounds. The present  
 CC sequence is a peptide substrate of human aggrecaanase-1 and -2 proteins  
 XX  
 XX SQ Sequence 11 AA;  
 Query Match 88.2%; Score 30; DB 7; Length 11;  
 Best Local Similarity 85.7%; Pred. No. 14;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KKLVPFA 7  
 Db 5 QKLVPFA 11  
 :|||||  
 :|||||  
 RESULT 52  
 ABR00147  
 ID ABR00147 standard; peptide; 11 AA.  
 XX  
 XX AC ABR00147;  
 XX  
 XX DT 15-JAN-2004 (first entry)  
 XX  
 XX DE Amyloid-beta (Abeta) peptide.  
 XX  
 XX KW Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;  
 KW Alzheimer's disease; amyloid-beta; Abeta.  
 XX  
 XX OS Unidentified.  
 XX  
 XX PN US2003087407-A1.  
 XX  
 XX PD 08-MAY-2003.  
 XX  
 XX PF 06-SEP-2002; 2002US-00235483.  
 XX  
 XX PR 07-JUN-1995; 95US-00478326.  
 XX PR 10-APR-1996; 96US-00630645.  
 XX PR 12-DEC-1996; 96US-00766596.  
 XX



```

PA (UUNY ) UNIV NEW YORK STATE.
XX
XX Soto-Jara C, Baumann MH, Frangione B;
XX WPI; 2003-616149/58.
XX
XX New inhibitory peptide, useful for preparing a composition for
PT diagnosing, preventing or treating disorders associated with amyloid-like
PT fibril deposits, e.g. Alzheimer's disease, or prion related
PT encephalopathies.
XX
XX Disclosure; Fig 9; 52pp; English.
XX
XX The invention relates to inhibitory peptide comprising a portion of at
XX least three amino acid residues and a sequence predicted not to adopt a
XX beta-sheet structure that associates with a hydrophobic beta-sheet
XX cluster on a protein or peptide involved in the abnormal folding into a
XX beta-sheet structure, to structurally block the abnormal folding of the
XX protein or peptide. The inhibitory peptide is useful for preparing a
XX composition for preventing, treating or detecting disorders or diseases
XX associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
XX prion related encephalopathies. The invention is also useful in gene
XX therapy. The present sequence is amyloid-beta (Abeta) peptide. This
XX peptide is used in the invention
XX
XX Sequence 11 AA;
SQ
Query Match 88.2%; Score 30; DB 7; Length 11;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPFFA 7
Db :|||||
1 QKLVPFFA 7

RESULT 53
AAE35464
ID AAE35464 standard; peptide; 12 AA.
XX
XX AAE35464;
XX
XX 17-JUN-2003 (first entry)
XX
XX Abeta peptide #35.
XX
XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
XX cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
XX psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
XX Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
XX chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotrophic;
XX Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
XX ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Misc-difference 7..12 /note= "D-form residues"
XX
XX WO200296937-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-CA000763.
XX
XX 29-MAY-2001; 2001US-00867847.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais P, Hebert L, Chalifour RJ, Kong X;
XX WPI; 2003-201269/19.
XX

XX Prevention and/or treatment of an amyloid-related disease e.g.
XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
XX
XX Claim 1; Page 61; 44pp; English.
XX
XX The invention relates to a method for prevention and/or treatment of an
XX amyloid-related disease which comprises administration of an all-D -
XX amyloid-beta peptide. The method is used for preventing and/or treating
XX Alzheimer's and other amyloid related disease e.g. cerebral amyloid
XX angiopathy; for altering serum levels of amyloid-beta in a mammal and
XX favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
XX the mammal; and reducing or inhibiting the formation of plaques. It is
XX also used for treating AA (reactive) amyloid diseases including
XX inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
XX arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
XX Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
XX disease. AA deposits are also produced as a result of chronic microbial
XX infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
XX ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
XX Certain malignant neoplasms can also result in AA fibril amyloid deposits
XX including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
XX and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
XX present sequence is an Abeta peptide used to illustrate the method of the
XX invention
XX
XX Sequence 12 AA;
SQ
Query Match 88.2%; Score 30; DB 6; Length 12;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPFFA 7
Db :|||||
6 QKLVPFFA 12

RESULT 54
AAE35435
ID AAE35435 standard; peptide; 12 AA.
XX
XX AAE35435;
XX
XX 17-JUN-2003 (first entry)
XX
XX Abeta peptide #6.
XX
XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
XX cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
XX psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
XX Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
XX chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotrophic;
XX Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
XX ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Misc-difference 1..12 /note= "D-form residues"
XX
XX WO200296937-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-CA000763.
XX
XX 29-MAY-2001; 2001US-00867847.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Hebert L, Chalifour RJ, Kong X;
XX PI
XX WPI; 2003-201269/19.
XX

```

DR WPI; 2003-201269/19.  
 XX Prevention and/or treatment of an amyloid-related disease e.g.  
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 PS Claim 1; Page 58; 44pp; English.  
 XX The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention  
 XX SQ Sequence 12 AA;  
 Query Match 88.2%; Score 30; DB 6; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db :|||||  
 6 QKLVPFA 12  
 RESULT 55  
 AAE35466  
 ID AAE35466 standard; peptide; 12 AA.  
 AC AAE35466;  
 XX 17-JUN-2003 (first entry)  
 DT Abeta peptide #37.  
 DE All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.  
 XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..12 /note= "D-form residues"  
 FT  
 FT WO200296937-A2.  
 FN 05-DEC-2002.  
 XX 29-MAY-2002; 2002WO-CA000763.  
 XX 29-MAY-2001; 2001US-00867847.  
 XX (NEUR-) NEUROCHEM INC.  
 PA Gervais F, Hebert L, Chalfour RJ, Kong X;

XX WPI; 2003-201269/19.  
 XX Prevention and/or treatment of an amyloid-related disease e.g.  
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 PS Claim 1; Page 61; 44pp; English.  
 XX The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention  
 XX SQ Sequence 12 AA;  
 Query Match 88.2%; Score 30; DB 6; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db :|||||  
 3 QKLVPFA 9  
 RESULT 56  
 ADD20745  
 ID ADD20745 standard; peptide; 12 AA.  
 AC ADD20745;  
 XX 15-JAN-2004 (first entry)  
 DT Human beta-amyloid 10-21 H13Q amino acid sequence SEQ ID NO:3.  
 DE self-assembly; peptide-based structure; beta-amyloid;  
 KW self-assembling structure; molecular-level probing; human.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX WO2003082900-A2.  
 XX 09-OCT-2003.  
 XX 24-MAR-2003; 2003WO-US009229.  
 XX 22-MAR-2002; 2002US-0366826P.  
 XX 23-OCT-2002; 2002US-0420746P.  
 XX 21-MAR-2003; 2003US-0456641P.  
 XX (UYEM-) UNIV EMORY.  
 XX Lynn D, Conticello V, Morgan DA, Dong J;  
 XX WPI; 2003-804023/75.  
 XX Controlling self-assembly of peptide-based structures (e.g. nanotubes)  
 PT comprises providing a controlled environment and placing segments of beta

PT -amyloids in the controlled environment to generate a self-assembling  
 PT structure.  
 XX  
 PS Claim 1; SEQ ID NO 3; 46pp; English.  
 XX  
 CC The present invention describes a method (M1) for controlling self-  
 CC assembly of self-assembling peptide-based structures by providing a  
 CC controlled environment and placing segments of beta-amyloids in the  
 CC controlled environment to generate a self-assembling structure. Also  
 CC described: (1) a method (M1a) for controlling self-assembly of peptide-  
 CC based structures comprising providing a controlled environment adapted to  
 CC redirect a self-assembly process, and generating a self-assembling  
 CC peptide-based structure by placing the self-assembling peptide in the  
 CC controlled environment; and (2) a self-assembling peptide-based structure  
 CC comprising beta-amyloid segments, optionally with a conservative amino  
 CC acid substitution; and hydrogen bonds formed between the segments of the  
 CC beta-amyloid. The method is useful in controlling the self-assembly of  
 CC self-assembling peptide-based structures. The self-assembling peptide  
 CC structures may be used in generating devices at a molecular level to  
 CC permit molecular-level probing. The present sequence represents a human  
 CC beta-amyloid 10-21 H13Q variant amino acid sequence, which is used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 12 AA;

Query Match 88.2%; Score 30; DB 7; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 :|||||  
 DB 6 QKLVPFA 12

RESULT 57  
 ADD20744  
 ID ADD20744 standard; peptide; 12 AA.  
 XX  
 AC ADD20744;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human beta-amyloid 10-21 E11N amino acid sequence SEQ ID NO:2.  
 XX  
 KW self-assembly; peptide-based structure; beta-amyloid;  
 KW self-assembling structure; molecular-level probing; human.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003082900-A2.  
 XX  
 PD 09-OCT-2003.  
 XX  
 PF 24-MAR-2003; 2003WO-US009229.  
 XX  
 PR 22-MAR-2002; 2002US-0366826P.  
 PR 23-OCT-2002; 2002US-0420746P.  
 PR 21-MAR-2003; 2003US-0456641P.  
 XX  
 PA (UYEM-) UNIV EMORY.  
 XX  
 XX Lynn D, Conticello V, Morgan DA, Dong J;  
 XX WPI; 2003-804023/75.  
 XX  
 XX Controlling self-assembly of peptide-based structures (e.g. nanotubes)  
 PT comprises providing a controlled environment and placing segments of beta  
 PT -amyloids in the controlled environment to generate a self-assembling  
 PT structure.  
 XX  
 XX Claim 1; SEQ ID NO 2; 46pp; English.

CC The present invention describes a method (M1) for controlling self-  
 CC assembly of self-assembling peptide-based structures by providing a  
 CC controlled environment and placing segments of beta-amyloids in the  
 CC controlled environment to generate a self-assembling structure. Also  
 CC described: (1) a method (M1a) for controlling self-assembly of peptide-  
 CC based structures comprising providing a controlled environment adapted to  
 CC redirect a self-assembly process, and generating a self-assembling  
 CC peptide-based structure by placing the self-assembling peptide in the  
 CC controlled environment; and (2) a self-assembling peptide-based structure  
 CC comprising beta-amyloid segments, optionally with a conservative amino  
 CC acid substitution; and hydrogen bonds formed between the segments of the  
 CC beta-amyloid. The method is useful in controlling the self-assembly of  
 CC self-assembling peptide-based structures. The self-assembling peptide  
 CC structures may be used in generating devices at a molecular level to  
 CC permit molecular-level probing. The present sequence represents a human  
 CC beta-amyloid 10-21 E11N variant amino acid sequence, which is used in the  
 CC exemplification of the present invention.

XX Sequence 12 AA;

Query Match 88.2%; Score 30; DB 7; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
 :|||||  
 DB 6 QKLVPFA 12

RESULT 58  
 ADJ71476  
 ID ADJ71476 standard; peptide; 12 AA.  
 XX  
 AC ADJ71476;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE N-terminal truncated beta-amyloid peptide, SEQ ID 139.  
 XX  
 KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;  
 KW amyloid precursor protein; APP; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004013172-A2.  
 XX  
 PD 12-FEB-2004.  
 XX  
 PF 18-JUL-2003; 2003WO-EP007833.  
 XX  
 PR 24-JUL-2002; 2002EP-00447147.  
 PR 06-AUG-2002; 2002US-0401497P.  
 XX  
 XX (INNO-) INNOGENETICS NV.  
 XX  
 PI Delacourte A, Sergeant N;  
 XX WPI; 2004-180423/17.  
 XX  
 PT New beta-amyloid or amyloid precursor protein preparation, useful as a  
 PT prophylactic vaccine or a therapeutic for preventing or treating a  
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.  
 PT Alzheimer's disease.  
 XX  
 PS Claim 4; Page 64; 104pp; English.

XX The present invention relates to preparations (I) comprising a beta-  
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-  
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal  
 CC fragment. The beta-amyloid or APP preparations are useful for  
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a  
 CC prophylactic vaccine for the prevention, or as a therapeutic for the  
 CC treatment of a disease associated with beta-amyloid formation and/or

CC aggregation, such as Alzheimer's disease.  
 XX Sequence 12 AA;  
 SQ Query Match 88.2%; Score 30; DB 8; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
 Db :|||||  
 6 QKLVPFA 12

RESULT 59  
 ADQ37407  
 ID ADQ37407 standard; peptide; 12 AA.  
 XX AC ADQ37407;  
 XX DT 07-OCT-2004 (first entry)  
 XX DE Amyloid-beta amino acid sequence.  
 XX KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX OS Synthetic.  
 XX XH Key Location/Qualifiers  
 FT Misc-difference 7.12 /note= "D-form residues"

XX WO2004058239-A1.  
 XX 15-JUL-2004.  
 XX 24-DEC-2003; 2003MO-CA002021.  
 XX 24-DEC-2002; 2002US-0436379P.  
 XX 23-JUN-2003; 2003US-0482214P.  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX Gervais F, Bellini F;  
 XX WPI; 2004-543342/52.  
 XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.  
 PS Disclosure; Page 68; 143pp; English.  
 XX The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have

CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an APOE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents an amyloid-  
 CC beta amino acid sequence, which can be used as a vaccine antigen in the  
 CC exemplification of the present invention.  
 XX SQ Sequence 12 AA;  
 Query Match 88.2%; Score 30; DB 8; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
 Db :|||||  
 6 QKLVPFA 12

RESULT 60  
 ADQ37289  
 ID ADQ37289 standard; peptide; 12 AA.  
 XX AC ADQ37289;  
 XX DT 07-OCT-2004 (first entry)  
 XX DE Vaccine antigen amyloid-beta related amino acid sequence.  
 XX KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX OS Synthetic.  
 XX XH Key Location/Qualifiers  
 FT Misc-difference 1.12

FT XX /note= "D-form residues"

PN WO2004058239-A1.

XX 15-JUL-2004.

PD 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

PA Gervais F, Bellini F;

XX WPI; 2004-543342/52.

DR Composition for treating e.g. Alzheimer's disease comprises first agent

PT that prevents or treats amyloid-beta related disease and second agent

PT that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 68; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

CC nontropic, neuroprotective, cerebroprotective, haemostatic,

CC ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,

CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,

CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,

CC and can be used as amyloid-beta fibril formation modulators, and as

CC immune system modulators. (C) can be used for preventing or treating an

CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic

CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,

CC mild-to-moderate cognitive impairment, vascular dementia, cerebral

CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,

CC Down's syndrome, inclusion body myositis, age-related macular

CC degeneration, or a condition associated with Alzheimer's disease

CC (including hypothyroidism, cerebrovascular disease, cardiovascular

CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

CC aggression, or incontinence), a neurological condition (e.g. Huntington's

CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,

CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia

CC with Lewy bodies), altered muscle tone, seizures, sensory loss, visual

CC field deficits, incoordination, gait disturbance, transient ischaemic

CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural

CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic

CC damage), or a psychological condition (e.g. depression, delusions,

CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep

CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal

CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or

CC excessive guilt)) in a subject e.g. human having a genomic mutation in an

CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;

CC having amyloid-beta deposits. The present sequence represents a peptide

CC that can be used as a vaccine antigen in the exemplification of the

XX present invention.

XX Sequence 12 AA;

Query Match 88.2%; Score 30; DB 8; Length 12;

Best Local Similarity 85.7%; Pred. No. 16;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

Db 3 QKLVPFA 9

RESULT 61

ADQ37259

ID ADQ37259 standard; peptide; 12 AA.

XX AC ADQ37259;

XX 07-OCT-2004 (first entry)

DT Vaccine antigen amyloid-beta related amino acid sequence.

DE amyloid-beta; amyloid-beta related disease;

XX amyloid-beta fibril formation; immune response; nontropic;

XX neuroprotective; cerebroprotective; haemostatic; ophthalmological;

XX antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;

XX anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

XX cardiant; antidepressant; endocrine; hypnotic;

XX amyloid-beta fibril formation modulator; immune system modulator;

XX Alzheimer's disease; mild cognitive impairment;

XX mild-to-moderate cognitive impairment; vascular dementia;

XX cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

XX senile dementia; Down's syndrome; inclusion body myositis;

XX age-related macular degeneration; hypothyroidism;

XX cerebrovascular disease; cardiovascular disease; memory loss; anxiety;

XX behavioural dysfunction; neurological condition; psychological condition;

XX vaccine antigen.

XX Synthetic.

OS Key Location/Qualifiers

FT Misc-difference 1..12 /note= "D-form residues"

FT WO2004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent

XX that prevents or treats amyloid-beta related disease and second agent

XX that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

CC nontropic, neuroprotective, cerebroprotective, haemostatic,

CC ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,

CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,

CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,

CC and can be used as amyloid-beta fibril formation modulators, and as

CC immune system modulators. (C) can be used for preventing or treating an

CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic

CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,

CC mild-to-moderate cognitive impairment, vascular dementia, cerebral

CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,

CC Down's syndrome, inclusion body myositis, age-related macular

CC degeneration, or a condition associated with Alzheimer's disease

CC (including hypothyroidism, cerebrovascular disease, cardiovascular

CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

CC aggression, or incontinence), a neurological condition (e.g. Huntington's

CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,

CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia

CC with Lewy bodies), altered muscle tone, seizures, sensory loss, visual

CC field deficits, incoordination, gait disturbance, transient ischaemic

CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural

CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic

CC damage), or a psychological condition (e.g. depression, delusions,

CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep

CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal

CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or

CC excessive guilt)) in a subject e.g. human having a genomic mutation in an

CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;

CC having amyloid-beta deposits. The present sequence represents a peptide

CC that can be used as a vaccine antigen in the exemplification of the

XX present invention.

CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt) in a subject e.g. human having a genomic mutation in or having amyloid precursor protein gene, an ApoE gene, or a presenilin gene; CC having amyloid-beta deposits. The present sequence represents a peptide CC that can be used as a vaccine antigen in the exemplification of the CC present invention.

XX SQ Sequence 12 AA;

Query Match 88.2%; Score 30; DB 8; Length 12;  
Best Local Similarity 85.7%; Pred. No. 16;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 6 QKLVPFA 12

RESULT 62

ADZ08890  
ID ADZ08890 standard; peptide; 12 AA.

XX AC ADZ08890;

XX DT 16-JUN-2005 (first entry)

XX DE Human beta-amyloid peptide (SEQ ID No:115) probed with anti-amyloid IgG.

XX KW amyloid; antibody engineering; antibody production;  
XX KW amyloid-associated disorder; Alzheimer's disease; cancer; allergy;  
XX KW autoimmune disease; Parkinson's disease;  
XX KW acquired immune deficiency syndrome; multiple sclerosis; migraine;  
XX KW dementia; infection; nootropic; neuroprotective; cytostatic;  
XX KW antiallergic; immunosuppressive; antiparkinsonian; antimigraine;  
XX KW antimicrobial; anti-HIV; beta-amyloid.

XX OS Homo sapiens.

XX FN WO2005028511-A2.

XX PD 31-MAR-2005.

XX PF 26-MAR-2004; 2004WO-US009522.

XX PR 28-MAR-2003; 2003US-0458469P.

XX PR 28-MAR-2003; 2003US-0458474P.

XX PR 28-MAR-2003; 2003US-0458509P.

XX PR 28-MAR-2003; 2003US-0458510P.

XX PA (CENZ ) CENTOCOR INC.

XX PA (MERC/) MERCKEN M.

XX PA (BENS/) BENSON J M.

XX PI Mercken M, Benson JM;

XX DR WPI; 2005-242565/25.

XX PT New isolated mammalian anti-amyloid antibodies useful for treating  
XX PT amyloid-associated disorders, such as Alzheimer's disease, cancer,  
XX PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,  
XX PT migraine and dementia.

XX Example 4; SEQ ID NO 115; 306pp; English.

XX The invention relates to at least one isolated mammalian amyloid antibody  
XX comprising at least one variable region comprising at least one heavy  
XX chain and at least one light chain, of a fully defined sequence of SEQ ID  
CC NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:  
CC (i) at least one isolated mammalian amyloid antibody that binds to the  
CC same region of an amyloid polypeptide as an antibody comprising at least  
CC one heavy chain or light chain complementarity determining region (CDR)  
CC having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)  
CC at least one isolated mammalian amyloid antibody, comprising at least one  
CC human CDR, where the antibody specifically binds at least one epitope  
CC selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined  
CC sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic  
CC acid encoding at least one of any of the isolated mammalian amyloid  
CC antibodies mentioned and having at least one human CDR of a fully defined  
CC sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an  
CC isolated nucleic acid vector comprising an isolated nucleic acid encoding  
CC an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising  
CC an isolated nucleic acid encoding an amyloid antibody, (vi) a method of  
CC producing at least one amyloid antibody, (vii) a composition comprising  
CC at least one of the isolated mammalian amyloid antibodies  
CC mentioned, and at least one pharmaceutical carrier or diluent, (viii) an  
CC anti-idiotypic antibody or fragment that specifically binds at least one  
CC of the amyloid antibodies mentioned, (ix) a method of diagnosing or  
CC treating an amyloid related condition in a cell, tissue, organ or animal,  
CC comprising contacting or administering a composition comprising at least  
CC one of the antibodies mentioned, with, or to, the cell, tissue, organ or  
CC animal, (x) a medical device comprising at least one amyloid antibody  
CC mentioned, where the device is suitable for contacting or administering  
CC at least one amyloid antibody, (xi) an article of manufacture for human  
CC pharmaceutical or diagnostic use, comprising packaging material and a  
CC container comprising a solution or a lyophilized form of at least one of  
CC the amyloid antibodies mentioned, and (xii) a method of producing at  
CC least one of the isolated mammalian amyloid antibodies, comprising  
CC providing a host cell or transgenic animal or transgenic plant or plant  
CC cell capable of expressing the antibody in recoverable amounts. The  
CC methods and compositions of the present invention are useful for  
CC producing therapeutic compositions and devices for treating amyloid-  
CC associated disorders, such as Alzheimer's disease, cancer, allergies,  
CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,  
CC migraine, dementia and infections. This sequence represents a peptide  
XX from human beta-amyloid probed with anti-beta-amyloid IgG antibodies.

XX SQ Sequence 12 AA;

Query Match 88.2%; Score 30; DB 9; Length 12;  
Best Local Similarity 85.7%; Pred. No. 16;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 6 QKLVPFA 12

RESULT 63

ADA37467

ID ADA37467 standard; peptide; 13 AA.

XX AC ADA37467;

XX DT 20-NOV-2003 (first entry)

XX DE Human amyloid precursor protein fragment.

XX KW ADAM; a disintegrin and metalloprotease; G-protein coupled receptor;  
XX KW GPCR; beta-amyloid precursor protein; APP; alpha-secretase site;  
XX KW Alzheimer's disease.

XX OS Homo sapiens.

XX FN US2003108978-A1.

XX PD 12-JUN-2003.  
 XX PF 25-OCT-2002; 2002US-00281458.  
 XX PR 25-OCT-2001; 2001US-0337641P.  
 XX PA (CIAM/) CIAMBRONE G J.  
 XX PI (GIBB/) GIBBONS I.  
 XX PI Ciambone GJ, Gibbons I;  
 XX WPI; 2003-626205/59.  
 XX PT Assaying activity of an a disintegrin and metalloprotease in whole cell  
 PT system combining soluble substrate with whole cell system, and  
 PT determining amount of product.  
 XX PT Disclosure; Page 9; 34pp; English.  
 XX CC The invention relates to the activity of a disintegrin and  
 CC metalloprotease (ADAM) in a whole cell system assayed by selecting a  
 CC soluble substrate that is specifically cleavable by the ADAM, combining  
 CC the soluble substrate with the whole cell system under conditions that  
 CC allow processing of the substrate to a product by the ADAM and  
 CC determining the amount of the product as an indication of the ADAM  
 CC activity. Also included is a method of determining the effect of a G-  
 CC protein coupled receptor (GPCR) on the activity of an ADAM in a whole  
 CC cell system comprising selecting a ligand known to modulate activity of  
 CC the GPCR and a soluble substrate that is cleavable by the ADAM, preparing  
 CC two mixtures of the whole cell system and the soluble substrate, where  
 CC only one of the mixtures contains the ligand, incubating the mixtures  
 CC under conditions that allow processing of the substrate to a product by  
 CC the ADAM, if the ADAM is active, determining the amount of the product  
 CC formed in each mixture and comparing the amount of product formed in  
 CC separate mixtures to determine effect of the GPCR on the ADAM activity.  
 CC The method may be adapted to assay the effect of a compound on the  
 CC cleavage of the Beta-amyloid precursor protein (APP) at its alpha-  
 CC secretase site by ADAM 17 or ADAM 10. The invention is used for the  
 CC assaying for the activity of an ADAM in a whole cell system. The assay  
 CC may be used in the diagnosis of diseases associated with ADAM activities  
 CC e.g. Alzheimer's disease. The present sequence is the human APP peptide  
 CC fragment containing the alpha-secretase site.  
 XX SQ Sequence 13 AA;  
 Query Match 88.2%; Score 30; DB 6; Length 13;  
 Best Local Similarity 85.7%; Pred. No. 17;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVFFA 7  
 Db :|||||  
 5 QKLVFFA 11  
 RESULT 64  
 ADJ71477  
 ID ADJ71477 standard; peptide; 13 AA.  
 AC ADJ71477;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE N-terminal truncated beta-amyloid peptide, SEQ ID 140.  
 XX KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;  
 KW amyloid precursor protein; APP; Alzheimer's disease.  
 XX OS Homo sapiens.  
 XX PN WO2004013172-A2.  
 XX PD 12-FEB-2004.  
 XX PF 18-JUL-2003; 2003WO-EP007833.  
 XX PR 24-JUL-2002; 2002EP-00447147.  
 XX PR 06-AUG-2002; 2002US-0401497P.  
 XX PA (INNO-) INNOGENETICS NV.  
 XX PI Delacourte A, Sergeant N;  
 XX WPI; 2004-180423/17.  
 XX PT New beta-amyloid or amyloid precursor protein preparation, useful as a  
 PT prophylactic vaccine or a therapeutic for preventing or treating a  
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.  
 PT Alzheimer's disease.

XX PF 18-JUL-2003; 2003WO-EP007833.  
 XX PR 24-JUL-2002; 2002EP-00447147.  
 XX PR 06-AUG-2002; 2002US-0401497P.  
 XX PA (INNO-) INNOGENETICS NV.  
 XX PI Delacourte A, Sergeant N;  
 XX WPI; 2004-180423/17.  
 XX PT New beta-amyloid or amyloid precursor protein preparation, useful as a  
 PT prophylactic vaccine or a therapeutic for preventing or treating a  
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.  
 PT Alzheimer's disease.  
 XX PS Claim 4; Page 64; 104pp; English.  
 XX CC The present invention relates to preparations (I) comprising a beta-  
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-  
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal  
 CC fragment. The beta-amyloid or APP preparations are useful for  
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a  
 CC prophylactic vaccine for the prevention, or as a therapeutic for the  
 CC treatment of a disease associated with beta-amyloid formation and/or  
 CC aggregation, such as Alzheimer's disease.  
 XX SQ Sequence 13 AA;  
 Query Match 88.2%; Score 30; DB 8; Length 13;  
 Best Local Similarity 85.7%; Pred. No. 17;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVFFA 7  
 Db :|||||  
 6 QKLVFFA 12  
 RESULT 65  
 ADJ71464  
 ID ADJ71464 standard; peptide; 13 AA.  
 XX AC ADJ71464;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE N-terminal truncated beta-amyloid peptide, SEQ ID 127.  
 XX KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;  
 KW amyloid precursor protein; APP; Alzheimer's disease.  
 XX OS Homo sapiens.  
 XX PN WO2004013172-A2.  
 XX PD 12-FEB-2004.  
 XX PF 18-JUL-2003; 2003WO-EP007833.  
 XX PR 24-JUL-2002; 2002EP-00447147.  
 XX PR 06-AUG-2002; 2002US-0401497P.  
 XX PA (INNO-) INNOGENETICS NV.  
 XX PI Delacourte A, Sergeant N;  
 XX WPI; 2004-180423/17.  
 XX PT New beta-amyloid or amyloid precursor protein preparation, useful as a  
 PT prophylactic vaccine or a therapeutic for preventing or treating a  
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.  
 PT Alzheimer's disease.



XX PS Claim 4; Page 63; 104pp; English.

XX CC The present invention relates to preparations (I) comprising a beta-amyloid peptide variant or beta-amyloid N-terminal fragment, or N-terminal amyloid precursor protein (APP) soluble fragment or C-terminal fragment. The beta-amyloid or APP preparations are useful for manufacturing a prophylactic vaccine or a therapeutic, or as a prophylactic vaccine for the prevention, or as a therapeutic for the treatment of a disease associated with beta-amyloid formation and/or aggregation, such as Alzheimer's disease.

XX CC Sequence 13 AA;

XX SQ Query Match 88.2%; Score 30; DB 8; Length 13;  
Best Local Similarity 85.7%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7  
Db 7 QKLVEFA 13

RESULT 66

ADA89887

ID ADA89887 standard; peptide; 14 AA.

XX AC ADA89887;

XX DT 20-NOV-2003 (first entry)

XX DE Beta-A4 second region peptide SEQ ID NO:2.

XX KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nontropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage with parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging.

XX OS Synthetic.

XX OS Homo sapiens.

XX FN WO2003070760-A2.

XX PD 28-AUG-2003.

XX PF 20-FEB-2003; 2003WO-EP001759.

XX PR 20-FEB-2002; 2002EP-00003844.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PA (MORP) MORPHOSYS AG.

XX PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T; Loehning C, Loetscher H, Nordstedt C, Rothe C;

XX DR WPI; 2003-663848/62.

XX PT New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia).

XX PS Claim 1; Page 99; 312pp; English.

XX CC The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule

CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (1), comprising culturing the host cell of (3) under conditions that allow synthesis of (1) and recovering (1) from the culture; (5) a composition comprising (1) or an antibody molecule produced by method (4); (6) a kit comprising (1), nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Fab optimisation library by panning against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a pharmaceutical composition prepared by method (8). (1) has neuroprotective, nontropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (I), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 14 AA;

Query Match 88.2%; Score 30; DB 6; Length 14;  
Best Local Similarity 85.7%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7  
Db 4 QKLVEFA 10

## RESULT 67

ADJ71452

ID ADJ71452 standard; peptide; 14 AA.

XX AC ADJ71452;

XX DT 06-MAY-2004 (first entry)

XX DE N-terminal truncated beta-amyloid peptide, SEQ ID 115.

XX KW Nontropic; Neuroprotective; Vaccine; beta Amyloid;  
KW amyloid precursor protein; APP; Alzheimer's disease.

XX OS Homo sapiens.

XX FN WO2004013172-A2.

XX PD 12-FEB-2004.

XX PF 18-JUL-2003; 2003WO-EP007833.

XX PR 24-JUL-2002; 2002EP-00447147.

XX PR 06-AUG-2002; 2002US-0401497P.

XX PA (INNO-) INNOGENETICS NV.

XX PI Delacourte A, Sergeant N;

XX DR WPI; 2004-180423/17.

XX PT New beta-amyloid or amyloid precursor protein preparation, useful as a prophylactic vaccine or a therapeutic for preventing or treating a disease associated with beta-amyloid formation and/or aggregation, e.g. Alzheimer's disease.



```

PS Claim 4; Page 63; 104pp; English.
XX
CC The present invention relates to preparations (I) comprising a beta-
CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
CC fragment. The beta-amyloid or APP preparations are useful for
CC manufacturing a prophylactic vaccine or a therapeutic, or as a
CC prophylactic vaccine for the prevention, or as a therapeutic for the
CC treatment of a disease associated with beta-amyloid formation and/or
CC aggregation, such as Alzheimer's disease.
XX
SQ Sequence 14 AA;

Query Match      88.2%; Score 30; DB 8; Length 14;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
DB 8 QKLVEFA 14
:|||||
XX

RESULT 68
ADJ71465
ID ADJ71465 standard; peptide; 14 AA.
XX
AC ADJ71465;
XX
DT 06-MAY-2004 (first entry)
XX
DE N-terminal truncated beta-amyloid peptide, SEQ ID 128.
XX
KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
KW amyloid precursor protein; APP; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO2004013172-A2.
XX
PD 12-FEB-2004.
XX
PF 18-JUL-2003; 2003WO-EP007833.
XX
PR 24-JUL-2002; 2002EP-00447147.
XX
PT 06-AUG-2002; 2002US-0401497P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Delacourte A, Sergeant N;
XX
DR WPI; 2004-180423/17.
XX
PT New beta-amyloid or amyloid precursor protein preparation, useful as a
PT prophylactic vaccine or a therapeutic for preventing or treating a
PT disease associated with beta-amyloid formation and/or aggregation, e.g.
PT Alzheimer's disease.
XX
PS Claim 4; Page 63; 104pp; English.
XX
CC The present invention relates to preparations (I) comprising a beta-
CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
CC fragment. The beta-amyloid or APP preparations are useful for
CC manufacturing a prophylactic vaccine or a therapeutic, or as a
CC prophylactic vaccine for the prevention, or as a therapeutic for the
CC treatment of a disease associated with beta-amyloid formation and/or
CC aggregation, such as Alzheimer's disease.
XX
SQ Sequence 14 AA;

Query Match      88.2%; Score 30; DB 8; Length 14;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
DB 8 QKLVEFA 14
:|||||
XX

RESULT 69
ADJ71478
ID ADJ71478 standard; peptide; 14 AA.
XX
AC ADJ71478;
XX
DT 06-MAY-2004 (first entry)
XX
DE N-terminal truncated beta-amyloid peptide, SEQ ID 141.
XX
KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
KW amyloid precursor protein; APP; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO2004013172-A2.
XX
PD 12-FEB-2004.
XX
PF 18-JUL-2003; 2003WO-EP007833.
XX
PR 24-JUL-2002; 2002EP-00447147.
XX
PT 06-AUG-2002; 2002US-0401497P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Delacourte A, Sergeant N;
XX
DR WPI; 2004-180423/17.
XX
PT New beta-amyloid or amyloid precursor protein preparation, useful as a
PT prophylactic vaccine or a therapeutic for preventing or treating a
PT disease associated with beta-amyloid formation and/or aggregation, e.g.
PT Alzheimer's disease.
XX
PS Claim 4; Page 64; 104pp; English.
XX
CC The present invention relates to preparations (I) comprising a beta-
CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
CC fragment. The beta-amyloid or APP preparations are useful for
CC manufacturing a prophylactic vaccine or a therapeutic, or as a
CC prophylactic vaccine for the prevention, or as a therapeutic for the
CC treatment of a disease associated with beta-amyloid formation and/or
CC aggregation, such as Alzheimer's disease.
XX
SQ Sequence 14 AA;

Query Match      88.2%; Score 30; DB 8; Length 14;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
DB 6 QKLVEFA 12
:|||||
XX

RESULT 70
ADZ08889
ID ADZ08889 standard; peptide; 14 AA.
XX
AC ADZ08889;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human beta-amyloid peptide (SEQ ID No:114) probed with anti-amyloid IgG.
XX

```

KW	amyloid; antibody engineering; antibody production;
KW	amyloid-associated disorder; Alzheimers disease; allergy;
KW	autoimmune disease; Parkinsons disease;
KW	acquired immune deficiency syndrome; multiple sclerosis; migraine;
KW	dementia; infection; nootropic; neuroprotective; cytosstatic;
KW	antiallergic; immunosuppressive; antiparkinsonian; antimigraine;
KW	antimicrobial; anti-Hiv; beta-amyloid.
XX	
OS	Homo sapiens.
XX	
WO	2005028511-A2.
PN	
XX	
PD	31-MAR-2005.
XX	
26-MAR-2004;	2004WO-US009522.
XX	
28-MAR-2003;	2003US-0458469P.
PR	
28-MAR-2003;	2003US-0458474P.
PR	
28-MAR-2003;	2003US-0458509P.
PR	
28-MAR-2003;	2003US-0458510P.
XX	
(CENZ )	CENTOCOR INC.
PA	
(MERC/)	MERCKEN M.
PA	
(BENS/)	BENSON J M.
XX	
Mercken M,	Benson JM;
PI	
WPI;	2005-342565/25.
DR	
XX	
PT	New isolated mammalian anti-amyloid antibodies useful for treating
PT	amyloid-associated disorders, such as Alzheimer's disease, cancer,
PT	allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
PT	migraine and dementia.
XX	
Example 4;	SEQ ID NO 114; 306pp; English.
PS	
XX	
CC	The invention relates to at least one isolated mammalian amyloid antibody
CC	comprising at least one variable region comprising at least one heavy
CC	chain and at least one light chain, of a fully defined sequence of SEQ ID
CC	NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
CC	(i) at least one isolated mammalian amyloid antibody that binds to the
CC	same region of an amyloid polypeptide as an antibody comprising at least
CC	one heavy chain or light chain complementarity determining region (CDR)
CC	having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
CC	at least one isolated mammalian amyloid antibody, comprising at least one
CC	human CDR, where the antibody specifically binds at least one epitope
CC	selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
CC	sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
CC	acid encoding at least one of any of the isolated mammalian amyloid
CC	antibodies mentioned and having at least one human CDR of a fully defined
CC	sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
CC	isolated nucleic acid vector comprising an isolated nucleic acid encoding
CC	an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
CC	an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
CC	producing at least one amyloid antibody, (vii) a composition comprising
CC	at least one of any of the isolated mammalian amyloid antibodies
CC	mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
CC	anti-idiotypic antibody or fragment that specifically binds at least one
CC	of the amyloid antibodies mentioned, (ix) a method of diagnosing or
CC	treating an amyloid related condition in a cell, tissue, organ or animal,
CC	comprising contacting or administering a composition comprising at least
CC	one of the antibodies mentioned, with, or to, the cell, tissue, organ or
CC	animal, (x) a medical device comprising at least one amyloid antibody
CC	mentioned, where the device is suitable for contacting or administering
CC	at least one amyloid antibody, (xi) an article of manufacture for human
CC	pharmaceutical or diagnostic use, comprising packaging material and a
CC	container comprising a solution or a lyophilized form of at least one of
CC	the amyloid antibodies mentioned, and (xii) a method of producing at
CC	least one of the isolated mammalian amyloid antibodies, comprising
CC	providing a host cell or transgenic animal or transgenic plant or plant
CC	cell capable of expressing the antibody in recoverable amounts. The
CC	methods and compositions of the present invention are useful for
CC	producing therapeutic compositions and devices for treating amyloid-

Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 5 QKLVPFA 11

RESULT 72  
ABU79064  
ID ABU79064 standard; peptide; 15 AA.  
XX  
AC ABU79064;

17-JUN-2003 (first entry)

Aggregation blocking peptide #16.

KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;  
KW pathological beta-sheet-rich conformation; Down's syndrome;  
KW amyloidosis disorder; human prion disease; kuru; CJD;  
KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;  
KW prion associated human neurodegenerative disease; animal prion disease;  
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;  
KW chronic wasting disease.

Unidentified.

US6462171-B1.

08-OCT-2002.

12-DEC-1996; 96US-00766596.

07-JUN-1995; 95US-00478326.

10-APR-1996; 96US-00630645.

(UUNY ) UNIV NEW YORK STATE.

Soto-Jara C, Baumann MH, Frangione B;

WPI; 2003-379012/36.

Novel inhibitory peptides which inhibit and structurally block abnormal  
folding of protein into amyloid or amyloid-like deposit and into  
pathological beta-sheet rich conformation, useful for treating  
Alzheimer's disease.

Disclosure; Col 51-52; 5lpp; English.

The invention describes an isolated inhibitory peptide (I) which  
interacts with a hydrophobic beta-sheet forming cluster of amino acid  
residues on a protein or peptide for amyloid or amyloid-like deposit  
formation, and inhibits or structurally blocks the abnormal folding of  
proteins and peptides into amyloid or amyloid-like deposits and into  
pathological beta-sheet-rich conformation. (I) is useful for disorders or  
diseases associated with abnormal protein folding into amyloid or amyloid  
-like deposits or into pathological beta-sheet-rich precursors of such  
deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis  
disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease  
(CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated  
human neurodegenerative diseases as well as animal prion diseases such as  
scrapie, spongiform encephalopathy, transmissible mink encephalopathy and  
chronic wasting disease of mule deer and elk. (I) is also useful for  
detecting and diagnosing the presence or absence of amyloid or amyloid-  
like deposits in vivo and its precursors. This is the amino acid sequence  
of peptide associated with the inhibition of amyloid or amyloid like  
deposits

Sequence 15 AA;

Query Match 88.2%; Score 30; DB 6; Length 15;  
Best Local Similarity 85.7%; Pred. No. 19;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 4 QKLVPFA 10

RESULT 73  
ABU79059  
ID ABU79059 standard; peptide; 15 AA.  
XX  
AC ABU79059;

17-JUN-2003 (first entry)

Aggregation blocking peptide #11.

KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;  
KW pathological beta-sheet-rich conformation; Down's syndrome;  
KW amyloidosis disorder; human prion disease; kuru; CJD;  
KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;  
KW prion associated human neurodegenerative disease; animal prion disease;  
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;  
KW chronic wasting disease.

Unidentified.

US6462171-B1.

08-OCT-2002.

12-DEC-1996; 96US-00766596.

07-JUN-1995; 95US-00478326.

10-APR-1996; 96US-00630645.

(UUNY ) UNIV NEW YORK STATE.

Soto-Jara C, Baumann MH, Frangione B;

WPI; 2003-379012/36.

Novel inhibitory peptides which inhibit and structurally block abnormal  
folding of protein into amyloid or amyloid-like deposit and into  
pathological beta-sheet rich conformation, useful for treating  
Alzheimer's disease.

Disclosure; Col 49-50; 5lpp; English.

The invention describes an isolated inhibitory peptide (I) which  
interacts with a hydrophobic beta-sheet forming cluster of amino acid  
residues on a protein or peptide for amyloid or amyloid-like deposit  
formation, and inhibits or structurally blocks the abnormal folding of  
proteins and peptides into amyloid or amyloid-like deposits and into  
pathological beta-sheet-rich conformation. (I) is useful for disorders or  
diseases associated with abnormal protein folding into amyloid or amyloid  
-like deposits or into pathological beta-sheet-rich precursors of such  
deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis  
disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease  
(CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated  
human neurodegenerative diseases as well as animal prion diseases such as  
scrapie, spongiform encephalopathy, transmissible mink encephalopathy and  
chronic wasting disease of mule deer and elk. (I) is also useful for  
detecting and diagnosing the presence or absence of amyloid or amyloid-  
like deposits in vivo and its precursors. This is the amino acid sequence  
of peptide associated with the inhibition of amyloid or amyloid like  
deposits

Sequence 15 AA;

Query Match 88.2%; Score 30; DB 6; Length 15;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7  
Db :|||||  
4 QKLVFPA 10

RESULT 74  
ABU79060  
ID ABU79060 standard; peptide; 15 AA.  
XX  
AC ABU79060;  
XX  
DT 17-JUN-2003 (first entry)  
XX  
DE Aggregation blocking peptide #12.  
XX  
KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;  
KW pathological beta-sheet-rich conformation; Down's syndrome;  
KW amyloidosis disorder; human prion disease; kuru; CJD;  
KW Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker syndrome; GSS;  
KW prion associated human neurodegenerative disease; animal prion disease;  
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;  
KW chronic wasting disease.  
XX  
OS Unidentified.  
XX  
PN US6462171-B1.  
XX  
PD 08-OCT-2002.  
XX  
PF 12-DEC-1996; 96US-00766596.  
XX  
PR 07-JUN-1995; 95US-00478326.  
PR 10-APR-1996; 96US-00630645.  
XX  
PA (UWNY ) UNIV NEW YORK STATE.  
XX  
PI Soto-Jara C, Baumann MH, Frangione B;  
XX  
DR WPI; 2003-379012/36.  
XX  
PT Novel inhibitory peptides which inhibit and structurally block abnormal  
PT folding of protein into amyloid or amyloid-like deposit and into  
PT pathological beta-sheet rich conformation, useful for treating  
PT Alzheimer's disease.  
XX  
PS Disclosure; Col 51-52; 51pp; English.  
XX  
CC The invention describes an isolated inhibitory peptide (I) which  
CC interacts with a hydrophobic beta-sheet forming cluster of amino acid  
CC residues on a protein or peptide for amyloid or amyloid-like deposit  
CC formation, and inhibits or structurally blocks the abnormal folding of  
CC proteins and peptides into amyloid or amyloid-like deposits and into  
CC pathological beta-sheet-rich conformation. (I) is useful for disorders or  
CC diseases associated with abnormal protein folding into amyloid or amyloid  
CC -like deposits or into pathological beta-sheet-rich precursors of such  
CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis  
CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease  
CC (CJD), Gerstmann-Straussler-Scheinker syndrome (GSS), prion associated  
CC human neurodegenerative diseases as well as animal prion diseases such as  
CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and  
CC chronic wasting disease of mule deer and elk. (I) is also useful for  
CC detecting and diagnosing the presence or absence of amyloid or amyloid-  
CC like deposits in vivo and its precursors. This is the amino acid sequence  
CC of peptide associated with the inhibition of amyloid or amyloid like  
CC deposits  
XX  
SQ Sequence 15 AA;

Query Match 88.2%; Score 30; DB 6; Length 15;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7

RESULT 75  
ABU79055  
ID ABU79055 standard; peptide; 15 AA.  
XX  
AC ABU79055;  
XX  
DT 17-JUN-2003 (first entry)  
XX  
DE Aggregation blocking peptide #7.  
XX  
KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;  
KW pathological beta-sheet-rich conformation; Down's syndrome;  
KW amyloidosis disorder; human prion disease; kuru; CJD;  
KW Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker syndrome; GSS;  
KW prion associated human neurodegenerative disease; animal prion disease;  
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;  
KW chronic wasting disease.  
XX  
OS Unidentified.  
XX  
PN US6462171-B1.  
XX  
PD 08-OCT-2002.  
XX  
PF 12-DEC-1996; 96US-00766596.  
XX  
PR 07-JUN-1995; 95US-00478326.  
PR 10-APR-1996; 96US-00630645.  
XX  
PA (UWNY ) UNIV NEW YORK STATE.  
XX  
PI Soto-Jara C, Baumann MH, Frangione B;  
XX  
DR WPI; 2003-379012/36.  
XX  
PT Novel inhibitory peptides which inhibit and structurally block abnormal  
PT folding of protein into amyloid or amyloid-like deposit and into  
PT pathological beta-sheet rich conformation, useful for treating  
PT Alzheimer's disease.  
XX  
PS Disclosure; Col 49-50; 51pp; English.  
XX  
CC The invention describes an isolated inhibitory peptide (I) which  
CC interacts with a hydrophobic beta-sheet forming cluster of amino acid  
CC residues on a protein or peptide for amyloid or amyloid-like deposit  
CC formation, and inhibits or structurally blocks the abnormal folding of  
CC proteins and peptides into amyloid or amyloid-like deposits and into  
CC pathological beta-sheet-rich conformation. (I) is useful for disorders or  
CC diseases associated with abnormal protein folding into amyloid or amyloid  
CC -like deposits or into pathological beta-sheet-rich precursors of such  
CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis  
CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease  
CC (CJD), Gerstmann-Straussler-Scheinker syndrome (GSS), prion associated  
CC human neurodegenerative diseases as well as animal prion diseases such as  
CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and  
CC chronic wasting disease of mule deer and elk. (I) is also useful for  
CC detecting and diagnosing the presence or absence of amyloid or amyloid-  
CC like deposits in vivo and its precursors. This is the amino acid sequence  
CC of peptide associated with the inhibition of amyloid or amyloid like  
CC deposits  
XX  
SQ Sequence 15 AA;

Query Match 88.2%; Score 30; DB 6; Length 15;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7

Db :|||||  
4 QXLVFFA 10

Search completed: December 29, 2005, 17:33:14  
Job time : 99.4032 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 91.2258 Seconds  
(without alignments)  
54.137 Million cell updates/sec

Title: US-10-009-122-18

Perfect score: 34

Sequence: 1 KLVFFPAQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	962	2	QANTX2_9DELTA
2	31	91.2	33	2	Q9UC33_HUMAN
3	31	91.2	42	2	Q56J06_GRAGR
4	31	91.2	42	2	Q56J07_TURTR
5	31	91.2	42	2	Q7M088_CAVPO
6	31	91.2	51	2	Q72A51_DESVH
7	31	91.2	52	1	Q8W299_HUMAN
8	31	91.2	57	1	A4_URDMA
9	31	91.2	58	1	A4_CANFA
10	31	91.2	58	1	A4_RABIT
11	31	91.2	58	1	A4_SHEEP
12	31	91.2	59	1	A4_BOVIN
13	31	91.2	79	2	Q35463_CRIGR
14	31	91.2	113	2	Q8JH58_CHESE
15	31	91.2	213	2	Q4ULC9_RICFE
16	31	91.2	218	2	Q8BPV5_MOUSE
17	31	91.2	357	2	Q8U118_BRARE
18	31	91.2	375	2	Q8SMFO_HORVU
19	31	91.2	384	2	Q8BPC7_MOUSE
20	31	91.2	417	1	Q865A_DROME
21	31	91.2	471	2	Q93YN7_ARATH
22	31	91.2	472	2	Q8UUSO_BRARE
23	31	91.2	534	2	Q93296_CHICK
24	31	91.2	569	2	Q9PVL1_CHICK
25	31	91.2	612	2	Q919E7_BRARE
26	31	91.2	678	2	Q7ZZT1_BRARE
27	31	91.2	693	2	Q98SG0_XENLA
28	31	91.2	695	2	Q5R477_PONPY
29	31	91.2	695	2	Q8RH29_CANIS
30	31	91.2	695	2	Q56J03_CANFA
31	31	91.2	695	2	Q6GR78_MOUSE

32	91.2	695	2	Q9DGJ8_CHICK
33	91.2	714	2	Q56JK4_CANFA
34	91.2	733	2	Q6P6Q5_RAT
35	91.2	738	2	Q6NUZ1_BRARE
36	91.2	738	2	Q9OW28_BRARE
37	91.2	745	2	Q7XZG7_ORYZA
38	91.2	747	2	Q91963_9PIPI
39	91.2	749	2	Q56JK2_STECO
40	91.2	749	2	Q6NRR1_XENLA
41	91.2	750	2	Q6DJB6_XENLA
42	91.2	751	2	A4_SAISC
43	91.2	751	2	Q6GSC0_HUMAN
44	91.2	751	2	Q6RH28_CANFA
45	91.2	751	2	Q56JK5_CANFA
46	91.2	751	2	Q4R4R8_MACFA
47	91.2	751	2	Q9DGJ7_CHICK
48	91.2	754	1	CHLD_PEA
49	91.2	754	2	Q6ATS0_ORYZA
50	91.2	754	2	Q4RY33_TETNG
51	91.2	758	1	CHLD_TOBAC
52	91.2	759	1	CHLD_ARATH
53	91.2	759	2	Q4S0J4_TETNG
54	91.2	760	2	Q8VZU7_ARATH
55	91.2	770	1	A4_CAVPO
56	91.2	770	1	A4_HUMAN
57	91.2	770	1	A4_MACFA
58	91.2	770	1	A4_MOUSE
59	91.2	770	1	A4_PANTR
60	91.2	770	1	A4_PIG
61	91.2	770	1	A4_RAT
62	91.2	770	2	Q6RH30_CANFA
63	91.2	770	2	Q56JK6_CANFA
64	91.2	770	2	Q53ZT3_MOUSE
65	91.2	770	2	Q547B7_RAT
66	91.2	780	1	A4_TETFL
67	88.2	355	2	Q87XV7_PSESM
68	88.2	364	2	Q4LMP3_9BURK
69	88.2	421	2	Q54L66_DICDI
70	88.2	480	2	Q4N8N8_THEPA
71	88.2	557	2	Q4UGZ4_THEAN
72	85.3	66	2	Q728F0_DESVH
73	85.3	81	2	Q6D3D0_ERWCT
74	85.3	95	2	Q8VOR5_ECOLI
75	85.3	97	2	Q6GZK0_ECOLI
76	85.3	115	1	YACC_ECOLI
77	85.3	115	2	Q57T88_SALCH
78	85.3	115	2	Q5PDA6_SALPA
79	85.3	115	2	Q7CR72_SALTY
80	85.3	115	2	Q8XGD8_SALTY
81	85.3	137	2	Q7UPR1_RHOBA
82	85.3	152	2	Q9STZ9_ARATH
83	85.3	156	2	Q7UDR8_SHIFL
84	85.3	156	2	Q8X949_ECOS7
85	85.3	172	2	Q83SM3_SHIFL
86	85.3	229	2	Q8VY56_ARATH
87	85.3	231	2	Q9SV79_ARATH
88	85.3	352	2	Q9XGY6_SIMCH
89	85.3	357	2	Q8U460_PYRFU
90	85.3	358	2	Q4WJL8_ASPFU
91	85.3	366	2	Q8PPL1_XANAC
92	85.3	381	2	Q4NSU7_THEPA
93	85.3	403	2	Q5L117_GEOKA
94	85.3	404	2	Q4UY85_XANCP
95	85.3	404	2	Q8P597_XANCP
96	85.3	428	2	Q9MIQ8_ARATH
97	85.3	461	2	Q89329_9POTV
98	85.3	470	2	Q7T310_9POTV
99	85.3	485	2	Q6C854_YARLI
100	85.3	485	2	Q8NQG2_CORGL
101	85.3	488	2	Q52NV6_9POTV
102	85.3	490	2	Q7T911_9POTV
103	85.3	490	2	Q7T912_9POTV
104	85.3	493	2	Q5K4D4_9POTV

Q9DGJ8	gallus gall
Q56JK4	canis famil
Q6P6Q5	rattus norv
Q6NUZ1	brachydanio
Q9OW28	brachydanio
Q7XZG7	oryza sativ
Q91963	xenopus ap
Q56JK2	stenella co
Q6NRR1	xenopus lae
Q6DJB6	xenopus tro
Q52121	s amyloid b
Q6GSC0	homo sapien
Q6RH28	canis famil
Q56JK5	canis famil
Q4R4R8	macaca fasc
Q9DGJ7	gallus gall
O22437	pisum sativ
Q6AT50	oryza sativ
O24133	tetradodon n
Q98J81	arabidopsis
Q480J4	tetradodon n
Q8VZU7	arabidopsis
Q60495	c amyloid b
P05067	h amyloid b
P53601	m amyloid b
P12023	m amyloid b
Q51880	p amyloid b
P79307	s amyloid b
P08592	r amyloid b
Q6RH30	canis famil
Q56JK6	canis famil
Q53ZT3	mus musculu
Q547B7	rattus norv
Q73683	tetradodon f
Q87XV7	pseudomonas
Q41MP3	burkholderi
Q54L66	dictyosteli
Q4N8N8	theileria p
Q4UGZ4	theileria a
Q728F0	desulfovibr
Q6D3D0	erwinia car
Q8VOR5	escherichia
Q6GZK0	escherichia
P23838	escherichia
Q57T88	salmonella
Q5PDA6	salmonella
Q7CR72	salmonella
Q8XGD8	salmonella
Q7UPR1	rhodospirill
Q9STZ9	arabidopsis
Q7UDR8	shigella fl
Q8X949	escherichia
Q83SM3	shigella fl
Q8VY56	arabidopsis
Q9SV79	arabidopsis
Q9XGY6	simmondsia
Q8U460	pyrococcus
Q4WJL8	aspergillus
Q8PPL1	xanthomonas
Q4NSU7	theileria p
Q5L117	geobacillus
Q4UY85	xanthomonas
Q8P597	xanthomonas
Q9MIQ8	arabidopsis
Q89329	zucchini ye
Q7T310	zucchini ye
Q6C854	yarrowia li
Q8NQG2	corynebacte
Q52NV6	zucchini ye
Q7T911	zucchini ye
Q7T912	zucchini ye
Q5K4D4	soybean mos

105	29	85.3	493	2	Q5K4D5_9POTV	Q5k4d5 soybean mos	178	28	82.4	685	2	Q5A951_CANAL	Q5a951 candida alb
106	29	85.3	505	2	Q6M5A9_CORGL	Q6m5a9 corynebacte	179	28	82.4	690	2	Q831B2_TROW8	Q831b2 tropheryma
107	29	85.3	508	2	Q5GV55_XANOR	Q5gv55 xanthomonas	180	28	82.4	691	2	Q9H7V0_HUMAN	Q9h7v0 homo sapien
108	29	85.3	512	1	CADC_ECOLI	P23g90 escherichia	181	28	82.4	691	2	Q5R745_PONPY	Q5r745 pongo pygma
109	29	85.3	512	2	Q8VR66_ECOLI	Q8vr66 escherichia	182	28	82.4	698	2	Q83GW3_TROWT	Q83gw3 tropheryma
110	29	85.3	512	2	Q8FAT2_ECOL6	Q8fat2 escherichia	183	28	82.4	699	2	Q7L1C9_HUMAN	Q7l1c9 homo sapien
111	29	85.3	512	2	Q8XDS2_ECO57	Q8xds2 escherichia	184	28	82.4	746	2	Q8ND40_HUMAN	Q8nda0 homo sapien
112	29	85.3	513	2	Q8ZMP6_SALTU	Q8zmp6 salmonella	185	28	82.4	771	2	Q4WPG0_ASFFU	Q4wpg0 aspergillus
113	29	85.3	570	2	Q4FTR5_9GAMM	Q4ftr5 psychrobact	186	28	82.4	881	2	Q6BM22_DBBHA	Q6bm22 debaryomyce
114	29	85.3	615	2	Q50285_ENTHI	Q50z85 entamoeba h	187	28	82.4	946	2	Q8WY25_HUMAN	Q8wy25 homo sapien
115	29	85.3	623	2	Q9VEV8_DROME	Q9v8v8 drosophila	188	28	82.4	957	2	Q7T3T7_OREMO	Q7t3t7 orochromis
116	29	85.3	638	2	Q5BZV4_EMENI	Q5bzv4 aspergillus	189	28	82.4	971	2	Q9VECS_DROME	Q9vecs drosophila
117	29	85.3	663	2	Q5BCB9_ASERGILL	Q5bcb9 aspergillus	190	28	82.4	1035	2	Q5T224_HUMAN	Q5t224 homo sapien
118	29	85.3	695	2	Q98SF9_XENLA	Q98sf9 xenopus lae	191	28	82.4	1049	2	Q81ZA0_HUMAN	Q81za0 homo sapien
119	29	85.3	695	2	Q7ZXQ0_XENLA	Q7zxq0 xenopus lae	192	28	82.4	1049	2	Q6PJJ7_HUMAN	Q6pjj7 homo sapien
120	29	85.3	737	1	A4_FURFU	Q93z79 fugu rubrip	193	28	82.4	1049	2	Q5RFP6_PONPY	Q5rfr6 pongo pygma
121	29	85.3	776	2	Q9SH68_ARATH	Q9sh68 arabidopsis	194	28	82.4	1058	2	Q5T225_HUMAN	Q5t225 homo sapien
122	29	85.3	851	2	Q6C4R4_YARLI	Q6czr4 yarrowia li	195	28	82.4	1080	2	Q8DT75_STRMU	Q8dt75 streptococc
123	29	85.3	955	2	Q8ORZ2_VIPOTV	Q8orz2 calla lily	196	28	82.4	1215	2	Q6L2N7_PICTO	Q6l2n7 picophilus
124	29	85.3	1016	2	Q05912_9POTV	Q05912 zucchini ye	197	28	82.4	1676	2	Q8A6R7_BACTN	Q8a6r7 bacteroides
125	29	85.3	1056	2	Q6FKH6_CANGA	Q6fkh6 candida gla	198	28	79.4	15	2	Q9TWFS_9CRUS	Q9twf5 artemia (br
126	29	85.3	1916	2	Q8OKU4_9POTV	Q8oku4 zucchini ye	199	27	79.4	46	2	Q8EXM4_LBPIN	Q8exm4 leptospira
127	29	85.3	3080	1	POLG_ZTWC	P18479 z genome po	200	27	79.4	91	2	Q5TT27_ANOGA	Q5tt27 anopheles g
128	29	85.3	3080	2	Q6WN47_9POTV	Q6wn47 zucchini ye	201	27	79.4	118	2	Q58M43_9CAUD	Q58m43 cyanophage
129	29	85.3	3080	2	Q6WN48_9POTV	Q6wn48 zucchini ye	202	27	79.4	132	2	Q4YR43_PLABE	Q4yr43 plasmodium
130	29	85.3	3080	2	Q6WN49_9POTV	Q6wn49 zucchini ye	203	27	79.4	164	2	Q73N39_TREDE	Q73n39 treponema d
131	29	85.3	3080	2	Q6Y2U7_9POTV	Q6y2u7 zucchini ye	204	27	79.4	165	2	Q6APD6_DSPPS	Q6apd6 desulfotale
132	29	85.3	3080	2	Q7T908_9POTV	Q7t908 zucchini ye	205	27	79.4	175	2	Q4UG67_THEAN	Q4ug67 theileria a
133	29	85.3	3080	2	Q7T914_9POTV	Q7t914 zucchini ye	206	27	79.4	175	2	Q4N989_THEPA	Q4n989 theileria p
134	29	85.3	3083	1	POLG_ZTWS	Q36979 z genome po	207	27	79.4	177	2	Q81JC9_PLAF7	Q81jc9 plasmodium
135	29	85.3	3105	2	Q70XR2_9POTV	Q70xr2 soybean mos	208	27	79.4	177	2	Q4YCE6_PLABE	Q4yce6 plasmodium
136	28	82.4	22	2	Q5C064_SCHJA	Q5c064 schistosoma	209	27	79.4	182	2	Q4XDG5_PLACH	Q4xdg5 streptomyc
137	28	82.4	49	2	Q4XA79_PLACH	Q4xa79 plasmodium	210	27	79.4	182	2	Q9Z588_STRCO	Q9z588 streptomyc
138	28	82.4	57	2	Q4XP83_PLACH	Q4xp83 plasmodium	211	27	79.4	185	2	Q89NA0_BRAJA	Q89na0 bradyrhizob
139	28	82.4	81	1	MOAD_ECOLI	P30748 escherichia	212	27	79.4	193	2	Q7RCA7_PLAYO	Q7rca7 plasmodium
140	28	82.4	81	2	Q9APP7_9BACT	Q9app7 uncultured	213	27	79.4	214	2	Q9LZY2_ARATH	Q9lzy2 arabidopsis
141	28	82.4	81	2	Q57RF2_SALCH	Q57rf2 salmonella	214	27	79.4	223	2	Q7P788_FUSNN	Q7p788 fusobacteri
142	28	82.4	81	2	Q65T70_MANSM	Q65tto manheimia	215	27	79.4	223	2	Q8RDM7_FUSNN	Q8rdm7 fusobacteri
143	28	82.4	81	2	Q7N6P4_PHOLL	Q7n6p4 photorhabdu	216	27	79.4	247	2	Q4Y236_PLACH	Q4y236 plasmodium
144	28	82.4	81	2	Q8D897_VIBUV	Q8d897 vibrio vuln	217	27	79.4	257	2	Q72V35_LBPIC	Q72v35 leptospira
145	28	82.4	81	2	Q9XT78_VIBCH	Q9xt78 vibrio chol	218	27	79.4	257	2	Q8EZT1_LBPIN	Q8ezt1 leptospira
146	28	82.4	81	2	Q83S38_SHIFL	Q83s38 shigella fl	219	27	79.4	272	2	Q54BA3_DICDI	Q54ba3 dictyostell
147	28	82.4	81	2	Q7MM72_VIBVY	Q7mm72 vibrio vuln	220	27	79.4	276	2	Q962V2_TRISP	Q962v2 trichinella
148	28	82.4	81	2	Q8X807_ECO57	Q8x807 escherichia	221	27	79.4	296	2	Q8XRD8_RALSO	Q8xrd8 ralestonia s
149	28	82.4	83	2	Q8ZQO0_SALTU	Q8zqo0 salmonella	222	27	79.4	300	2	Q9XU61_CAEEL	Q9xu61 caenorhabdi
150	28	82.4	85	2	Q87MY3_VIBPA	Q87my3 vibrio para	223	27	79.4	314	2	Q9Z2H7_MOUSE	Q9z2h7 m semaf cyt
151	28	82.4	105	2	Q64CV5_9ARCH	Q64cv5 uncultured	224	27	79.4	315	2	Q74N48_NANEQ	Q74n48 nanocarchaeu
152	28	82.4	132	2	Q7VL67_HAEDU	Q7vl67 haemophilus	225	27	79.4	316	1	TRUB_PHOPR	Q6luj0 photobacter
153	28	82.4	182	2	Q835H4_ENTFA	Q835h4 enterococcu	226	27	79.4	329	1	EB43_FLAME	P36913 flavobacter
154	28	82.4	223	2	Q89219_CLOTE	Q89219 clostridium	227	27	79.4	330	1	SYW_DEIRA	Q9twv7 deinococcus
155	28	82.4	270	2	Q7MV75_PORGI	Q7mv75 porphyromon	228	27	79.4	331	2	Q6BMW6_DBBHA	Q6bmw6 debaryomyce
156	28	82.4	276	2	Q4XE69_PLACH	Q4xe69 plasmodium	229	27	79.4	341	1	Y665_METJA	Q58079 methanococc
157	28	82.4	279	2	Q4YWA7_PLABE	Q4ywa7 plasmodium	230	27	79.4	342	2	Q86QP4_TRISP	Q86qp4 trichinella
158	28	82.4	284	2	Q4XZ22_PSRSD	Q4xz22 pseudomonas	231	27	79.4	349	2	Q9XU59_CAEEL	Q9xu59 caenorhabdi
159	28	82.4	306	2	Q9AZG0_9CAUD	Q9azg0 bacterioph	232	27	79.4	350	2	Q552M0_DICDI	Q552m0 dictyostell
160	28	82.4	306	2	Q9CEB2_LACIA	Q9ceb2 lactococcus	233	27	79.4	364	2	Q93CU7_SHIBO	Q93cu7 shigella bo
161	28	82.4	321	1	Y189_RICPR	Q9zdx5 rickettsia	234	27	79.4	387	2	Q81FHS_BACCR	Q81fhs bacillus ce
162	28	82.4	336	2	Q94155_ORYSA	Q94155 oryza sativ	235	27	79.4	399	2	Q5WPU9_LUTLO	Q5wpu9 lutzonvial
163	28	82.4	346	2	Q9SYB5_ARATH	Q9syb5 arabidopsis	236	27	79.4	410	2	Q8L2B4_PICTO	Q8l2b4 picophilus
164	28	82.4	353	2	Q961C3_HUMAN	Q961c3 homo sapien	237	27	79.4	421	2	Q6G1K7_BARHE	Q6g1k7 bartonella
165	28	82.4	357	2	Q4R803_MACFA	Q4r803 macaca fasc	238	27	79.4	432	2	Q5U3S9_BRARE	Q5u3s9 brachydanio
166	28	82.4	439	2	Q7SFH1_NEUCR	Q7sfh1 neurospora	239	27	79.4	436	2	Q4YRG0_PLABE	Q4yrg0 plasmodium
167	28	82.4	449	2	Q6NKH0_CORDI	Q6nkh0 corynebacte	240	27	79.4	437	1	DNAA_MYCEA	P35888 mycoplasma
168	28	82.4	450	2	Q5WFB7_BACSK	Q5wfb7 bacillus cl	241	27	79.4	437	2	Q5KUT3_GFOKA	Q5kut3 geobacillus
169	28	82.4	473	1	CYSG_BUCAI	P57500 b siroheme	242	27	79.4	450	2	Q4TRF8_9SPHN	Q4trf8 erythrobaet
170	28	82.4	479	2	Q9QLS5_9POTV	Q9qls5 sarcophilus	243	27	79.4	456	2	Q6GVJ4_9BURK	Q6gvj4 burkholderi
171	28	82.4	479	2	Q4F979_9POTV	Q4f979 eustrephus	244	27	79.4	464	2	Q4S4T5_TETNG	Q4s4t5 tetrahodon n
172	28	82.4	491	2	Q8N2B3_HUMAN	Q8n2b3 homo sapien	245	27	79.4	470	2	Q8EDU7_MYCPS	Q8euw7 mycoplasma
173	28	82.4	583	2	Q9XZ66_CAEEL	Q9xz66 caenorhabdi	246	27	79.4	477	2	Q81729_CRAGI	Q81729 crassostrea
174	28	82.4	639	2	Q96JJO_HUMAN	Q96jjo homo sapien	247	27	79.4	496	2	Q5K4D0_9POTV	Q5k4d0 daheen mos
175	28	82.4	651	2	Q9PYV4_GVXN	Q9pyv4 xestia c-ni	248	27	79.4	498	2	Q5NX24_AZOSE	Q5nx24 azoarcus ap
176	28	82.4	681	2	Q5WLL8_BACSK	Q5wll8 bacillus cl	249	27	79.4	498	2	Q5NWB1_AZOSE	Q5nwb1 azoarcus ap
177	28	82.4	685	1	MDU1_CANAL	P97998 candida alb	250	27	79.4	517	1	SEST_CAEEL	Q9n4d6 caenorhabdi

251 27 79.4 531 2 O65536 ARATH  
 252 27 79.4 532 2 Q9PTB2 ICTFU  
 253 27 79.4 571 2 Q97KU8 CLOAB  
 254 27 79.4 606 2 Q91VU5 MOUSE  
 255 27 79.4 624 2 O5E6S4 VIBF1  
 256 27 79.4 627 2 O57B48 BRUAB  
 257 27 79.4 627 2 O8G1M1 BRUSU  
 258 27 79.4 646 2 O8YGA2 BRUCEA  
 259 27 79.4 663 2 Q6RUU2 MOUSE  
 260 27 79.4 667 2 O5B3H6 EMENI  
 261 27 79.4 667 2 O4U8H8 THEAN  
 262 27 79.4 679 2 O4WXW0 ASPFU  
 263 27 79.4 685 2 O5AGS1 DICDI  
 264 27 79.4 711 2 Q99YU3 STRPY  
 265 27 79.4 711 2 Q8K670 STRF3  
 266 27 79.4 721 2 O6AG25 LEIXX  
 267 27 79.4 729 2 O8XZK4 STRP6  
 268 27 79.4 729 2 O8N2X4 STRP8  
 269 27 79.4 741 2 O5NHQ1 PRATT  
 270 27 79.4 808 2 Q8DK23 STNEL  
 271 27 79.4 810 2 O59JZ3 CANAL  
 272 27 79.4 810 2 O5ABW6 CANAL  
 273 27 79.4 810 2 O5AC87 CANAL  
 274 27 79.4 810 2 Q9P852 CANAL  
 275 27 79.4 811 2 O5A8N0 CANAL  
 276 27 79.4 811 2 O5AC07 CANAL  
 277 27 79.4 811 2 O5ACC8 CANAL  
 278 27 79.4 819 2 O4JCD0 SULAC  
 279 27 79.4 821 2 O6ZRO2 HUMAN  
 280 27 79.4 933 2 O6ZU08 HUMAN  
 281 27 79.4 1013 2 Q6BNQ9 DEBHA  
 282 27 79.4 1054 2 O67430 AQUAE  
 283 27 79.4 1105 2 Q9VX31 DROME  
 284 27 79.4 1179 2 O15206 HUMAN  
 285 27 79.4 1191 2 Q756U3 ASHGO  
 286 27 79.4 1265 2 O6Z031 MOUSE  
 287 27 79.4 1273 2 Q5UFH2 HUMAN  
 288 27 79.4 1412 2 Q5F3M1 CHICK  
 289 27 79.4 1492 2 Q83Y21 FEWBP  
 290 27 79.4 1566 2 Q7RIX3 PLAYO  
 291 27 79.4 1661 2 O69223 MOUSE  
 292 27 79.4 1775 2 O6CT24 KULUA  
 293 27 79.4 2584 2 Q65Z23 MONAN  
 294 27 79.4 4488 2 Q9QZH1 MOUSE  
 295 27 79.4 4511 2 Q7PXX5 ANOGE  
 296 26 76.5 40 2 Q87MN1 VIBPA  
 297 26 76.5 41 2 O4YAX8 PLABE  
 298 26 76.5 61 2 Q4XX51 FLACH  
 299 26 76.5 70 2 Q6HN03 BACHK  
 300 26 76.5 75 2 Q81UQ0 BACAN

## ALIGNMENTS

RESULT 1  
 Q4NTK2\_9DELTA PRELIMINARY; PRT; 962 AA.  
 ID Q4NTK2\_9DELTA PRELIMINARY; PRT; 962 AA.  
 AC Q4NTK2\_9DELTA PRELIMINARY; PRT; 962 AA.  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Pyruvate, phosphate dikinase (BC 2.7.9.1).  
 GN ORFNames=AdhDRAFT\_2040;  
 OS Anaeromyxobacter dehalogenans 2CP-C.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;  
 OC Cytophactineae; Myxococcaceae; Anaeromyxobacter.  
 OX NCBI\_TaxID=290397;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=2CP-C;  
 RG US DOE Joint Genome Institute (JGI-PGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,

RA Hammon N., Israeli S., Pitluck S., Richardson P.;  
 RT "Sequencing of the draft genome assembly of Anaeromyxobacter  
 RT dehalogenans 2CP-C."; EMBL/GenBank/DBJ databases.  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=2CP-C;  
 RG US DOE Joint Genome Institute (JGI-ORNL);  
 RA Larimer F., Land M.;  
 RT "Annotation of the draft genome assembly of Anaeromyxobacter  
 RT dehalogenans 2CP-C."; EMBL/GenBank/DBJ databases.  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AAHD01000017; EAL78925.1; -; Genomic\_DNA.  
 KW Kinase; Pyruvate; Transferase.  
 SQ SEQUENCE 962 AA; 104247 MW; CP843895DC5C3790 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 962;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7  
 Db 420 KLVFFFAQ 426

RESULT 2  
 Q9UC33\_HUMAN PRELIMINARY; PRT; 33 AA.  
 ID Q9UC33\_HUMAN PRELIMINARY; PRT; 33 AA.  
 AC Q9UC33;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Beta-amyloid peptide (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RL MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;  
 RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,  
 RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;  
 RT "Isolation and quantification of soluble Alzheimer's beta-peptide from  
 RT biological fluids."; Nature 359:325-327(1992).  
 RL Nature 359:325-327(1992).  
 DR HSSP; Q16019; 1BA4.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 33;  
 Best Local Similarity 85.7%; Pred. No. 9.7;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7  
 Db 16 KLVFFFAE 22

RESULT 3  
 Q56JJ6 GRAGR  
 ID Q56JJ6 GRAGR PRELIMINARY; PRT; 42 AA.  
 AC Q56JJ6;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)



```

DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampidae.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926589; AAX81918.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAE 22

RESULT 4
ID Q56J77 TURTR
AC Q56J77; PRT; 42 AA.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Tursiops truncatus (Atlantic bottlenose dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926588; AAX81917.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAE 22

RESULT 5
ID Q7M088 CAVPO
AC Q7M088; PRT; 42 AA.
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93290653; PubMed=7685598;

```

```

RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
RT protein fragment for NK-1 substance p receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
DR PIR; P0512; P0512.
DR HSP; Q16019; 11YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 42
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAE 22

RESULT 6
ID Q72A51 DESVH
AC Q72A51; PRT; 51 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=DVU2146;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC Desulfobacteriaceae; Desulfobacter.
OX NCBI_TaxID=882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Meche B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.";
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AB017316; AAS96619.1; -; Genomic_DNA.
DR TIGR; DVU2146; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 51 AA; 6205 MW; E7F69C0D8432B7F5 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 51;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 18 KLVFFAQ 24

RESULT 7
ID Q8WZ99 HUMAN
AC Q8WZ99; PRT; 52 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

```

```

DE Amyloid protein (Fragment).
GN Name=APP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15201367; DOI=10.1136/jnmp.2003.010611;
RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
RA Ninomiya H., Salido T.C., Hashimoto T., Iwatsubo T., Nakashima K.;
RT "Novel amyloid precursor protein gene missense mutation (D678N) in
RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
DE EMBL; AB066441; BAB71958.2; -; mRNA.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR FT NON_TER 1 52
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5597 MW; 3F08E9EC18011AD CRC64;

Query Match 91.2%; Score 31; DB 2; Length 52;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 16 KLVFFAE 22
|||||:

RESULT 8
A4_URSWA
ID A4_URSWA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalassos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G10) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

```

```

DR EMBL; X56128; CAA39593.1; -; mRNA.
DR FIR; B60045; B60045.
DR HSSP; P08592; INMU.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SP6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >57 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT NON_TER 1 57
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBAB82DFA CRC64;

Query Match 91.2%; Score 31; DB 1; Length 57;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 21 KLVFFAE 27
|||||:

RESULT 9
A4_CANFA
ID A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G10) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; X56125; CAA39590.1; -; mRNA.
DR HSSP; P08592; INMU.

```

```

DR Ensembl; ENSCAFG0000008557; Canis familiaris.
DR InterPro; IPR008155; A4 APP.
DR PRINTS; PRO001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PTHR10083:SF6; Beta-APP; 1.
DR PRINTS; PRO0204; BETAAPP.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >58 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 1 1
FT NON_TER 58 58
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match          91.2%; Score 31; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 22 KLVFFAE 28

RESULT 10
A4 RABBIT
ID A4 RABBIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; X56129; CAA39594.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4 APP.
DR PANTHER; PTHR10083:SF6; Beta-APP.
DR InterPro; IPR001255; Beta-APP.

```

```

DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PRO0204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match          91.2%; Score 31; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 21 KLVFFAE 27

RESULT 11
A4 SHEEP
ID A4 SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; X56130; CAA39595.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.

```

DR PRINTS: PR00204; BETAAMYLOID  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Amyloid; Transmembrane.  
 FT CHAIN <1 5  
 FT CHAIN 6 >58 Soluble APP-beta (By similarity).  
 FT CHAIN 6 >58 CTF-alpha (By similarity).  
 FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).  
 FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).  
 FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).  
 FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).  
 FT TOPO\_DOM <1 33 Extracellular (Potential).  
 FT TRANSMEM 34 57 Potential.  
 FT TOPO\_DOM 58 >58 Cytoplasmic (Potential).  
 FT NON\_TER 1 1  
 FT NON\_TER 58 58  
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA92D CRC64;  
 Query Match 91.2%; Score 31; DB 1; Length 59;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 Db 21 KLVFFAE 27  
 RESULT 12  
 A4\_BOVIN  
 ID A4\_BOVIN STANDARD; PRT; 59 AA.  
 AC Q28053;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-  
 beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);  
 DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase  
 DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal  
 DE fragment 57)] (Fragment).  
 GN Name=APP;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -1- FUNCTION: Functional neuronal receptor which couples to  
 CC intracellular signaling pathway through the GTP-binding protein  
 CC G1O (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the APP family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X56124; CAA39589.1; -; mRNA.  
 CC EMBL; X56126; CAA39591.1; -; mRNA.  
 DR HSSP; P08592; 1NMJ.  
 DR InterPro; IPR008155; A4 APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Amyloid; Transmembrane.  
 FT CHAIN <1 6  
 FT CHAIN 7 >59 Soluble APP-beta (By similarity).  
 FT CHAIN 7 48 CTF-alpha (By similarity).  
 FT CHAIN 7 46 Beta-amyloid protein 42 (By similarity).  
 FT CHAIN 47 >59 Beta-amyloid protein 40 (By similarity).  
 FT CHAIN 49 >59 Gamma-CTF(59) (By similarity).  
 FT TOPO\_DOM <1 34 Extracellular (Potential).  
 FT TRANSMEM 35 58 Potential.  
 FT TOPO\_DOM 59 >59 Cytoplasmic (Potential).  
 FT NON\_TER 1 1  
 FT NON\_TER 59 59  
 SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;  
 Query Match 91.2%; Score 31; DB 1; Length 59;  
 Best Local Similarity 85.7%; Pred. No. 17;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 Db 22 KLVFFAE 28  
 RESULT 13  
 O35463 CRIGR  
 ID O35463 CRIGR PRELIMINARY; PRT; 79 AA.  
 AC O35463;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Alzheimer's amyloid beta protein (fragment).  
 GN Name=beta APP;  
 OS Cricetus lagurus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Cricetinae; Cricetulus.  
 OC NCBI\_TaxID=10029;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sambamurti K., Pinnix I., Gandhi S.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF030413; AAB86608.1; -; mRNA.  
 DR HSSP; P08592; 1NMJ.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 FT NON\_TER 1 1  
 FT NON\_TER 79 79  
 SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 79;  
 Best Local Similarity 85.7%; Pred. No. 22;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 Db 36 KLVFFAE 42  
 RESULT 14  
 O8JH58 CHESE  
 ID O8JH58 CHESE PRELIMINARY; PRT; 113 AA.  
 AC O8JH58;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Amyloid beta protein (fragment).  
 DE Chelydra serpentina serpentina (common snapping turtle).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Testudines; Cryptodira; Testudinoidae; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN NUCLEOTIDE SEQUENCE.
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RX MEDLINE=21876906; PubMed=11882478;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AAN04908.1; -; mRNA.
DR HSSP; Q16019; 11YT.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF03494; Beta_APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 30 KLVFFAE 36

RESULT 15
Q4ULC9 RICFE PRELIMINARY; PRT; 213 AA.
AC Q4ULC9
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Uncharacterized phage-associated protein.
GN OrderedLocustNames=RF_0793;
OS Rickettsia felis (Rickettsia azadi).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxID=42862;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=URWKC12;
RX PubMed=15984913; DOI=10.1371/journal.pbio.0030248;
RA Ogata H., Renesto P., Audic S., Robert C., Blanc G., Fournier P.-E.,
RA Parinello H., Claverie J.-M., Raoult D.;
RT "The genome sequence of Rickettsia felis identifies the first putative
RT conjugative plasmid in an obligate intracellular parasite.";
RL PLoS Biol. 3:E248-E248(2005).
DR EMBL; CP000053; AY61644.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 213 AA; 24651 MW; 35852F551672389E CRC64;

Query Match 91.2%; Score 31; DB 2; Length 213;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 38 KLVYFAQ 44

RESULT 16
QBPPV5 MOUSE PRELIMINARY; PRT; 218 AA.
ID QBPPV5
AC QBPPV5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

```

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
DE library, clone:D430025B14 product:amyloid beta (A4) protein, full
DE insert sequence. (Fragment).
CN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:695-690(2001).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Izawa Y., Tanaka T., Matsuda S., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Watahiki M.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipillary sequencer.";
RL Genome Res. 10:1757-1771(2000).

```

RP NUCLEOTIDE SEQUENCE  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takabashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK052448; BAC34997.1; -; mRNA.  
DR HGSP; P08592; INMJ.  
DR MGI; MGI:88059; APP.  
DR GO; GO:0016021; C:integral to membrane; IDA.  
DR GO; GO:0016020; C:membrane; TAS.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:00030198; F:extracellular matrix organization and bioge. . .; IGI.  
DR InterPro; IPR008155; A4\_APP.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAMYLOID.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
FT NON TER 1  
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;  
Query Match 91.2%; Score 31; DB 2; Length 218;  
Best Local Similarity 85.7%; Pred. No. 57;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVPFAQ 7  
DB 135 KLVPFAE 141  
RESULT 17  
Q8UUI8 BRARE  
ID Q8UUI8 BRARE PRELIMINARY; PRT; 357 AA.  
AC Q8UUI8;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Putative membrane protein (Fragment).  
GN Name=appa;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN 1  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Whole embryo;  
RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;  
RA Musa A., Lehrach H., Russo V.R.A.;  
RT "Distinct expression patterns of two zebrafish homologues of the human  
RT APP gene during embryonic development."  
RL Dev. Genes Evol. 211:563-567(2001).  
DR EMBL; AJ315637; CAC85734.1; -; mRNA.  
DR HSSP; Q16019; 1H23.  
DR SMR; Q8UUI8; 62-170.  
DR ZFIN; ZDB-GENE-000616-13; appa.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR008155; A4\_APP.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAMYLOID.  
DR PROSITE; PS00320; A4\_INTRA; 1.

FT NON TER 1  
SQ SEQUENCE 357 AA; 40962 MW; 07D99BEF6C5B2D8 CRC64;  
Query Match 91.2%; Score 31; DB 2; Length 357;  
Best Local Similarity 85.7%; Pred. No. 91;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVPFAQ 7  
DB 274 KLVPFAE 280  
RESULT 18  
Q9SMFO HORVU  
ID Q9SMFO HORVU PRELIMINARY; PRT; 375 AA.  
AC Q9SMFO;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Mg-protoporphyrin IX (Fragment).  
GN Name=xantha-g;  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN 1  
RP NUCLEOTIDE SEQUENCE.  
RA Petersen B.L., Morrell J., Moeller M.G., Jensen P.E., Henningsen K.W.;  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ011926; CAB58179.1; -; mRNA.  
DR InterPro; IPR002035; VWF\_A.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS0234; VWEA; 1.  
FT NON TER 1  
SQ SEQUENCE 375 AA; 41123 MW; 563BC063F425DCF3 CRC64;  
Query Match 91.2%; Score 31; DB 2; Length 375;  
Best Local Similarity 85.7%; Pred. No. 95;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVPFAQ 7  
DB 84 KLVPFAQ 90  
RESULT 19  
Q8BPC7 MOUSE  
ID Q8BPC7 MOUSE PRELIMINARY; PRT; 384 AA.  
AC Q8BPC7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched  
DE library, clone:4833432109 product:amyloid beta (A4) protein, full  
DE insert sequence. (Fragment).  
GN Name=App;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN 1  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
RN 2  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bargh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
 RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RT Nature 409:685-690(2001).  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Head;  
 RC The FANTOM Consortium,  
 RC the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RT Nature 420:563-573(2002).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Head;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RT Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Head;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RX Shibata K., Itoh M., Aizawa K., Nagasaki S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multiplexed capillary sequencer.";  
 RT Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Head;  
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohashi N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tsgami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AK076506; BAC36369.1; -; mRNA.  
 DR HSSP: P08592; 1NWJ.  
 DR SRR: Q8BPC7; 74-183.  
 DR MGI: MGI:88059; App.  
 DR GO: GO:0016021; C:integral to membrane; IDA.  
 DR GO: GO:0016020; C:membrane; TAS.

DR	GO: 0005515; F:protein binding; IPI.
DR	GO: 0030198; P:extracellular matrix organization and bioge. .; IGO
DR	InterPro; IPR008155; A4 APP.
DR	InterPro; IPR001255; Beta-APP.
DR	Pfam; PF03494; Beta-APP; 1.
DR	PRINTS; PR00203; ANYLOIDA4.
DR	PRINTS; PR00204; BETAAMYLOID.
DR	PROSITE; PS00320; A4 INTRA; 1.
FT	NON TER 1
SQ	SEQUENCE 384 AA; 43990 MW; A81BIAD8AE683173 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 384;	
Best Local Similarity 85.7%; Pred. No. 97;	
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps	
Qy	1 KLWFFAQ 7
Db	301 KLWFFAE 307
RESULT 20	
OR65A_DROME	
ID	OR65A_DROME STANDARD; PRT; 417 AA.
AC	P82982;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)
DE	Putative odorant receptor 65a.
GN	Names:Or65a; ORFNames=CG32401;
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [Large Scale Genomic DNA].
RC	STRAIN=Berkeley;
RX	MDLLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.E., Vandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abriel J.F., Achyani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Fosler C., Evangelista A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Mileshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Swirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,







RESULT 24  
O9PVL1 CHICK

DR Pfam; PF02177; A4 EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR PROSITE; PS00319; A4 EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON TER 1  
 SQ SEQUENCE 612 AA; 69710 MW; 59A9ACBDF9C59BEFF CRC64;

Query Match 91.2%; Score 31; DB 2; Length 612;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
 |||||:  
 Db 529 KLVFFAE 535

## RESULT 26

Q7ZZT1\_BRARE PRELIMINARY; PRT; 678 AA.  
 AC Q7ZZT1;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Amyloid protein a variant 2.  
 GN Name=appa;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Groth C., Lardelli M.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY271746; AAP22958.1; -; mRNA.  
 DR HSP; Q16019; 1H23.  
 DR SMR; Q7ZZT1; 29-124, 383-491.  
 DR ZFIN; ZDB-GENE-000616-13; appa.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0005488; F: binding; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4 EXTRA; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4 EXTRA; 1.  
 DR PROSITE; PS00319; A4 EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 678 AA; 76755 MW; 94163778444FD0BC CRC64;

Query Match 91.2%; Score 31; DB 2; Length 678;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
 |||||:  
 Db 595 KLVFFAE 601

## RESULT 27

Q98SGO\_XENLA PRELIMINARY; PRT; 693 AA.  
 AC Q98SGO;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Beta-amyloid precursor protein A.  
 GN Name=app;  
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE-21610087; PubMed-11744158; DOI=10.1016/S0169-328X(01)00279-0;  
 RA van den Hurk W.H., Bloemen M., Martens G.J.M.;  
 RT "Expression of the gene encoding the beta-amyloid precursor protein  
 RT APP in Xenopus laevis.";  
 RL Brain Res. Mol. Brain Res. 97:13-20(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Van den Hurk W.H.;  
 RL Thesis (2001), Department of Biological Sciences, University of  
 RL Nijmegen, Nijmegen, Netherlands.  
 DR EMBL; AJ298150; CAC37193.1; -; mRNA.  
 DR HSP; Q16019; 1H23.  
 DR SMR; Q98SGO; 27-122, 383-492.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0005488; F: binding; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4 EXTRA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4 EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR SMART; SM00006; A4 EXTRA; 1.  
 DR PROSITE; PS00319; A4 EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 KW SIGNAL.  
 FT SIGNAL 1 19 Potential.  
 SQ SEQUENCE 693 AA; 78567 MW; CAF1DF655CIAB653 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 693;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
 |||||:  
 Db 610 KLVFFAE 616

## RESULT 28

Q5R477\_PONPY PRELIMINARY; PRT; 695 AA.  
 AC Q5R477;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Hypothetical protein DKFZp459D212.  
 GN Name=DKFZp459D212;  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Pongo.  
 OX NCBI\_TaxID=9600;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUR=Cortex;  
 RG The German cDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR861380; CH93439.1; -; mRNA.  
 DR SMR; Q5R477; 28-123, 124-189, 385-494.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0005488; F: binding; IEA.  
 DR GO; GO:0020037; F: heme binding; IEA.  
 DR GO; GO:0006118; P: electron transport; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_EXTRA.

0;

QY 1 KLVFFPAQ 7  
DB 612 KLVFFFAE 618

RESULT 32  
Q9DGJ8\_CHICK  
ID Q9DGJ8\_CHICK PRELIMINARY; PRT; 695 AA.  
AC Q9DGJ8;  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Beta-amyloid protein 695 isoform.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]

NUCLEOTIDE SEQUENCE.  
RP Sarasa M., Rodolose A., Sorribas V.;  
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF289218; AAG00593.1; -, mRNA.  
DR HSSP; Q16019; 11YT.  
DR SMR; Q9DGJ8; 28-123, 124-189, 385-494.  
DR Ensembl; ENSGALG00000015770; Gallus gallus.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0005488; F: binding; IEA.  
DR InterPro; IPR008155; A4 APP.  
DR InterPro; IPR008154; A4 EXTRA.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF021177; A4 EXTRA; 1.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAAMYL0ID.  
DR SMART; SM00006; A4 EXTRA; 1.  
DR PROSITE; PS00319; A4 EXTRA; 1.  
DR PROSITE; PS00320; A4 INTRA; 1.  
DR PROSITE; PS00320; A4 INTRA; 1.  
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 695;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
DB 612 KLVFFFAE 618

RESULT 33  
Q56JK4\_CANFA  
ID Q56JK4\_CANFA PRELIMINARY; PRT; 714 AA.  
AC Q56JK4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Beta-amyloid protein 714.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
RN [1]

NUCLEOTIDE SEQUENCE.  
RP Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;  
RA "Relationship between canine dementia and Alzheimer's disease.";  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY926581; AAX81910.1; -, mRNA.  
SQ SEQUENCE 714 AA; 80826 MW; 50DD851FB9E90EC5 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 714;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
DB 631 KLVFFFAE 637

RESULT 34  
Q6P6Q5\_RAT  
ID Q6P6Q5\_RAT PRELIMINARY; PRT; 733 AA.  
AC Q6P6Q5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE App protein.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]

NUCLEOTIDE SEQUENCE.  
RP TISSUE=Prostate;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toohyiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]

NUCLEOTIDE SEQUENCE.  
RP TISSUE=Prostate;  
RC Strausberg R.;  
RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
RL -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
CC EMBL; BC062082; AAH62082.1; -, mRNA.  
DR HSSP; Q16019; 1AAP.  
DR SMR; Q6P6Q5; 28-123, 124-189, 287-342, 441-550.  
DR Ensembl; ENSRNOG00000006997; Rattus norvegicus.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0005488; F: binding; IEA.  
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.  
DR InterPro; IPR008155; A4 APP.  
DR InterPro; IPR008154; A4 EXTRA.  
DR InterPro; IPR001255; Beta-APP.  
DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
DR Pfam; PF021177; A4 EXTRA; 1.  
DR Pfam; PF03494; Beta-APP; 1.  
DR Pfam; PF00014; Kunitz\_BPTI; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00759; BASICPTASE.  
DR PRINTS; PR00204; BETAAMYL0ID.  
DR ProDom; PD000222; Prot\_inh\_Kunz-m; 1.  
DR SMART; SM00006; A4 EXTRA; 1.  
DR SMART; SM00131; KU; 1.  
DR PROSITE; PS00319; A4 EXTRA; 1.  
DR PROSITE; PS00320; A4 INTRA; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 1.

```
SQ SEQUENCE 733 AA; 82797 MW; 8538F36FF73762F1 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 733;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
    |||||:
Db 650 KLVFFPAE 656

RESULT 35
Q6NUZ1 BRARE
ID Q6NUZ1 BRARE PRELIMINARY; PRT; 738 AA.
AC Q6NUZ1;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Amyloid beta (A4) protein a.
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D.K., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC068375; AAH68375.1; -; mRNA.
DR HSSP; Q16019; 1BA4.
DR SMR; Q6NUZ1; 29-124, 443-551.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0015021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008154; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4 EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR InterPro; IPR008154; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.

SQ SEQUENCE 733 AA; 83577 MW; AF480F6D308FD298 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 738;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
    |||||:
Db 655 KLVFFPAE 661

RESULT 37
Q7XZG7_ORYSA
```

```
DR SMART; SM00006; A4 EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 738 AA; 83577 MW; 3A02A6C158AF57B1 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 738;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
    |||||:
Db 655 KLVFFPAE 661

RESULT 36
Q90W28 BRARE
ID Q90W28 BRARE PRELIMINARY; PRT; 738 AA.
AC Q90W28;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Amyloid protein.
GN Name=appa; Synonym=app;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Groth C., Lardelli M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF389401; AAK64495.1; -; mRNA.
DR HSSP; Q16019; 1H23.
DR SMR; Q90W28; 29-124, 443-551.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008154; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4 EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 738 AA; 83577 MW; AF480F6D308FD298 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 738;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
    |||||:
Db 655 KLVFFPAE 661

RESULT 37
Q7XZG7_ORYSA
```

```
ID QTXZG7 ORYSA PRELIMINARY; PRT; 745 AA.
AC QTXZG7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative magnesium chelatase subunit chld.
GN Names:OSUNB0033J23.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Rhizophytidae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Teitlin T., Kim M.M., Bera J.J., Jin S.S.,
RA Padrosh D.W., Tallon L.J., Koo H., Ziemann V., Heiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP Buell R.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC137507; AAP73850.1; -; Genomic_DNA.
DR HSSP; P26239; IG8P.
DR Gramene; QTXZG7; -.
DR GO; GO:0016851; F:magnesium chelatase activity; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0015995; P:chlorophyll biosynthesis; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011776; BchD-ChlD.
DR InterPro; IPR012174; Mgchl ChlD.
DR InterPro; IPR000523; Mg_chelatase_chII.
DR InterPro; IPR002035; VNF_A.
DR Pfam; PF01078; Mg_chelatase; 1.
DR PIRSF; PIRSF036550; Mgchl ChlD; 1.
DR PRINTS; PR00453; VNFADOMAIN.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRFAMs; TIGR02031; BchD-ChlD; 1.
DR PROSITE; PS02034; VNF_A; 1.
SQ SEQUENCE 745 AA; 80846 MW; 4A347B2PB9PC6646 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 745;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 455 KLVFFAQ 461

RESULT 38
Q91963_9PIPI PRELIMINARY; PRT; 747 AA.
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE APP747.
GN Name=APP747;
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae.
OX NCBI_TaxID=8353;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93129227; PubMed=1282805;

ID Q91963_9PIPI PRELIMINARY; PRT; 747 AA.
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE APP747.
GN Name=APP747;
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae.
OX NCBI_TaxID=8353;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93129227; PubMed=1282805;
```

```
RA Okado H., Okamoto H.;
RT "A xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression.";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; S52417; AAB24853.1; -; mRNA.
DR HSSP; Q16019; 1H23.
DR SMR; Q91963; 26-119, 283-338, 437-546.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 747;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 664 KLVFFAQ 670

RESULT 39
Q56JK2_STECO PRELIMINARY; PRT; 749 AA.
ID Q56JK2
AC Q56JK2
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Beta-amyloid protein 749.
OS Stenella coeruleoalba (Striped dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Stenella.
OX NCBI_TaxID=9737;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY926583; AAX81912.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020377; F:heme binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
SQ SEQUENCE 749 AA; 84542 MW; 426599887C2A95D6 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 749;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 666 KLVFFAQ 672
```

DR	PROSITE; PS00319; A4_EXTRA; 1.
DR	PROSITE; PS00320; A4_INTRA; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ	SEQUENCE 749 AA; 84766 MW; 33478C6B6A8C295D CRC64;

  

Query Match	91.2%;	Score 31;	DB 2;	Length 749;
Best Local Similarity	85.7%;	Pred. NO. 1.8e+02;		
Matches 6;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps

  

Qy	1	KLVFFQAQ 7
		:
Db	666	KLVFFFAE 672

  

RESULT 41

Q6DUJB6_XENTR	IC	Q6DUJB6_XENTR PRELIMINARY;	PRT;	750 AA.
ID	Q6DUJB6;			
DT	25-OCT-2004	(TrEMBLrel. 28, Created)		
DT	25-OCT-2004	(TrEMBLrel. 28, Last sequence update)		
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)		
DE	Amyloid beta (A4) protein (protease nexin-II, Alzheimer disease).			
GN	Name=app-prov;			
OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;			
OC	Xenopodinae; Xenopus; Silurana.			
OX	NCBI_TaxID=8364;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TTSSUE=Whole body;			
XC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klauser R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,			
RA	Aletschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieih F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Brownstein M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Prange C.,			
RA	Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,			
RA	Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Whole body;			
RA	Klein S., Gerhard D.S.;			
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBIJ databases.			
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.			
DR	EMBL; BC075266; AAH75266.1; -; mRNA.			
DR	SNR; Q6DUJB6; 27-122, 285-340, 440-549.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0005488; F:binding; IEA.			
DR	GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.			
DR	InterPro; IPR008155; A4_APP.			
DR	InterPro; IPR008154; A4_extra.			
DR	InterPro; IPR001255; Beta-APP.			
DR	InterPro; IPR002223; Prot_inh_kunz-m.			
DR	Pfam; PF02177; A4_EXTRA; 1.			
DR	Pfam; PF00014; Kunitz_BPTI; 1.			
DR	PRINTS; PR00203; AMYLOIDA4.			



DR PRINTS; PRO0759; BASICPTASE.  
 DR PRINTS; PRO0204; BETAAMYLOID.  
 DR PRODOM; PD000222; Prot Inh\_Kunz-m; 1.  
 DR SMART; SM00006; A4 EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4 EXTRA; 1.  
 DR PROSITE; PS00320; A4 INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 1.  
 KW Protease.  
 SQ SEQUENCE 750 AA; 84927 MW; 4222350843147CAF CRC64;

Query Match 91.28; Score 31; DB 2; Length 750;  
 Best Local Similarity 85.74; Pred. NO. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPAQ 7  
 |||||  
 667 KLVPPAE 673

Db

RESULT 42  
 A4\_SAISS  
 ID\_ A4\_SAISS STANDARD; PRT; 751 AA.  
 AC Q95241;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid  
 protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble  
 APP-beta (S-APP-beta); C95; Beta-amyloid protein 42 (Beta-APP42);  
 DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-  
 CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)  
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-  
 secretase C-terminal fragment 50); C31].  
 GN Name=APP;  
 OS Saimiri sciureus (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;  
 OC Cebinae; Saimiri.  
 OX NCBI\_TaxID=9521;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney, and Liver;  
 RX MEDLINE=96108492; PubMed=8532114; DOI=10.1016/0197-4580(95)00090-2;  
 RA Levy E., Amorim A., Frangione B., Walker L.C.;  
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral  
 amyloid angiopathy.";  
 RL Neurobiol. Aging 16:805-808(1995).  
 CC -1- FUNCTION: Functions as a cell surface receptor and performs  
 physiological functions on the surface of neurons relevant to  
 neurite growth, neuronal adhesion and axonogenesis. Involved in  
 cell motility and transcription regulation through protein-protein  
 interactions (By similarity). Can promote transcription activation  
 through binding to APBB1/rip60 and inhibit Notch signaling through  
 interaction with Numb (By similarity). Couples to apoptosis-  
 inducing pathways such as those mediated by G(O) and JIP (By  
 similarity). Inhibits G(o) alpha ATPase activity (By similarity).  
 CC Acts as a kinesin I membrane receptor, mediating the axonal  
 transport of beta-secretase and presenilin 1 (By similarity). May  
 be involved in copper homeostasis/oxidative stress through copper  
 ion reduction. In vitro, copper-metalated APP induces neuronal  
 death directly or is potentiated through Cu(2+)-mediated low-  
 density lipoprotein oxidation (By similarity). Can regulate  
 neurite outgrowth through binding to components of the  
 extracellular matrix such as heparin and collagen I and IV (By  
 similarity). The splice isoforms that contain the BPTI domain  
 possess protease inhibitor activity (By similarity).  
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 with metal-reducing activity. Bind transient metals such as  
 copper, zinc and iron (By similarity).  
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 peptides, including C31, are potent enhancers of neuronal

CC apoptosis (By similarity).  
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several  
 cytoplasmic proteins, including APBB family members, the APBA  
 family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding  
 to Dab1 inhibits its serine phosphorylation (By similarity). Also  
 interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2  
 (via its TPR domains) (By similarity), APPBP2 (via BASS) and DDB1.  
 CC In vitro, it binds MAPT via the WT-binding domains (By  
 CC similarity). Associates with microtubules in the presence of ATP  
 CC and in a kinesin-dependent manner (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the  
 CC endoplasmic reticulum) moves to the Golgi complex where complete  
 CC maturation occurs (O-glycosylated and sulfated). After alpha  
 CC secretase cleavage, soluble APP is released into the extracellular  
 CC space and the C-terminal is internalized into endosomes and  
 CC lysosomes. Some APP accumulates in secretory transport vesicles  
 CC leaving the late Golgi compartment and returns to the cell  
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm  
 CC and nuclei of neurons (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=APP770;  
 CC IsoId=Q95241-1; Sequence=Displayed;  
 CC Name=APP695;  
 CC IsoId=Q95241-2; Sequence=Not described;  
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for  
 CC sorting of membrane proteins to the basolateral surface of  
 CC epithelial cells (By similarity).  
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-  
 CC phosphorylated proteins is required for the specific binding of  
 CC the PID domain. However additional amino acids either N- or C-  
 CC terminal to the NPXY motif are often required for complete  
 CC interaction. The PID domain-containing proteins which bind APP  
 CC require the YENPTY motif for full interaction. These interactions  
 CC are independent of phosphorylation on the terminal tyrosine  
 CC residue. The NPXY site is also involved in clathrin-mediated  
 CC endocytosis (By similarity).  
 CC -1- PTM: Proteolytically processed or alternatively by beta-secretase  
 CC cleavage by alpha-secretase and extracellular release of soluble APP  
 CC leads to generation and S-APP-beta, respectively, and the  
 CC retention of corresponding membrane-anchored C-terminal fragments,  
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase  
 CC yields P3 peptides. This is the major secretory pathway and is  
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated  
 CC gamma-secretase processing of C99 releases the amyloid beta  
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),  
 CC major components of amyloid plaques, and the cytotoxic C-terminal  
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By  
 CC similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis  
 CC (By similarity). Cleavage at App-720 by either caspase-3, -8 or -9  
 CC results in the production of the neurotoxic C31 peptide and the  
 CC increased production of beta-amyloid peptides (By similarity).  
 CC -1- PTM: N- and O-glycosylated (By similarity).  
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and  
 CC serine residues is neuron-specific. Phosphorylation can affect APP  
 CC processing, neuronal differentiation and interaction with other  
 CC proteins (By similarity).  
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and  
 CC zinc, can induce histidine-bridging between beta-amyloid molecules  
 CC resulting in beta-amyloid-metal aggregates (By similarity).  
 CC Extracellular zinc-binding increases binding of heparin to APP and  
 CC inhibits collagen-binding (By similarity).  
 CC -1- SIMILARITY: Belongs to the APP family.  
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its



use as long as its content is in no way modified and this statement is not removed.

EMBL; S81024; AAD14347.1; -; mRNA.  
PDB; 1RW6; X-ray; A=346-551.  
SMR; Q95241; 28-123, 124-189, 287-342.  
InterPro; IPR008155; A4\_APP.  
InterPro; IPR001255; Beta-APP.  
InterPro; IPR002223; Prot inh Kunz-m.  
PANTHER; PTHR10083.SF6; Beta-APP; 5.  
Pfam; PF02177; A4\_EXTRA; 1.  
Pfam; PF03494; Beta-APP; 1.  
Pfam; PF00014; Kunitz BPTI; 1.  
PRINTS; PR00203; AMYLOIDA4.  
PRINTS; PR00759; BASICPTASE.  
PRINTS; PR00204; BETAAMYLOID.  
ProDom; PD000222; Prot inh Kunz-m; 1.  
SMART; SM00006; A4\_EXTRA; 1.  
SMART; SM00131; KU; 1.  
PROSITE; PS00319; A4\_EXTRA; 1.  
PROSITE; PS00320; A4\_INTRA; 1.  
PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
PROSITE; PS00279; BPTI\_KUNITZ\_2; 1.  
3D-structure; Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Metal-binding; Notch signaling pathway; Phosphorylation; Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal; Transmembrane; Zinc.  
SIGNAL 1 17 By similarity.  
CHAIN 18 751 Amyloid beta A4 protein.  
CHAIN 18 668 Soluble APP-alpha (Potential).  
CHAIN 18 652 Soluble APP-beta (Potential).  
CHAIN 653 751 C99 (Potential).  
CHAIN 653 694 Beta-amyloid protein 42 (Potential).  
CHAIN 653 692 Beta-amyloid protein 40 (Potential).  
CHAIN 669 751 C93 (Potential).  
PEPTIDE 669 694 P3 (42) (Potential).  
PEPTIDE 669 692 P3 (40) (Potential).  
CHAIN 693 751 Gamma-CTF (59) (Potential).  
CHAIN 695 751 Gamma-CTF (57) (Potential).  
CHAIN 702 751 Gamma-CTF (50) (Potential).  
CHAIN 721 751 C31 (Potential).  
TOPO\_DOM 18 680 Extracellular (Potential).  
TRANSMEM 681 704 Potential.  
TOPO\_DOM 705 751 Cytoplasmic (Potential).  
DOMAIN 291 341 BPTI/Kunitz inhibitor.  
REGION 96 110 Heparin-binding (By similarity).  
REGION 181 188 Zinc-binding (By similarity).  
REGION 316 344 Heparin-binding (By similarity).  
REGION 363 428 Heparin-binding (By similarity).  
REGION 504 521 Collagen-binding (By similarity).  
REGION 713 732 Interaction with G(o)-alpha (By similarity).  
MOTIF 705 715 Basolateral sorting signal (By similarity).  
MOTIF 740 743 NPXY motif.  
COMPBIAS 230 260 Asp/Glu-rich (acidic).  
METAL 137 137 Poly-Thr.  
METAL 147 147 Copper (By similarity).  
METAL 149 149 Copper (By similarity).  
METAL 151 151 Copper (By similarity).  
METAL 658 658 Copper or zinc (By similarity).  
METAL 662 662 Copper or zinc (By similarity).  
METAL 665 665 Copper or zinc (By similarity).  
METAL 666 666 Copper or zinc (By similarity).  
SITE 144 144 Required for Cu(2+) reduction (By similarity).  
SITE 301 302 Reactive bond.  
SITE 652 653 Cleavage (by beta-secretase) (By similarity).  
SITE 653 654 Cleavage (by caspase-6) (By similarity).

FT SITE 668 669 Cleavage (by alpha-secretase) (By similarity).  
FT SITE 685 685 Implicated in free radical propagation (By similarity).  
Query Match 91.2%; DB 1; Length 751;  
Best Local Similarity 85.7%; Pred. NO. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVFFAQ 7  
Db 668 KLVFFAE 674  
RESULT 43  
Q6GSC0 HUMAN PRELIMINARY; PRT; 751 AA.  
AC Q6GSC0;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE Amyloid beta A4 protein,, isoform b.  
GN Name=APP;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Eye;  
RG NIH MGC Project;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
DR EMBL; BC065529; AA065529.1; -; mRNA.  
DR SMR; Q6GSC0; 28-123, 124-189, 287-342, 441-550.  
DR Ensembl; ENSG00000142192; Homo sapiens.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0020037; F:heme binding; IEA.  
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
DR GO; GO:0006118; F:electron transport; IEA.  
DR InterPro; IPR008155; A4\_APP.  
DR InterPro; IPR008154; A4\_extra.  
DR InterPro; IPR01255; Beta-APP.  
DR InterPro; IPR01282; Cytochrome c R.  
DR InterPro; IPR002223; Prot inh Kunz-m.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR Pfam; PF03494; Beta-APP; 1.

Db 668 KLVPFAE 674

RP	NUCL
RA	Inte
RT	"DNA

International consortium for macaque cDNA sequencing, analysis; "DNA sequences of macaque genes expressed in brain or testis and its



DR PROSITE; PS0234; VWFA; 1;  
 KW ATP-binding; Chlorophyll biosynthesis; Chloroplast; Ligase;  
 NM Nucleotide-binding; Photosynthesis; Transit peptidase;  
 FT TRANSIT 1 ? Chloroplast (Potential).  
 FT CHAIN ? 754  
 FT DOMAIN 551 751 VWFA.  
 FT COMPIAS 398 449 Glu/Pro-rich.  
 FT COMPIAS 405 412 Poly-Pro.  
 FT COMPIAS 423 432 Poly-Glu.  
 SQ SEQUENCE 754 AA; 82865 MW; 1D56BA3139080A90 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 754;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVEPFAQ 7  
 ||:||||  
 Db 462 KLVEPFAQ 468

## RESULT 49

Q6ATS0 ORYSA  
 ID Q6ATS0 ORYSA PRELIMINARY; PRT; 754 AA.  
 AC Q6ATS0;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Putative magnesium chelatase.  
 GN Name=OSJNB0028F23.2;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoideae; Oryza.  
 ON NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,  
 RA Overton I.L., Teitran T., Kim M.M., Bera J.J., Jin S.S.,  
 RA Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,  
 RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,  
 RA Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,  
 RA White O., Salzberg S.L., Fraser C.M.;  
 RT "Oryza sativa chromosome 3 BAC OSJNB0028F23 genomic sequence.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Buell R.;  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC135595; AAT77900.1; -; Genomic\_DNA.  
 DR Gramene; Q6ATS0; -.  
 DR GO; GO:0016851; F:magnesium chelatase activity; IEA.  
 DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0015995; P:chlorophyll biosynthesis; IEA.  
 DR GO; GO:0015979; P:photosynthesis; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR011776; BchD-Chld.  
 DR InterPro; IPR012174; Mgchl Chld.  
 DR InterPro; IPR000523; Mg chelatase\_chII.  
 DR InterPro; IPR002035; VWFA.  
 DR Pfam; PF01078; Mg\_chelatase; 1.  
 DR PIRSF; PIRSF036550; Mgchl Chld; 1.  
 DR PRINTS; PR00453; VWFADOMAIN.  
 DR SMART; SM00382; AAA; 1.  
 DR SMART; SM00327; VWFA; 1.  
 DR TIGRFAMs; TIGR02031; BchD-Chld; 1.  
 DR PROSITE; PS0234; VWFA; 1.  
 SQ SEQUENCE 754 AA; 81878 MW; 8B9PFAA055401164D CRC64;

Query Match 91.2%; Score 31; DB 2; Length 754;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVEPFAQ 7  
 ||:||||  
 Db 464 KLVEPFAQ 470

## RESULT 50

Q4RY33 TETNG  
 ID Q4RY33 TETNG PRELIMINARY; PRT; 754 AA.  
 AC Q4RY33;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome 3 SCAF14978, whole genome shotgun sequence.  
 DE (Fragment).  
 GN ORFNAMES=GSTENG00027170001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 ON NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli S., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Weissenbach J., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissbach J., Roest Crullius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; CAAE01014978; CAG06699.1; -; Genomic\_DNA.  
 FT NON\_TER 1 1  
 FT NON\_TER 754 754  
 SQ SEQUENCE 754 AA; 84740 MW; 4A37B051A9FAD777 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 754;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVEPFAQ 7  
 ||:||||  
 Db 671 KLVEPFAE 677

## RESULT 51

CHLD\_TOBAC  
 ID CHLD\_TOBAC STANDARD; PRT; 758 AA.  
 AC O24133;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Magnesium-chelatase subunit chld, chloroplast precursor (EC 6.6.1.1)  
 DE (Mg-protoporphyrin IX chelatase) (Mg-chelatase subunit D).  
 GN Name=CHLD;  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC asterids; lamids; Solanales; Solanaceae; Nicotiana.

```

OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Papanbrock J., Graefe S., Kruse E., Haenel F., Grimm B.;
RT "Mg-chelate of tobacco: identification of a chl D cDNA sequence
RT encoding a third subunit, analysis of the interaction of the three
RT subunits with the yeast two-hybrid system, and reconstitution of the
RT enzyme activity by co-expression of recombinant CHL D, CHL H and CHL
RT I.";
RL Plant J. 12:981-990(1997).
CC -!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a
CC magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
CC IX.
CC -!- CATALYTIC ACTIVITY: ATP + protoporphyrin IX + Mg(2+) + H(2)O = ADP
CC + phosphate + Mg-protoporphyrin IX + 2 H(+).
CC -!- PATHWAY: Chlorophyll biosynthesis.
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma.
CC -!- SIMILARITY: Belongs to the Mg-chelatase subunits D/I family.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Y10022; CAA71128.1; -; mRNA.
DR F1R; T02925; T02925.
DR HSSP; P26239; 1G8P.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011776; BchD-Chld.
DR InterPro; IPR000523; Mg_chelatase_chII.
DR InterPro; IPR012174; MgChl_Chld.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01078; Mg_chelatase; 1.
DR PRINTS; FIRSF036550; Mgchl_Chld; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRfam; TIGR02031; BchD-Chld; 1.
DR PROSITE; PS50234; VWFA; 1.
KW ATP-binding; Chlorophyll biosynthesis; Chloroplast; Ligase;
KW Nucleotide-binding; Photosynthesis; Transit peptide.
FT TRANSIT 1 62 Chloroplast (Potential).
FT CHAIN 63 758 Magnesium-chelatase subunit chld.
FT DOMAIN 556 752 VWFA.
FT COMPIAS 399 445 Glu/Pro-rich.
FT COMPIAS 409 416 Poly-Pro.
FT COMPIAS 427 434 Poly-Glu.
SQ SEQUENCE 758 AA; 83013 MW; ED531E85D5FAFEF8 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 758;
Best Local Similarity 85.7%; Pred.No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KLVFFAQ 7
Db 467 KLVFFAQ 473

RESULT 52
CHLD ARATH
ID CHLD ARATH STANDARD; PRT; 759 AA.
AC Q9SJ61; Q9SWY5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Magnesium-chelatase subunit chld, chloroplast
DE (Mg-protoporphyrin IX chelatase) (Mg-chelatase subunit D).
GN Name=CHLD; OrderedLocNames=At1G08520; ORFNames=T2G7.20;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

OC OC
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=9418040;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.-H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltcher J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 32-759.
RC STRAIN=cv. C24;
RA Green J., Jensen P.E., Gibson L.C.D., Hunter C.N.;
RT "Characterization of the magnesium protoporphyrin chelatase chld
RT subunit from Arabidopsis thaliana cv. C24.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a
CC magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
CC IX.
CC -!- CATALYTIC ACTIVITY: ATP + protoporphyrin IX + Mg(2+) + H(2)O = ADP
CC + phosphate + Mg-protoporphyrin IX + 2 H(+).
CC -!- PATHWAY: Chlorophyll biosynthesis.
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma.
CC -!- SIMILARITY: Belongs to the Mg-chelatase subunits D/I family.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AC006932; AAF22895.1; ALT SEQ; Genomic_DNA.
DR EMBL; AF083555; AAD52031.1; -; mRNA.
DR HSSP; P26239; 1G8P.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011776; BchD-Chld.
DR InterPro; IPR000523; Mg_chelatase_chII.
DR InterPro; IPR012174; MgChl_Chld.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01078; Mg_chelatase; 1.
DR PRINTS; FIRSF036550; Mgchl_Chld; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRfam; TIGR02031; BchD-Chld; 1.
DR PROSITE; PS50234; VWFA; 1.
KW ATP-binding; Chlorophyll biosynthesis; Chloroplast; Ligase;
KW Nucleotide-binding; Photosynthesis; Transit peptide.
FT TRANSIT 1 759 Magnesium-chelatase subunit chld.
FT CHAIN 557 753 VWFA.
FT DOMAIN 411 418 Poly-Pro.
FT COMPIAS 425 438 Poly-Glu.

```

FT CONFLICT 70 70 D -> B (in Ref. 2).  
 FT CONFLICT 150 150 D -> N (in Ref. 2).  
 FT CONFLICT 270 270 G -> S (in Ref. 2).  
 FT CONFLICT 285 286 Missing (in Ref. 2).  
 FT CONFLICT 314 314 R -> S (in Ref. 2).  
 FT CONFLICT 379 379 E -> K (in Ref. 2).  
 FT CONFLICT 426 426 E -> D (in Ref. 2).  
 SQ SEQUENCE 759 AA; 83155 MW; A4169319E1247BD1 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 759;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
 ||:||||  
 DB 468 KLVFFAQ 474

RESULT 53  
 Q4S0J4\_TETNG PRELIMINARY; PRT; 759 AA.  
 ID Q4S0J4\_TETNG PRELIMINARY; PRT; 759 AA.  
 AC Q4S0J4;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome 2 SCAP14781, whole genome shotgun sequence.  
 GN ORFNames=GSTENG00025991001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OC NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 Blumont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,  
 Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
 Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 Winkler P., Lander E.S., Weissenbach J., Roest Croliis H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE  
 RG Genoscope: Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 DR EMBL; CAAB01014781; CAG05838.1; -, Genomic\_DNA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Prot. inh. Kunz-m.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR ProDom; PD000222; Prot. inh. Kunz-m; 1.  
 DR SMART; SM00006; A4\_EXTEA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.

DR PROSITE; PS00320; A4\_INTEA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 1.  
 SQ SEQUENCE 759 AA; 85017 MW; 5EEF9B8B6C273233 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 759;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
 ||:||||  
 DB 676 KLVFFAQ 682

RESULT 54  
 Q8VZU7\_ARATH PRELIMINARY; PRT; 760 AA.  
 ID Q8VZU7\_ARATH PRELIMINARY; PRT; 760 AA.  
 AC Q8VZU7;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Putative Mg-chelatease.  
 GN Name=At1g08520;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
 Goldsmith A.D., Lee J.M., Toriumi M., Yu G., Bowser L.,  
 Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
 Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
 Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
 Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
 Theologis A.,  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE  
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,  
 Dang J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,  
 Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,  
 Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
 Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
 Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
 Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,  
 Davis R.W., Ecker J.R., Theologis A.,  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY063821; AAL36177.1; -, mRNA.  
 DR EMBL; AY091402; AAM14341.1; -, mRNA.  
 DR HSP; P26239; 1G8P.  
 DR GO; GO:0016851; P.magnesium chelatease activity; IEA.  
 DR GO; GO:0017111; P.nucleoside-triphosphatase activity; IEA.  
 DR GO; GO:0000166; P.nucleoside binding; IEA.  
 DR GO; GO:0015995; P.chlorophyll biosynthesis; IEA.  
 DR GO; GO:0015979; P.photosynthesis; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR011776; BchD-Chld.  
 DR InterPro; IPR012174; Mgchl\_Chld.  
 DR InterPro; IPR00523; Mg\_chelatease\_chII.  
 DR InterPro; IPR002035; VWF\_A.  
 DR PIRSF; PIRSF036550; Mgchl\_Chld; 1.  
 DR PRINTS; PR00453; VWFADOMAIN.  
 DR SMART; SM00382; AAA; 1.  
 DR SMART; SM00327; VWA; 1.  
 DR TIGRFAMs; TIGR02031; BchD-Chld; 1.  
 DR PROSITE; PS0234; VWFA; 1.  
 SQ SEQUENCE 760 AA; 83283 MW; A3A2D92DF93D4F43 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 760;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;



Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFQAQ 7  
 DB 469 KLVFFQAQ 475

RESULT 55  
 A4\_CAVPO STANDARD; PRT; 770 AA.

AC Q60495; Q60496;  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
 DE amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha);  
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid  
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3 (42);  
 DE P3 (40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-  
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].  
 GN Name=APP;  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 OC Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.  
 RC TISSUE=Brain, and Liver;  
 RX MEDLINE=97236426; PubMed=9116031; DOI=10.1016/S0167-4781(96)00232-1;  
 RA Beck M., Mueller D., Bigl V.;  
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and  
 RT alternative splicing";  
 RL Biochim. Biophys. Acta 1351:17-21(1997).  
 RN [2]  
 RP INTERACTION OF BETA-APP40 WITH APOE.  
 RX MEDLINE=98007700; PubMed=9349544;  
 RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,  
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;  
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on  
 RT cerebral capillary sequestration and blood-brain barrier transport of  
 RT circulating Alzheimer's amyloid beta.";  
 RL J. Neurochem. 69:1995-2004(1997).  
 RN [3]  
 RP PROCESSING.  
 RX MEDLINE=20084499; PubMed=10619481; DOI=10.1016/S0306-4522(99)00390-5;  
 RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,  
 RA Bigl V.;  
 RT "Guinea-pig primary cell cultures provide a model to study expression  
 RT and amyloidogenic processing of endogenous amyloid precursor  
 RT protein.";  
 RL Neuroscienc 95:243-254(2000).  
 RN [4]  
 RP GAMMA-SECRETASE PROCESSING.  
 RX MEDLINE=20576391; PubMed=11035007; DOI=10.1074/jbc.M005968200;  
 RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,  
 RA Ziani-Cherif C., Onstead L., Sambamurti K.;  
 RT "A novel gamma -secretase assay based on detection of the putative C-  
 RT terminal fragment-gamma of amyloid beta protein precursor.";  
 RL J. Biol. Chem. 276:481-487(2001).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions (By similarity). Can promote transcription activation  
 CC through binding to APPB1/Tip60 and inhibit Notch signaling through  
 CC interaction with Numb (By similarity). Couples to apoptosis-  
 CC inducing pathways such as those mediated by G(O) and JIP (By  
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).  
 CC Acts as a kinesin I membrane receptor, mediating the axonal  
 CC transport of beta-secretase and presenilin 1 (By similarity). May  
 CC be involved in copper homeostasis/oxidative stress through copper  
 CC ion reduction (By similarity). In vitro, copper-metallated APP

induces neuronal death directly or is potentiated through Cu(2+)-  
 mediated low-density lipoprotein oxidation (By similarity). Can  
 regulate neurite outgrowth through binding to components of the  
 extracellular matrix such as heparin and collagen I and IV (By  
 similarity). The splice isoforms that contain the BPTI domain  
 possess protease inhibitor activity (By similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins  
 CC and apolipoproteins E and J in the CSF and to HDL particles in  
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.  
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the  
 CC extracellular matrix and may regulate neurite outgrowth in the  
 CC brain (By similarity).  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminus, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK3IP1, SHC1 and Numb and Dab1 (By similarity). Also  
 CC interacts with GPCR-like protein BPP, PPRL1, APPBP1, IB1, KNS2  
 CC (via its TPR domain), APPBP2 (via BASS) and DDB1 (By similarity).  
 CC Associates with microtubules in the presence of ATP and in a  
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds  
 CC all three isoforms of APOE, in vitro and in vivo. When lipidated,  
 CC ApoE3 appears to be the preferred amyloid binding isoform, while  
 CC the apoE4 isoform-beta-APP40 complex is capable of being  
 CC transported across the blood-brain barrier.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated pits  
 CC (By similarity). During maturation, the immature APP (N-  
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi  
 CC complex where complete maturation occurs (O-glycosylated and  
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble  
 CC APP is released into the extracellular space and the C-terminal is  
 CC internalized to endosomes and lysosomes (By similarity). Some APP  
 CC accumulates in secretory transport vesicles leaving the late Golgi  
 CC compartment and returns to the cell surface (By similarity). APP  
 CC sorts to the basolateral surface in epithelial cells (By  
 CC similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms, missing exons 7,8 and 15, seem to  
 CC exist. The L-isoforms, missing exon 15, are referred to as  
 CC appicans;  
 CC Name=APP770;  
 CC IsoId=Q60495-1; Sequence=Displayed;  
 CC Name=APP695;  
 CC IsoId=Q60495-2; Sequence=VSP\_007221, VSP\_007222;  
 CC -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in  
 CC brain. The longer isoforms containing the BPTI domain are  
 CC predominantly expressed in peripheral organs such as muscle and  
 CC liver.  
 CC -!- INDUCTION: Increased levels during neuronal differentiation.  
 CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for  
 CC sorting of membrane proteins to the basolateral surface of  
 CC epithelial cells.  
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-  
 CC phosphorylated proteins is required for the specific binding of  
 CC the PID domain. However additional amino acids either N- or C-  
 CC terminal to the NPXY motif are often required for complete  
 CC interaction. The PID domain-containing proteins which bind APP  
 CC require the YENPTY motif for full interaction. These interactions  
 CC are independent of phosphorylation on the terminal tyrosine  
 CC residue (By similarity). The NPXY site is also involved in  
 CC clathrin-mediated endocytosis.  
 CC -!- PTM: Proteolytically processed  
 CC Cleavage by alpha-secretase or alternatively by beta-secretase  
 CC leads to generation and extracellular release of soluble APP  
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the  
 CC retention of corresponding membrane-anchored C-terminal fragments,  
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by  
 CC gamma-secretase yields P3 peptides. This is the major secretory

pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of CTF-beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the corresponding cytotoxic C-terminal fragments (CTFs).

-1- PTM: Proteolytically cleaved by caspase-3 during neuronal apoptosis (By similarity).

-1- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to the L-APP isoforms produces the APP proteoglycan core proteins, the appicans (By similarity).

-1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific (By similarity).

Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins.

-1- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

-1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates.

-1- SIMILARITY: Belongs to the APP family.

-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

-----

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

-----

EMBL; X97631; CAA6230.1; -; mRNA.  
 DR EMBL; X99198; CAA67589.1; -; mRNA.  
 DR HSSP; P08592; INMJ.  
 DR SMR; Q60495; 28-123, 124-189, 287-342, 460-569.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta\_APP.  
 DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR PANTHER; PTHR10083:SF6; Beta\_APP; 6.  
 DR Pfam; PF021177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta\_APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR ProDom; PD000222; Prot\_inh\_Kunz-m; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 1.  
 KW Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;  
 KW Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;  
 KW Metal-binding; Notch signaling pathway; Phosphorylation;  
 KW Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;  
 KW Transmembrane; Zinc.  
 FT SIGNAL 1 17 By similarity.  
 FT CHAIN 18 770 Amyloid beta A4 protein.  
 FT CHAIN 18 687 Soluble APP-alpha (By similarity).  
 FT CHAIN 18 671 Soluble APP-beta (By similarity).  
 FT CHAIN 672 770 CTF-alpha (By similarity).  
 FT CHAIN 672 713 Beta-amyloid protein 42 (By similarity).  
 Query Match 91.2%; Score 31; DB 1; Length 770;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KLVFFAQ 7  
 |||||:  
 687 KLVFFAE 693

## RESULT 56

A4\_HUMAN STANDARD; PRT; 770 AA.  
 AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;  
 Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCB8; Q9UCD1; Q9QUS8;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
 amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease  
 nexin-II) (PN-II) (APP1) (PreA4) [Contains: Soluble APP-alpha (S-APP-  
 alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42  
 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);  
 P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)  
 (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-  
 secretase C-terminal fragment 57) (Amyloid intracellular domain 57)  
 (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)  
 (Amyloid intracellular domain 50) (AID(50)); C31].  
 GN Name=APP, Synonyms=A4, AD1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP695).  
 RC TISSUE=Brain;  
 RX MEDLINE=87144572; PubMed=2881207; DOI=10.1038/325733a0;  
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,  
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a  
 cell-surface receptor.";  
 RL Nature 325:733-736(1987).  
 [2]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP751).  
 RC TISSUE=Brain;  
 RX MEDLINE=88122639; PubMed=2893289; DOI=10.1038/331525a0;  
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,  
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,  
 RA Cordell B.;  
 RT "A new A4 amyloid mRNA contains a domain homologous to serine  
 protease inhibitors.";  
 RL Nature 331:525-527(1988).  
 [3]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP695).  
 RC MEDLINE=89128427; PubMed=2783775;  
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayne R.M.,  
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;  
 RT "The PreA4 (695) precursor protein of Alzheimer's disease A4 amyloid is  
 encoded by 16 exons.";  
 RL Nucleic Acids Res. 17:517-522(1989).  
 [4]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP770).  
 RC MEDLINE=90236318; PubMed=2110105; DOI=10.1016/0378-1119(90)90310-N;  
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sasaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 gene.";  
 RL Gene 87:257-263(1990).  
 [5]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM L-APP733).  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=9228136; PubMed=1587857;  
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,  
 RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;  
 RT "Identification and differential expression of a novel alternative  
 splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in  
 leukocytes and brain microglial cells.";  
 RL J. Biol. Chem. 267:10804-10809(1992).



RN [7]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).  
 RX MEDLINE=97263807; PubMed=9108164; DOI=10.1093/nar/25.9.1802;  
 RA Hattori M., Teukahara F., Furuhata Y., Tanahashi H., Hirose M.,  
 RA Saito M., Teukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for  
 RT sequencing of a 300 kb region of human APP locus";  
 RL Nucleic Acids Res. 25:1802-1808(1997).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP639).  
 RC TISSUE=Brain;  
 RX MEDLINE=22744650; PubMed=12859342;  
 RX DOI=10.1046/j.1460-9568.2003.02731.x;  
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;  
 RT "Identification of a novel alternative splicing isoform of human  
 RT amyloid precursor protein gene, APP639";  
 RL Eur. J. Neurosci. 18:102-108(2003).  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA), AND VARIANT LYS-501.  
 RA Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,  
 RA Nguyen C.P., Gildersleeve H., Cassidy C.M., Johnson E.J.,  
 RA Swanson J.E., McFarland I., Yool B., Park C., Nickerson D.A.;  
 RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department  
 RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>)";  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS APP305 AND APP751).  
 RC TISSUE=Eye, and Pancreas;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Tothyluki S., Carninci P., Frange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany P.H.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [11]  
 RP NUCLEOTIDE SEQUENCE OF 1-10.  
 RC TISSUE=Liver;  
 RX MEDLINE=89016647; PubMed=3140222;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [12]  
 RP ERRATUM, AND SEQUENCE REVISION.  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RL Nucleic Acids Res. 16:11402-11402(1988).  
 RN [13]  
 RP NUCLEOTIDE SEQUENCE OF 1-75.  
 RX MEDLINE=89165870; PubMed=2538123;  
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;  
 RT "Characterization of the 5'-end region and the first two exons of the  
 RT beta-protein precursor gene";  
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).  
 RN [14]  
 RP PROTEIN SEQUENCE OF 18-50.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=87350462; PubMed=3597385;  
 RA van Nostrand W.E., Cunningham D.B.;

RT "Purification of protease nexin II from human fibroblasts.";  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [15]  
 RP PROTEIN SEQUENCE OF 18-40.  
 RC TISSUE=Platelet;  
 RX MEDLINE=22608298; PubMed=12658801; DOI=10.1038/nbt810;  
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,  
 RA Thomas G.R., Vandekerckhove J.;  
 RT "Exploring proteomes and analyzing protein processing by mass  
 RT spectrometric identification of sorted N-terminal peptides";  
 RL Nat. Biotechnol. 21:566-569(2003).  
 RN [16]  
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP751).  
 RC TISSUE=Brain;  
 RX MEDLINE=89346754; PubMed=2569763;  
 RA de Sauvage F., Octave J.N.;  
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly  
 RT secreted protein";  
 RL Science 245:651-653(1989).  
 RN [17]  
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP695).  
 RC TISSUE=Brain;  
 RX MEDLINE=87231971; PubMed=30355574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RN [18]  
 RP NUCLEOTIDE SEQUENCE OF 286-366.  
 RX MEDLINE=88122640; PubMed=2893290; DOI=10.1038/331528a0;  
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
 RA Gusella J.P., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease";  
 RL Nature 331:528-530(1988).  
 RN [19]  
 RP NUCLEOTIDE SEQUENCE OF 287-367.  
 RX MEDLINE=88122641; PubMed=2893291; DOI=10.1038/331530a0;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease  
 RT inhibitory activity";  
 RL Nature 331:530-532(1988).  
 RN [20]  
 RP NUCLEOTIDE SEQUENCE OF 507-770.  
 RC TISSUE=Brain cortex;  
 RX MEDLINE=88124954; PubMed=2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [21]  
 RP PROTEIN SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.  
 RX MEDLINE=96139497; PubMed=8576160; DOI=10.1074/jbc.271.3.1613;  
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;  
 Query Match 91.2%; Score 31; DB 1; Length 770;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 Db 687 KLVFFAE 693  
 RESULT 57  
 A4 MACFA STANDARD; PRT; 770 AA.  
 ID A4 MACFA  
 AC P53601; Q60HH7; Q95KN7;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);  
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-  
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);  
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)  
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-  
DE secretase C-terminal fragment 50); C31].  
DE Name=APP; ORFNames=QCC8-1594;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORMS APP695 AND APP770).  
RC TISSUE=Cerebellum;  
RX MEDLINE=91273117; PubMed=1905108;  
RA Podlany M.B., Tolan D.R., Selkoe D.J.;  
RT "Homology of the amyloid beta protein precursor in monkey and human  
RT supports a primate model for beta amyloidosis in Alzheimer's  
RT disease.";  
RL Am. J. Pathol. 138:1423-1435(1991).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).  
RC TISSUE=Brain cortex;  
RA Kusuda J., Oeada N., Tanuma R., Hirata M., Sugano S., Hashimoto K.;  
RT "Isolation and characterization of cDNA for macaque neurological  
RT disease genes";  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Functions as a cell surface receptor and performs a  
CC physiological functions on the surface of neurons relevant to  
CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
CC cell motility and transcription regulation through protein-protein  
CC interactions (By similarity). Can promote transcription activation  
CC through binding to APPB1/Tip60 and inhibit Notch signaling through  
CC interaction with Numb (By similarity). Couples to apoptosis-  
CC inducing pathways such as those mediated by G(O) and JIP (By  
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).  
CC Acts as a kinesin I membrane receptor, mediating the axonal  
CC transport of beta-secretase and presenilin 1 (By similarity). May  
CC be involved in copper homeostasis/oxidative stress through copper  
CC ion reduction. In vitro, copper-metallated APP induces neuronal  
CC death directly or is potentiated through Cu(2+)-mediated low-  
CC density lipoprotein oxidation (By similarity). Can regulate  
CC neurite outgrowth through binding to components of the  
CC extracellular matrix such as heparin and collagen I and IV (By  
CC similarity). The splice isoforms that contain the BPTI domain  
CC possess protease inhibitor activity (By similarity).  
CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
CC with metal-reducing activity. Bind transient metals such as  
CC copper, zinc and iron (By similarity).  
CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
CC peptides, including C31, are potent enhancers of neuronal  
CC apoptosis (By similarity).  
CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several  
CC cytoplasmic proteins, including APBB family members, the APBA  
CC family, MAPK3IP1, and SHC1. Numb and Dab1 (By similarity). Binding  
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also  
CC interacts with GPCR-like protein BPR, FPR1L, APPBP1, IBL, KNS2  
CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DOB1.  
CC In vitro, it binds MAPT via the MT-binding domains (By  
CC similarity). Associates with microtubules in the presence of ATP  
CC and in a kinesin-dependent manner (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
CC protein that rapidly becomes internalized via clathrin-coated  
CC pits. During maturation, the immature APP (N-glycosylated in the  
CC endoplasmic reticulum) moves to the Golgi complex where complete  
CC maturation occurs (O-glycosylated and sulfated). After alpha-  
CC secretase cleavage, soluble APP is released into the extracellular  
CC space and the C-terminal is internalized to endosomes and  
CC lysosomes. Some APP accumulates in secretory transport vesicles  
CC leaving the late Golgi compartment and returns to the cell  
CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm

CC and nuclei of neurons (By similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Additional isoforms seem to exist;  
CC Name=APP770;  
CC IsoId=PS3601-1; Sequence=Displayed;  
CC Name=APP695;  
CC IsoId=PS3601-2; Sequence=VSP\_000010, VSP\_000011;  
CC Name=3;  
CC IsoId=PS3601-3; Sequence=VSP\_013360, VSP\_013361;  
CC -1- DOMAIN: The basolateral sorting signal (BaSS) is required for  
CC sorting of membrane proteins to the basolateral surface of  
CC epithelial cells (By similarity).  
CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-  
CC phosphorylated proteins is required for the specific binding of  
CC the PID domain. However additional amino acids either N- or C-  
CC terminal to the NPXY motif are often required for complete  
CC interaction. The PID domain-containing proteins which bind APP  
CC require the YENPTY motif for full interaction. These interactions  
CC are independent of phosphorylation on the terminal tyrosine  
CC residue. The NPXY site is also involved in clathrin-mediated  
CC endocytosis (By similarity).  
CC -1- PTM: Proteolytically processed under normal cellular conditions.  
CC Cleavage by alpha-secretase or alternatively by beta-secretase  
CC leads to generation and extracellular release of soluble APP  
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the  
CC retention of corresponding membrane-anchored C-terminal fragments,  
CC C83 and C99. Subsequent processing of C83 by gamma-secretase  
CC yields P3 peptides. This is the major secretory pathway and is  
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated  
CC gamma-secretase processing of C99 releases the amyloid beta  
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),  
CC major components of amyloid plaques, and the cytotoxic C-terminal  
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By  
CC similarity).  
CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis  
CC (By similarity). Cleavage at Asp-739 by either caspase-3, 8 or -9  
CC results in the production of the neurotoxic C31 peptide and the  
CC increased production of beta-amyloid peptides (By similarity).  
CC -1- PTM: N- and O-glycosylated (By similarity).  
CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and  
CC serine residues is neuron-specific. Phosphorylation can affect APP  
CC processing, neuronal differentiation and interaction with other  
CC proteins (By similarity).  
CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and  
CC zinc, can induce histidine-bridging between beta-amyloid molecules  
CC resulting in beta-amyloid-metal aggregates (By similarity).  
CC Extracellular zinc-binding increases binding of heparin to APP and  
CC inhibits collagen-binding (By similarity).  
CC -1- SIMILARITY: Belongs to the APP family.  
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; M58726; AAA36828.1; -; mRNA.  
CC EMBL; M58727; AAA36829.1; -; mRNA.  
CC EMBL; AB125150; BAD51938.1; -; mRNA.  
CC HSSP; P08592; 1NMJ.  
CC SMR; P53601; 28-123, 124-189, 287-342, 460-569.  
CC InterPro; IPR008155; A4\_APP.  
CC InterPro; IPR008154; A4\_extra.  
CC InterPro; IPR001255; Beta-APP.  
CC InterPro; IPR002223; Prot inh. Kunitz-m.  
CC PANTHER; PTHR10083:SF6; Beta-APP; 6.  
CC Pfam; PF02177; A4\_EXTRA; 1.  
CC Pfam; PF03494; Beta-APP; 1.  
CC Pfam; PF00014; Kunitz\_BPTI; 1.  
CC Pfam; PR00203; AMYLOIDA.  
CC PRINTS; PR00759; BASICPTASE.

DR PRINTS; PR00204; BETAAMYLOID.  
 DR ProDom; PD000222; Prot\_Inh\_Kunz-m; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 1.  
 DR Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;  
 KW Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;  
 KW Metal-binding; Notch signaling pathway; Phosphorylation;  
 KW Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;  
 KW Transmembrane; Zinc.  
 FT SIGNAL 1 17 By similarity.  
 FT CHAIN 18 770 Amyloid beta A4 protein.  
 FT CHAIN 18 687 Soluble APP-alpha (Potential).  
 FT CHAIN 18 671 Soluble APP-beta (Potential).  
 FT CHAIN 672 770 C99 (Potential).  
 FT CHAIN 672 713 Beta-amyloid protein 42 (Potential).  
 FT CHAIN 672 711 Beta-amyloid protein 40 (Potential).  
 FT CHAIN 688 770 C83 (Potential).  
 FT CHAIN 688 713 P3(42) (Potential).  
 FT CHAIN 688 711 P3(40) (Potential).  
 FT CHAIN 712 770 Gamma-CTF(59) (Potential).  
 FT CHAIN 714 770 Gamma-CTF(57) (Potential).  
 FT CHAIN 721 770 Gamma-CTF(50) (Potential).  
 FT CHAIN 740 699 C31 (Potential).  
 FT CHAIN 740 659 Extracellular (Potential).  
 FT CHAIN 700 723 Potential.  
 FT CHAIN 724 770 Cytoplasmic (Potential).  
 FT DOMAIN 291 341 BPTI/Kunitz inhibitor.  
 FT REGION 96 110 Heparin-binding (By similarity).  
 FT REGION 181 188 Zinc-binding (By similarity).  
 FT REGION 391 423 Heparin-binding (By similarity).  
 FT REGION 491 522 Heparin-binding (By similarity).  
 FT REGION 523 540 Collagen-binding (By similarity).  
 FT REGION 732 751 Interaction with G(o)-alpha (By similarity).  
 FT MOTIF 724 734 Basolateral sorting signal (By similarity).  
 FT MOTIF 759 762 NPXY motif.  
 FT COMEPIAS 230 260 Asp/Glu-rich (acidic).  
 FT METAL 137 137 Poly-Thr.  
 FT METAL 147 147 Copper (By similarity).  
 FT METAL 149 149 Copper (By similarity).  
 FT METAL 151 151 Copper (By similarity).  
 FT METAL 677 677 Copper or zinc (By similarity).  
 FT METAL 681 681 Copper or zinc (By similarity).  
 Query Match 91.2%; Score 31; DB 1; Length 770;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 Db 687 KLVFFAE 693  
 RESULT 58  
 A4 MOUSE  
 ID AA MOUSE STANDARD; PRT; 770 AA.  
 AC P12023; P97487; P97942; Q99K32;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
 DE Amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:  
 DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99  
 DE (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein  
 DE 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secre  
 DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59)  
 DE (APP-C59); Gamma-CTF(57) (Gamma-secretease C-terminal fragment 57)

DE DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)  
 DE (Gamma-secretease C-terminal fragment 50) (Amyloid intracellular domain  
 DE 50) (AID(50)); C31].  
 GN Name=App;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).  
 RC TISSUE=Brain;  
 RX MEDLINE=68106489; PubMed=3322280;  
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;  
 RT "Complementary DNA for the mouse homolog of the human amyloid beta  
 RL protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
 RN [2]  
 RP SEQUENCE REVISION.  
 RC Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
 RA Yamada T.;  
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).  
 RC STRAIN=BALE/c; TISSUE=Brain;  
 RX MEDLINE=92096458; PubMed=1756177; DOI=10.1016/0167-4781(91)90231-A;  
 RA de Strooper B., van Leuven F., van den Bergh H.;  
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse  
 RL is closer related to its human homolog than previously reported.";  
 RL Biochim. Biophys. Acta 1129:141-143(1991).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).  
 RC STRAIN=SAMP8; TISSUE=Hippocampus;  
 RX MEDLINE=21130647; PubMed=11235921; DOI=10.1139/bcb-79-1-57;  
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,  
 RA Alvarez J., Worley J.E.;  
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid  
 RL precursor protein of senescence accelerated mouse (SAMP8).";  
 RL Biochem. Cell Biol. 79:57-67(2001).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE OF 1-19.  
 RX MEDLINE=92209998; PubMed=1555768; DOI=10.1016/0378-1119(92)90375-Y;  
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M., Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RL Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
 RN Gene 112:189-195(1992).  
 RN [6]  
 RP PARTIAL NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM APP770).  
 RC TISSUE=Mammary tumor;  
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE OF 281-380, AND ALTERNATIVE SPLICING.  
 RC TISSUE=Brain, and Kidney;  
 RX MEDLINE=89149013; PubMed=2493250;

RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;  
 RT "Structure and expression of the alternatively-spliced forms of mRNA  
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
 RT precursor.";  
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE OF 289-364.  
 RC STRAIN=CD-1; TISSUE=Placenta;  
 RX MEDLINE=89345111; PubMed=2569710;  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of Mus domesticus";  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE OF 656-737.  
 RC STRAIN=129/Sv;  
 RA Wrang M.A., Busfield F., Duff K., Korenblat K., Capecci M.,  
 RA Loring J.P., Goate A.M.;  
 RT "Introduction of six mutations into the mouse genome using 'Hit and  
 RT Run' gene-targeting: introduction of familial Alzheimer's disease  
 RT mutations into the mouse amyloid precursor protein gene and  
 RT humanization of the A-beta fragment.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.  
 RX MEDLINE=93287808; PubMed=8510506; DOI=10.1016/0169-328X(93)90020-P;  
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;  
 RT "Regional distribution of the alternatively spliced isoforms of beta  
 RT APP RNA transcript in the brain of normal, heterozygous and homozygous  
 RT weaver mutant mice as revealed by in situ hybridization  
 RT histochemistry.";  
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).  
 RN [11]  
 RP INTERACTION WITH KNS2.  
 RX MEDLINE=21010507; PubMed=11443355; DOI=10.1016/S0896-6273(00)00124-0;  
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;  
 RT "Axonal transport of amyloid precursor protein is mediated by direct  
 RT binding to the kinesin light chain subunit of kinesin-I.";  
 RL Neuron 28:449-459(2000).  
 RN [12]  
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;  
 RC THR-743; TYR-757; ASN-759 AND TYR-762.  
 RX MEDLINE=21406156; PubMed=1157249;  
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,  
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,  
 RA Kyriakis J.M., Nishimoto I.;  
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/isolet-brain-1  
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";  
 RL J. Neurosci. 21:6597-6607(2001).  
 RN [13]  
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.  
 RX MEDLINE=22028091; PubMed=11912189; DOI=10.1074/jbc.M108372200;  
 RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;  
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins  
 RT with scaffold proteins of the JNK signaling cascade.";  
 RL J. Biol. Chem. 277:20070-20078(2002).  
 RN [14]  
 RP INTERACTION OF CTF PEPTIDES WITH NUBB.  
 RX MEDLINE=22008109; PubMed=12011466; DOI=10.1073/pnas.102192599;  
 RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,  
 RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;  
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid  
 RT precursor protein binds Numb and inhibits Notch signaling.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).  
 RN [15]  
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.  
 RX MEDLINE=21437805; PubMed=11553691;  
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;  
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by  
 RT gamma-secretase is rapidly degraded but distributes partially in a  
 RT nuclear fraction of neurons in culture.";  
 RL J. Neurochem. 78:1168-1178(2001).  
 RN [1]  
 RP FUNCTION: Functions as a cell surface receptor and performs

CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions. Can promote transcription activation through binding  
 CC to APBB1/Tip60 and inhibit Notch signaling through interaction  
 CC with Numb. Couples to apoptosis-inducing pathways such as those  
 CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By  
 CC similarity). Acts as a kinesin I membrane receptor, mediating the  
 CC axonal transport of beta-secretase and presenilin 1. May be  
 CC involved in copper homeostasis/oxidative stress through copper ion  
 CC reduction. Can regulate neurite outgrowth through binding to  
 CC components of the extracellular matrix such as heparin and  
 CC collagen I and IV (By similarity). The splice isoforms that  
 CC contain the BPTI domain possess protease inhibitor activity (By  
 CC similarity).  
 CC FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind  
 CC only weakly transient metals and have little reducing activity due  
 CC to substitutions of transient metal chelating residues. Beta-APP42  
 CC may activate mononuclear phagocytes in the brain and elicit  
 CC inflammatory responses. Promotes both tau aggregation and TPK II-  
 CC mediated phosphorylation (By similarity).  
 CC FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis.  
 CC FUNCTION: Binds, via its C-terminus, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits  
 CC its serine phosphorylation. Also interacts with GPCR-like protein  
 CC BPP, PPRL1, APPBP1, IBI, KNS2 (via its TPR domains), APPBP2 (via  
 CC BASS) and DDB1 (By similarity). In vitro, it binds MAPT via the  
 CC MT-binding domain (By similarity). Associates with microtubules  
 CC in the presence of ATP and in a kinesin-dependent manner (By  
 CC similarity). Interacts, through a C-terminal domain, with GNAO1  
 CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal  
 CC neurons (By similarity). Beta-amyloid associates with HADH2 (By  
 CC similarity).  
 CC INTERACTION:  
 CC P98084:Apba2; NbExp=1; IntAct=EBI-78814, EBI-81669;  
 CC Q90XJ1:Apbb1; NbExp=1; IntAct=EBI-78814, EBI-81338;  
 CC P97318:Dab1; NbExp=1; IntAct=EBI-78814, EBI-81660;  
 CC  
 CC Query Match 91.2%; Score 31; DB 1; Length 770;  
 CC Best Local Similarity 85.7%; Pred. NO. 1.9e+02;  
 CC Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 KLVFFQAQ 7  
 CC DB 687 KLVFFPAE 693  
 CC  
 CC RESULT 59  
 CC A4\_PANTR STANDARD; PRT; 770 AA.  
 CC ID A4\_PANTR  
 CC AC Q5IS80;  
 CC DT 10-MAY-2005 (Rel. 47, Created)  
 CC DT 10-MAY-2005 (Rel. 47, Last sequence update)  
 CC DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 CC DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
 CC DE amyloid beta A4 protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha);  
 CC DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-  
 CC DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);  
 CC DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)  
 CC DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-  
 CC DE secretase C-terminal fragment 50); C31].  
 CC GN Name:APP;  
 CC OS Pan troglodytes (Chimpanzee).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 CC OC Pan.  
 CC OX NCBI\_TaxID=9598;  
 CC RN [1]

RP NUCLEOTIDE SEQUENCE [RNA].  
RX PubMed=15620360; DOI=10.1016/j.cell.2004.11.040;  
RA Dorus S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L.,  
RA Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.,  
RT "Accelerated evolution of nervous system genes in the origin of Homo  
RT sapiens".  
RL Cell 119:1027-1040 (2004).

CC -!- FUNCTION: Functions as a cell surface receptor and performs  
CC physiological functions on the surface of neurons relevant to  
CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
CC cell mobility and transcription regulation through protein-protein  
CC interactions (By similarity). Can promote transcription activation  
CC through binding to APBB1/rip60 and inhibit Notch signaling through  
CC interaction with Numb (By similarity). Couples to apoptosis-  
CC inducing pathways such as those mediated by G(O) and JIP (By  
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).  
CC Acts as a kinesin I membrane receptor, mediating the axonal  
CC transport of beta-secretase and presenilin 1 (By similarity). May  
CC be involved in copper homeostasis/oxidative stress through copper  
CC ion reduction. In vitro, copper-metallated APP induces neuronal  
CC death directly or is potentiated through Cu(2+)-mediated low-  
CC density lipoprotein oxidation (By similarity). Can regulate  
CC neurite outgrowth through binding to components of the  
CC extracellular matrix such as heparin and collagen I and IV (By  
CC similarity). The splice isoforms that contain the BPTI domain  
CC possess protease inhibitor activity (By similarity).  
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
CC with metal-reducing activity. Bind transient metals such as  
CC copper, zinc and iron (By similarity).  
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
CC peptides, including C31, are potent enhancers of neuronal  
CC apoptosis (By similarity).  
CC -!- SUBUNIT: Binds, via its C-terminus, to the PID domain of several  
CC cytoplasmic proteins, and SHC1, Numb and Dab1 (By similarity). Binding  
CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding  
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also  
CC interacts with GPCR-like protein BPP, FRLP1, APPBP1, IBL, KNS2  
CC (via its TPR domains) (By similarity), APPBP2 (via Bass) and DBP1.  
CC In vitro, it binds MAPT via the WT-binding domains (By  
CC similarity). Associates with microtubules in the presence of ATP  
CC and in a kinesin-dependent manner (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
CC protein that rapidly becomes internalized via clathrin-coated  
CC pits. During maturation, the immature APP (N-glycosylated in the  
CC endoplasmic reticulum) moves to the Golgi complex where complete  
CC maturation occurs (O-glycosylated and sulfated). After alpha-  
CC secretase cleavage, soluble APP is released into the extracellular  
CC space and the C-terminal is internalized to endosomes and  
CC lysosomes. Some APP accumulates in secretory transport vesicles  
CC leaving the late Golgi compartment and returns to the cell  
CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm  
CC and nuclei of neurons (By similarity).  
CC -!- DOMAIN: The basolateral sorting signal (Bass) is required for  
CC sorting of membrane proteins to the basolateral surface of  
CC epithelial cells (By similarity).  
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-  
CC phosphorylated proteins is required for the specific binding of  
CC the PID domain. However additional amino acids either N- or C-  
CC terminal to the NPXY motif are often required for complete  
CC interaction. The PID domain-containing proteins which bind APP  
CC require the YENPY motif for full interaction. These interactions  
CC are independent of phosphorylation on the terminal tyrosine  
CC residue. The NPXY site is also involved in clathrin-mediated  
CC endocytosis (By similarity).  
CC -!- PTM: Proteolytically processed under normal cellular conditions.  
CC Cleavage by alpha-secretase or alternatively by beta-secretase  
CC leads to generation and extracellular release of soluble APP  
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the  
CC retention of corresponding membrane-anchored C-terminal fragments,  
CC C83 and C99. Subsequent processing of C83 by gamma-secretase  
CC yields p3 peptides. This is the major secretory pathway and is  
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated  
CC gamma-secretase processing of C99 releases the amyloid beta

CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),  
CC major components of amyloid plaques, and the cytotoxic C-terminal  
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By  
CC similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis  
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9  
CC results in the production of the neurotoxic C31 peptide and the  
CC increased production of beta-amyloid peptides (By similarity).  
CC -!- PTM: N- and O-glycosylated (By similarity).  
CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and  
CC serine residues is neuron-specific. Phosphorylation can affect APP  
CC processing, neuronal differentiation and interaction with other  
CC proteins (By similarity).  
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and  
CC zinc, can induce histidine-bridging between beta-amyloid molecules  
CC resulting in beta-amyloid-metal aggregates (By similarity).  
CC Extracellular zinc-binding increases binding of heparin to APP and  
CC inhibits collagen-binding (By similarity).  
CC -!- SIMILARITY: Belongs to the APP family.  
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; AY655248; AAV74286.1; -; mRNA.  
CC SMR; Q5IS80; 28-123, 124-189, 287-342, 460-569.  
CC InterPro; IPR008155; A4\_APP.  
CC InterPro; IPR008154; A4\_extra.  
CC InterPro; IPR012255; Beta-APP.  
CC InterPro; IPR012282; Cytochrome C R.  
CC PANTHER; PTHR10083\_SF6; Beta-APP; 6.  
CC Pfam; PF02177; A4\_EXTRA; 1.  
CC Pfam; PF03494; Beta-APP; 1.  
CC Pfam; PF00014; Kunitz BPTI; 1.  
CC PRINTS; PR00203; AMYLOIDA4.  
CC PRINTS; PR00759; BASICPTASE.  
CC PRINTS; PR00204; BETAMAMLOID.  
CC ProDom; PD000222; Prot\_inh\_Kunz-m; 1.  
CC SMART; SM00006; A4\_EXTRA; 1.  
CC SMART; SM00131; KU; 1.  
CC PROSITE; PS00319; A4\_EXTRA; 1.  
CC PROSITE; PS00320; A4\_INTRA; 1.  
CC PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
CC PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
CC KW Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;  
CC KW Glycoprotein; Heparin-binding; Iron; Metal-binding;  
CC KW Notch signaling pathway; Phosphorylation; Protease inhibitor;  
CC KW Proteoglycan; Serine protease inhibitor; Signal; Transmembrane; Zinc.  
CC SIGNAL 1 17 By similarity.  
CC FT CHAIN 18 770 Amyloid beta A4 protein.  
CC FT CHAIN 18 687 Soluble APP-alpha (Potential).  
CC FT CHAIN 18 671 Soluble APP-beta (Potential).  
CC FT CHAIN 672 770 C99 (Potential).  
CC FT CHAIN 672 713 Beta-amyloid protein 42 (Potential).  
CC FT CHAIN 672 711 Beta-amyloid protein 40 (Potential).  
CC FT CHAIN 688 770 C83 (Potential).  
CC FT PEPTIDE 688 713 P3(42) (Potential).  
CC FT PEPTIDE 688 711 Gamma-CTF(59) (Potential).  
CC FT CHAIN 712 770 Gamma-CTF(57) (Potential).  
CC FT CHAIN 714 770 Gamma-CTF(50) (Potential).  
CC FT CHAIN 721 770 Gamma-CTF(50) (Potential).  
CC FT CHAIN 740 770 C31 (Potential).  
CC FT TOPO\_DOM 18 699 Extracellular (Potential).  
CC FT TRANSMEM 700 723 Potential.  
CC FT TOPO\_DOM 724 770 Cytoplasmic (Potential).  
CC FT DOMAIN 291 341 BPTI/Kunitz inhibitor.  
CC FT REGION 96 110 Heparin-binding (By similarity).  
CC FT REGION 181 188 Zinc-binding (By similarity).  
CC FT REGION 391 423 Heparin-binding (By similarity).



PT REGION 491 522 Heparin-binding (By similarity).  
PT REGION 523 540 Collagen-binding (By similarity).  
PT REGION 732 751 Interaction with G(o)-alpha (By similarity).  
FT MOTIF 724 734 Basolateral sorting signal (By similarity).  
FT MOTIF 759 762 NPXY motif.  
FT COMPBIAS 230 260 Asp/Glu-rich (acidic).  
FT METAL 137 137 Copper (By similarity).  
FT METAL 147 147 Copper (By similarity).  
FT METAL 149 149 Copper (By similarity).  
FT METAL 151 151 Copper (By similarity).  
FT METAL 677 677 Copper or zinc (By similarity).  
FT METAL 681 681 Copper or zinc (By similarity).  
FT METAL 684 684 Copper or zinc (By similarity).  
FT METAL 685 685 Copper or zinc (By similarity).  
FT SITE 144 144 Required for Cu(2+) reduction (By similarity).  
FT SITE 301 302 Reactive bond (By similarity).  
FT SITE 671 672 Cleavage (by beta-secretase) (By similarity).  
FT SITE 672 673 Cleavage (by caspase-6) (By similarity).  
FT SITE 687 688 Cleavage (by alpha-secretase) (By similarity).  
FT SITE 704 704 Implicated in free radical propagation (By similarity).  
FT SITE 706 706 Susceptible to oxidation (By similarity).  
FT SITE 711 712 Cleavage (by gamma-secretase; site 1) (By similarity).  
FT SITE 713 714 Cleavage (by gamma-secretase; site 2) (By similarity).  
FT SITE 720 721 Cleavage (by gamma-secretase; site 3) (By similarity).  
FT SITE 739 740 Cleavage (by caspases-6, -8 or -9) (By similarity).  
Query Match 91.28; Score 31; DB 1; Length 770;  
Best Local Similarity 85.74; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVFFAQ 7  
DB 687 KLVFFAE 693  
RESULT 60  
A4\_PIG STANDARD; PRT; 770 AA.  
AC P75307; Q29023; Q9TU10;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C311).  
GN Name=APP;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Suidae.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Kimura A., Takahashi T.;  
RT "Amyloid precursor protein 770";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-136.  
RC TISSUE=Small intestine;

RA Winteroe A.K., Fredholm M.;  
RT "Evaluation and characterization of a porcine small intestine CDNA library.";  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 667-723.  
RX TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -I- FUNCTION: Functions as a cell surface receptor and performs physiological functions on the surface of neurons relevant to neurite growth, neuronal adhesion and axonogenesis. Involved in cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G(O) and JIP (By similarity). Inhibits G(o) alpha ATPase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction (By similarity). In vitro, copper-metalated APP induces neuronal death directly or is potentiated through Cu(2+)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity).  
CC -I- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).  
CC -I- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).  
CC -I- SUBUNIT: Binds, via its C-terminus, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FPR1, APPBP1, IBI, KNS2 (via its TPR domains) (By similarity), APPBP2 (via BASS) and DDB1. In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).  
CC -I- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).  
CC -I- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).  
CC -I- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the.

retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF (50), gamma-CTF (57) and gamma-CTF (59) (By similarity).

-!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-!- PTM: N- and O-glycosylated (By similarity).

-!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-!- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-!- SIMILARITY: Belongs to the APP family.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; AB032550; BAA84580.1; -; mRNA.  
EMBL; Z84022; CAB06313.1; -; mRNA.  
EMBL; X56127; CAA39592.1; -; mRNA.  
HSSP; P08592; 1NMJ.  
SMR; P79307; 28-123, 124-189, 287-342, 460-569.  
InterPro; IPR008155; A4\_APP.  
InterPro; IPR008154; A4\_extra.  
InterPro; IPR001255; Beta\_APP.  
InterPro; IPR002223; Prot\_inh\_Kunz-m.  
PANTHER; PTHR10083.SF6; Beta\_APP; 6.  
Pfam; PF02177; A4\_EXTRA; 1.  
Pfam; PF03494; Beta\_APP; 1.  
Pfam; PF00014; Kunitz\_BPTI; 1.  
PRINTS; PR00203; AMYLOID4.  
PRINTS; PR00759; BASICPTASE.  
PRINTS; PR00204; BETAAMYLOID.  
ProDom; PD000222; Prot\_inh\_Kunz-m; 1.  
SMART; SM00006; A4\_EXTRA; 1.  
SMART; SM00131; KU; 1.  
PROSITE; PS00319; A4\_EXTRA; 1.  
PROSITE; PS00320; A4\_INTRA; 1.  
PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
PROSITE; PS00279; BPTI\_KUNITZ\_2; 1.  
Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Metal-binding; Notch signaling pathway; Phosphorylation; Protease inhibitor; Serine protease inhibitor; Signal; Transmembrane; Zinc.  
SIGNAL 1 17 By similarity.  
CHAIN 18 770 Amyloid beta A4 protein.  
CHAIN 18 687 Soluble APP-alpha (Potential).  
CHAIN 18 671 Soluble APP-beta (Potential).  
CHAIN 672 713 C99 (By similarity).  
CHAIN 672 713 Beta-amyloid protein 40 (By similarity).  
CHAIN 672 713 Beta-amyloid protein 42 (By similarity).  
CHAIN 688 713 C83 (By similarity).  
CHAIN 688 713 P3(42) (By similarity).  
CHAIN 688 711 P3(40) (By similarity).  
CHAIN 712 770 Gamma-CTF(59).

FT	CHAIN	714	770	Gamma-CTF(57).
FT	CHAIN	721	770	Gamma-CTF(50) (By similarity).
FT	CHAIN	740	770	C31 (By similarity).
FT	TOPO_DOM	18	699	Extracellular (Potential).
FT	TRANSMEM	700	723	Potential.
FT	TOPO_DOM	724	770	Cytoplasmic (Potential).
FT	DOMAIN	291	341	BPTI/Kunitz inhibitor.
FT	REGION	96	110	Heparin-binding (By similarity).
FT	REGION	135	155	Copper-binding (By similarity).
FT	REGION	181	188	Zinc-binding (By similarity).
FT	REGION	391	423	Heparin-binding (By similarity).
FT	REGION	491	522	Heparin-binding (By similarity).
FT	REGION	523	540	Collagen-binding (By similarity).
FT	REGION	732	751	Interaction with G(o)-alpha (By similarity).
FT	MOTIF	724	734	Basolateral sorting signal.
FT	MOTIF	759	762	NPXY motif.
FT	COMPBIAS	230	260	Asp/Glu-rich (acidic).
FT	COMPBIAS	274	280	Poly-Thr.
FT	METAL	137	137	Copper (By similarity).
FT	METAL	147	147	Copper (By similarity).
FT	METAL	149	149	Copper (By similarity).
FT	METAL	151	151	Copper (Probable).
FT	METAL	677	677	Copper or zinc (By similarity).
FT	METAL	681	681	Copper or zinc (Probable).
FT	METAL	684	684	Copper or zinc (By similarity).
FT	METAL	685	685	Copper or zinc (By similarity).
FT	SITE	144	144	Required for Cu(2+) reduction (By similarity).

Query Match 91.2%; Score 31; DB 1; Length 770;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
| | | | |  
Db 687 KLVFFPAE 693

RESULT 61  
A4\_RAT  
ID A4\_RAT STANDARD; PRT; 770 AA.  
AC P08592;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid  
DE protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble  
DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-  
DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);  
DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal  
DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);  
DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].  
GN Name-APP;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).  
RC TISSUE=Brain;  
RX MEDLINE=88312583; PubMed=2900758;  
RA Shivers B.D.; Hilbich C.; Multhaup G.; Salbaum J.M.; Beyreuther K.,  
RA Seeburg P.H.;  
RA "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in  
rat brain suggests a role in cell contact.";  
RL EMBJ 7.1:1365-1370(1988).  
RN [2]  
RP PROTEIN SEQUENCE OF 18-44.  
RX MEDLINE=88264430; PubMed=2968652;  
RA Schubert D., Schroeder R., LaCorbiere M., Saitoh T., Cole G.;  
RT "Amyloid beta protein precursor is possibly a heparan sulfate  
proteoglycan core protein.";

RL Science 241:223-226 (1988).  
 RN [3]  
 RP PROTEIN SEQUENCE OF 18-32.  
 RX MEDLINE=91217087; PubMed=1673681;  
 RA Potempa A., Styles J., Mehta P., Kim K.S., Miller D.L.;  
 RT "Purification and tissue level of the beta-amyloid peptide precursor  
 of rat brain.";  
 RL J. Biol. Chem. 266:8464-8469 (1991).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE OF 289-364.  
 RC TISSUE=Liver;  
 RX MEDLINE=89183625; PubMed=2648331;  
 RA Kang J., Mueller-Hill B.;  
 RT "The sequence of the two extra exons in rat preA4.";  
 RL Nucleic Acids Res. 17:2130-2130 (1989).  
 RN [5]  
 RP PROTEIN SEQUENCE OF 720-730, AND MASS SPECTROMETRY.  
 RX MEDLINE=21443797; PubMed=11483588; DOI=10.1074/jbc.C100357200;  
 RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;  
 RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein  
 family resembling gamma-secretase-like cleavage of Notch.";  
 RL J. Biol. Chem. 276:35235-35238 (2001).  
 RN [6]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=96187032; PubMed=8624099;  
 RA Sandbrink R., Masters C.L., Beyreuther K.;  
 RT "APP gene family. Alternative splicing generates functionally related  
 isoforms.";  
 RL Ann. N. Y. Acad. Sci. 777:281-287 (1996).  
 RN [7]  
 RP TISSUE SPECIFICITY OF APPICAN.  
 RX MEDLINE=9526326; PubMed=7744833; DOI=10.1074/jbc.270.20.11839;  
 RA Shioi J., Pangalos M.N., Ripellino J.A., Vassiliacopoulou D.,  
 MYtilineou C., Margolis R.U., Robakis N.K.;  
 RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in  
 brain and is produced by astrocytes but not by neurons in primary  
 neural cultures.";  
 RL J. Biol. Chem. 270:11839-11844 (1995).  
 RN [8]  
 RP TISSUE SPECIFICITY OF ISOFORMS.  
 RX MEDLINE=97150061; PubMed=8995834;  
 RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;  
 RT "Expression of the APP gene family in brain cells, brain development  
 and aging.";  
 RL Gerontology 43:119-131 (1997).  
 RN [9]  
 RP INTERACTION WITH DBL1, AND MUTAGENESIS OF TYR-757; ASN-759 AND  
 TYR-762.  
 RX MEDLINE=99127916; PubMed=9930726;  
 RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,  
 Suzuki T., Nairn A.C., Greengard P.;  
 RT "A 127-kDa protein (UV-DBB) binds to the cytoplasmic domain of the  
 Alzheimer's amyloid precursor protein.";  
 RL J. Neurochem. 72:549-556 (1999).  
 RN [10]  
 RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.  
 RX MEDLINE=99162676; PubMed=10024359;  
 RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,  
 Valenza C., Prochiantz A., Allinquant B.;  
 RT "The amyloid precursor protein interacts with Go heterotrimeric  
 protein within a cell compartment specialized in signal  
 transduction.";  
 RL J. Neurosci. 19:1717-1727 (1999).  
 RN [11]  
 RP COPPER-BINDING.  
 RX MEDLINE=94320627; PubMed=7913895; DOI=10.1016/0014-5793(94)00658-X;  
 RA Heese L., Behr D., Masters C.L., Multhaup G.;  
 RT "The beta A4 amyloid precursor protein binding to copper.";  
 RL FEBS Lett. 349:109-116 (1994).  
 RN [12]  
 RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.  
 RX MEDLINE=95256193; PubMed=7737970; DOI=10.1074/jbc.270.18.10388;  
 RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;  
 RT "The chondroitin sulfate attachment site of appican is formed by  
 splicing out exon 15 of the amyloid precursor gene.";  
 RL J. Biol. Chem. 270:10388-10391 (1995).  
 RN [13]  
 RP BETA-AMYLOID METAL-BINDING.  
 RX MEDLINE=99116162; PubMed=10386999; DOI=10.1021/bi990438f;  
 RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,  
 Scarpa R.C., Cuaungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,  
 Bush A.I.;  
 RT "The A beta peptide of Alzheimer's disease directly produces hydrogen  
 peroxide through metal ion reduction.";  
 RL Biochemistry 38:7609-7616 (1999).  
 RN [14]  
 RP BETA-AMYLOID ZINC-BINDING.  
 RX MEDLINE=99343552; PubMed=10413512; DOI=10.1021/bi990205o;  
 RA Liu S.T., Howlett G., Barrow C.J.;  
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation  
 of the A beta peptide of Alzheimer's disease.";  
 RL Biochemistry 38:9373-9378 (1999).  
 RN [15]  
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF  
 GLY-704.  
 RX MEDLINE=21956095; PubMed=11959460; DOI=10.1016/S0925-4439(01)00097-7;  
 RA Kaneki J., Varadarajan S., Aksanova M., Butterfield D.A.;  
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-  
 peptide 1-42-associated oxidative stress and neurotoxicity.";  
 RL Biochim. Biophys. Acta 1586:190-198 (2001).  
 RN [16]  
 RP PHOSPHORYLATION.  
 RX MEDLINE=97239592; PubMed=9085254;  
 RA Olshi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,  
 Greengard P., Suzuki T.;  
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is  
 phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and  
 cultured cells.";  
 RL Mol. Med. 3:111-123 (1997).  
 RN [17]  
 RP PHOSPHORYLATION SITE SER-730.  
 RX MEDLINE=99262094; PubMed=10329382; DOI=10.1006/bbrc.1999.0637;  
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,  
 Greengard P., Nairn A.C., Suzuki T.;  
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid  
 precursor protein at Ser655 by a novel protein kinase.";  
 RL Biochem. Biophys. Res. Commun. 258:300-305 (1999).  
 RN [18]  
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF  
 THR-743.  
 RX MEDLINE=99274744; PubMed=10341243;  
 RA Ando K., Olshi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,  
 Kirino Y., Greengard P., Suzuki T.;  
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein  
 during neuronal differentiation.";  
 RL J. Neurosci. 19:4421-4427 (1999).  
 RN [19]  
 RP PHOSPHORYLATION SITE THR-743.  
 RX MEDLINE=20396183; PubMed=10336190;  
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,  
 Greengard P., Kirino Y., Nairn A.C., Suzuki T.;  
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor  
 protein by cyclin-dependent kinase 5.";  
 RL J. Neurochem. 75:1085-1091 (2000).  
 RN [20]  
 RP CARBOHYDRATE STRUCTURE OF APPICAN.  
 RX MEDLINE=21463085; PubMed=11479316; DOI=10.1074/jbc.M105818200;  
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,  
 Suganara K., Robakis N.K.;  
 RT "Appican, the proteoglycan form of the amyloid precursor protein,  
 contains chondroitin sulfate E in the repeating disaccharide region  
 and 4-O-sulfated galactose in the linkage region.";  
 RL J. Biol. Chem. 276:37155-37160 (2001).  
 RN [21]  
 RP FUNCTION: Functions as a cell surface receptor and performs  
 physiological functions on the surface of neurons relevant to  
 neurite growth, neuronal adhesion and axonogenesis. Involved in



cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G(O) and JIP. Inhibits G(O) alpha Arpase activity. Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

-!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron. Rat and mouse beta-amyloid peptides bind only weakly transient metals and have little reducing activity due to substitutions of transient metal chelating residues. Beta-APP42 may activate mononuclear phagocytes in the brain and elicit inflammatory responses. Promotes both tau aggregation and TPK II-mediated phosphorylation (By similarity).

Query Match 91.2%; Score 31; DB 1; Length 770;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||||:  
Db 687 KLVFFPAE 693

## RESULT 62

Q6RH30 CANFA  
ID Q6RH30 CANFA PRELIMINARY; PRT; 770 AA.

AC Q6RH30  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Beta amyloid protein isoform APP770.

GN Name=beta APP;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Nakata M.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR EMBL; AY498706; AAR9726.1; -; mRNA.

DR HSSP; Q16019; 1AAP.

DR SMR; Q6RH30; 28-123, 124-189, 287-342, 460-569.

DR Ensembl; ENSCARG0000008557; Canis familiaris.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR008155; A4\_APP.

DR InterPro; IPR001255; Beta-APP.

DR InterPro; IPR002223; Prot\_inh\_Kunz-m.

DR Pfam; PF02117; A4\_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR Pfam; PF00014; Kunitz BPTI; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR PRINTS; PR00204; BETAAMYLOID.

DR ProDom; PD000222; Prot\_inh\_Kunz-m; 1.

DR SMART; SM00006; A4\_EXTRA; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4\_EXTRA; 1.

DR PROSITE; PS00320; A4\_INTRA; 1.

DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.

DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
SQ SEQUENCE 770 AA; 86929 MW; 4560E18BB405F588 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 770;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||||:  
Db 687 KLVFFPAE 693

## RESULT 63

Q56JK6 CANFA  
ID Q56JK6 CANFA PRELIMINARY; PRT; 770 AA.

AC Q56JK6

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Beta-amyloid protein 770.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

OC Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Gallego C.; Sanchez-Diaz R.; Sarasa L.; Sarasa M.;

RT "Relationship between canine dementia and Alzheimer's disease.";

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY926579; AAX81908.1; -; mRNA.

DR SMR; Q56JK6; 28-123, 124-189, 287-342, 460-569.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0020037; F:heme binding; IEA.

DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR008155; A4\_APP.

DR InterPro; IPR001255; Beta-APP.

DR InterPro; IPR012282; Cytochrome\_c\_R.

DR InterPro; IPR002223; Prot\_inh\_Kunz-m.

DR Pfam; PF02177; A4\_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR Pfam; PF00014; Kunitz BPTI; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR PRINTS; PR00204; BETAAMYLOID.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00320; A4\_INTRA; 1.

DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.

DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.

SQ SEQUENCE 770 AA; 86998 MW; 81ADD82D3FB8DC6D CRC64;

## Query Match

Best Local Similarity 91.2%; Score 31; DB 2; Length 770;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|||||:  
Db 687 KLVFFPAE 693

## RESULT 64

Q53ZT3 MOUSE  
ID Q53ZT3 MOUSE PRELIMINARY; PRT; 770 AA.

AC Q53ZT3

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Amyloid-beta protein-like protein long isoform.

GN Name=App;

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6;  
 RA Szendro P.I., Cadenas C., Eichele G.;  
 RT "Sequence of an alternative spliced amyloid-beta precursor protein  
 RT homolog.";  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 DR EMBL; AY267348; AAP23169.1; -; mRNA.  
 DR MGI; MGI:88059; App.  
 DR GO; GO:0016021; C:integral to membrane; IDA.  
 DR GO; GO:0016020; C:membrane; TAS.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IGI.  
 SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;

Query Match 91.2%; Score 31; DB 2; Length 770;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7  
 |||||  
 Db 687 KLVPFAE 693

RESULT 65  
 ID Q547B7 RAT PRELIMINARY; PRT; 770 AA.  
 AC Q547B7;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE APP770.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Feng J., Song S., Zheng J.;  
 RT "A new beta amyloid precursor protein cDNA found in Rat6 embryo  
 RT fibroblasts.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 DR EMBL; AF513015; AAM90259.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR GO; GO:0020037; F:heme binding; IEA.  
 DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 SQ SEQUENCE 770 AA; 86704 MW; C26C9D6B52929A7 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 770;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7  
 |||||  
 Db 687 KLVPFAE 693

RESULT 66  
 A4 TETFL  
 ID A4\_TETFL STANDARD; PRT; 780 AA.  
 AC O73683;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog precursor (Contains:  
 DE Beta-amyloid protein (Beta-APP) (A-beta)).  
 GN Name=APP;  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OC NCBI\_TaxID=47145;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=98252138; PubMed=9599080; DOI=10.1016/S0378-1119(98)00032-8;  
 RA Villard L., Tasone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;  
 RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";  
 RL Gene 210:17-24(1998).  
 CC -1- FUNCTION: Functional neuronal receptor which couples to  
 CC intracellular signaling pathway through the GTP-binding protein  
 CC G(O) (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the APP family.  
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 DR EMBL; AF018165; AAC41275.1; -; mRNA.  
 DR HSP; P10646; IIRH.  
 DR SNR; O73683; 23-124, 478-586.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Prot inh Kunz-m.  
 DR PANTHER; PTHR10083:SF6; Beta-APP; 5.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR ProDom; PD000222; Prot inh Kunz-m; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; FALSE\_NEG.  
 DR PROSITE; PS02279; BPTI\_KUNITZ\_2; 1.  
 KW Amyloid; Glycoprotein; Protease inhibitor; Serine protease inhibitor;  
 KW Signal; Transmembrane.  
 FT SIGNAL 1 18 Potential.  
 FT CHAIN 19 780 Alzheimer's disease amyloid A4 protein  
 FT homolog.  
 FT TOPO\_DOM 682 724 Beta-amyloid protein (Potential).  
 FT TRANSMEM 712 732 Extracellular (Potential).  
 FT TOPO\_DOM 733 780 Potential.  
 FT DOMAIN 323 382 Cytoplasmic (Potential).  
 FT SITE 769 772 BPTI/Kunitz inhibitor.  
 FT CARBOHYD 560 560 Clathrin-binding (By similarity).  
 FT DISULFID 327 378 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 336 361 By similarity.  
 SQ SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;

Query Match 91.2%; Score 31; DB 1; Length 780;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7  
 |||||  
 Db 697 KLVPFAE 703

```

RESULT 67
Q87XV7 PSES
ID Q87XV7_PSES PRELIMINARY; PRT; 355 AA.
AC
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcriptional regulator, AraC family.
GN OrderedLocusNames=PSPT04068;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DC3000.
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Jørgensen V., Lindeberg M., Selenkov J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidovitz T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
DR EMBL; AB016853; AA057525.1; -; Genomic DNA.
DR TIGR; PSPT04068; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR012287; HTH domain-rel.
DR InterPro; IPR002197; HTH F18.
DR InterPro; IPR000005; HTHARAC.
DR Pfam; PF00165; HTH_AraC; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR TIGRFAMs; TIGR01199; HTH_f18; 1.
DR PROSITE; PS01124; HTH_ARAC FAMILY 2; 1.
KW Activator; Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 355 AA; 39416 MW; F59F8756270F310B CRC64;

Query Match 88.2%; Score 30; DB 2; Length 355;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 150 KLVFFVQ 156
|||||

RESULT 68
Q4LMP3 9BURK
ID Q4LMP3_9BURK PRELIMINARY; PRT; 364 AA.
AC
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Helix-turn-helix, AraC type.
DE ORFNames=Bcen2424DRAFT_2820.
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;

Query Match 88.2%; Score 30; DB 2; Length 421;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;

```

```

RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RA Larimer F., Land M.;
RG "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
-!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AALH01000042; EMBL17351.1; -; Genomic DNA.
SQ SEQUENCE 364 AA; 40535 MW; 7A0B6786C815E29 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 364;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 157 KLVFFVQ 163
|||||

RESULT 69
Q54L66 DICDI
ID Q54L66_DICDI PRELIMINARY; PRT; 421 AA.
AC Q54L66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD0187166;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugeng B., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Turggal R., Kummerfeld S., Madera M., Konfortov B.A., Rivo F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Filcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lousaged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF101000141; EAL63992.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 421 AA; 48326 MW; EA92A3934FE63F36 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 421;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;

```

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7  
 DB 75 KLIFPAQ 81

# RESULT 70

Q4N8N8 THEPA  
 ID Q4N8N8 THEPA PRELIMINARY; PRT; 480 AA.  
 AC Q4N8N8;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=TP01\_0426;  
 OS Theileria parva.  
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;  
 OC Theileria.  
 OX NCBI\_TaxID=5875;  
 RN [1]  
 RC STRAIN=Muguga;  
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M., Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L., Lynn J., Weaver B., Shoabi A., Wasawo D., Crabtree J., Wortman J.R., Haas B., Anguoli S.V., Creasy T.H., Lu C., Suh B., Silva J.C., Uterback T.R., Feldblyum T.V., Pertea M., Allen J., Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;  
 RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;  
 RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an preliminary data.  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC EMBL; AAG0100001; EAN3670.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 480 AA; 58211 MW; 042C35CDC02A7158 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 480;  
 Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7  
 DB 108 KLIFPAE 114

# RESULT 71

Q4UGZ4 THEAN  
 ID Q4UGZ4 THEAN PRELIMINARY; PRT; 557 AA.  
 AC Q4UGZ4;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=TA20805;  
 OS Theileria annulata.  
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;

OC Theileria.  
 OX NCBI\_TaxID=5874;  
 RN [1]  
 RC NUCLEOTIDE SEQUENCE.  
 RA STRAIN=Ankara isolate clone C9;  
 RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M., Hall N., Barrell B.G.;  
 RA "The chromosome 1 sequence of Theileria annulata.";  
 RT Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; CR940347; CAI73645.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 557 AA; 64191 MW; 203AA30E5F22D073 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 557;  
 Best Local Similarity 71.4%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7  
 DB 191 KLIFPAE 197

# RESULT 72

Q728F0 DESVH  
 ID Q728F0 DESVH PRELIMINARY; PRT; 66 AA.  
 AC Q728F0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocusNames=DVU2653;  
 OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;  
 OC Desulfovibrionaceae; Desulfovibrio.  
 OX NCBI\_TaxID=882;  
 RN [1]  
 RC NUCLEOTIDE SEQUENCE.  
 RA PubMed=15077118; DOI=10.1038/nbt959;  
 RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Daviden T.M., Zafar N., Zhou L., Radune D., Dmitrov G., Hance M., Tran K., Khouri H.M., Gill J., Uterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;  
 RA "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough.";  
 RT Nat. Biotechnol. 22:554-559(2004).  
 RL EMBL; AB017318; AAS97125.1; -; Genomic\_DNA.  
 KW TIGR; DVU2653; -;  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 66 AA; 7605 MW; 633FBB080C3962A6 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 66;  
 Best Local Similarity 71.4%; Pred. No. 56;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7  
 DB 35 KLIFPAK 41

# RESULT 73

Q6D3D0 ERWCT  
 ID Q6D3D0 ERWCT PRELIMINARY; PRT; 81 AA.  
 AC Q6D3D0;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Molybdopterin converting factor subunit 1.  
 GN Namemoad; Synonyms=chlA4, chlM; OrderedLocusNames=ECA2814;  
 OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmon G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG75714.1; -; Genomic_DNA.
DR GO; GO:0008777; P:mo-molybdopterine cofactor biosynthesis; IEA.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR010034; Moad.
DR InterPro; IPR003749; This.
DR Pfam; PF02597; This; 1.
DR TIGRfam; TIGR01682; moad; 1.
KW Complete proteome.
SQ SEQUENCE 81 AA; 8998 MW; 81EBB4AB90A96911 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 81;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
|:|||||
Db 3 KILFFAQ 9

RESULT 74
QBVR5 ECOLI
ID Q8VR5 ECOLI PRELIMINARY; PRT; 95 AA.
AC QBVR5;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE CadC (Fragment).
GN Name=cadC;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=83/39;
RX MEDLINE=22063667; PubMed=12067342;
RA Tauschek M., Strugnelli R.A., Robins-Browne R.M.;
RT "Characterization and evidence of mobilization of the LEE
RT pathogenicity island of rabbit-specific strains of enteropathogenic
RT Escherichia coli.";
RL Mol. Microbiol. 44:1533-1550(2002).
DR EMBL; AF453441; AAL57517.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; P:two-component response regulator activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR001867; Trans_reg_C.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00486; Trans_reg_C; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
FT NON_TER 95
SQ SEQUENCE 95 AA; 10865 MW; 1569318B458687D5 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
|:|||||
Db 3 KILFFAQ 9

RESULT 75
Q6GZK0 ECOLI
ID Q6GZK0 ECOLI PRELIMINARY; PRT; 97 AA.
AC Q6GZK0;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Cad operon transcriptional activator (Fragment).
GN Name=cadC;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=4787;
RX PubMed=15358417; DOI=10.1016/j.femsle.2004.07.052;
RA Derfulian H., Tremblay D., Hazel J.;
RT "Molecular characterization of extraintestinal pathogenic Escherichia
RT coli (ExPEC) pathogenicity islands in F165-positive E. coli strain
RT from a diseased animal.";
RL FEMS Microbiol. Lett. 238:321-332(2004).
DR EMBL; AY560911; AAT48691.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; P:two-component response regulator activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00486; Trans_reg_C; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
FT NON_TER 97
SQ SEQUENCE 97 AA; 11079 MW; B4DC0569318B4586 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFAQ 7
|:|||||
Db 37 LVFFAQ 42

Search completed: December 29, 2005, 17:47:37
Job time : 99.2258 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 15.129 Seconds  
(without alignments)  
44.518 Million cell updates/sec

Title: US-10-009-122-18  
Perfect score: 34  
Sequence: 1 KLVFFAQ 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : PIR\_80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	91.2	33	S23094	beta-amyloid prote
2	31	91.2	42	PN0512	beta-amyloid prote
3	31	91.2	57	A60045	Alzheimer's diseas
4	31	91.2	57	F60045	Alzheimer's diseas
5	31	91.2	57	D60045	Alzheimer's diseas
6	31	91.2	57	E60045	Alzheimer's diseas
7	31	91.2	57	G60045	Alzheimer's diseas
8	31	91.2	57	B60045	Alzheimer's diseas
9	31	91.2	82	PQ0438	Alzheimer's diseas
10	31	91.2	695	A49795	Alzheimer's diseas
11	31	91.2	695	A27485	Alzheimer's diseas
12	31	91.2	695	S00550	Alzheimer's diseas
13	31	91.2	747	JH0773	Alzheimer's diseas
14	31	91.2	754	T06249	protoporphyrin IX
15	31	91.2	758	T02925	protoporphyrin IX
16	31	91.2	770	QKH044	Alzheimer's diseas
17	31	91.2	778	B86218	protein T27G7.20 [
18	29	85.3	115	AE0523	conserved hypothet
19	29	85.3	152	T06645	hypothetical prote
20	29	85.3	156	B64735	yacc protein - Esc
21	29	85.3	156	F85495	hypothetical prote
22	29	85.3	156	F90644	hypothetical prote
23	29	85.3	231	H85138	hypothetical prote
24	29	85.3	247	T32514	wax synthase [impo
25	29	85.3	352	T48903	hypothetical prote
26	29	85.3	428	T48008	transcription acti
27	29	85.3	512	C91288	transcription acti
28	29	85.3	512	A86109	transcription acti
29	29	85.3	512	C41968	transcription acti

protein F22C12.6 l  
genome polyprotein  
molybdopterin bios  
molybdenum cofacto  
molybdopterin bios  
molybdopterin bios  
prophage p33 prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
valine-tRNA ligase  
hypothetical prote  
hypothetical prote  
hypothetical prote  
tryptophanyl-tRNA  
endoglycosidase F3  
hypothetical prote  
replication initia  
hypothetical prote  
diguanilate cyclas  
ABC transporter AT  
hypothetical prote  
conserved hypothet  
hypothetical prote  
(3R)-hydroxymyrist  
hypothetical prote  
19K globulin precu  
alpha-globulin pre  
phosphoribosylform  
hypothetical prote  
hypothetical prote  
ABC transporter (A  
ABC transporter (A  
hypothetical prote  
cell fusion protei  
sorbitol dehydroge  
hypothetical prote  
hypothetical prote  
zootin-like protei  
probable integral  
hypothetical prote  
hypothetical prote  
sodium/galactoside  
aminoacyl-histidin  
11S globulin beta  
Trk7.22 protein -  
ABC transporter re  
ABC transporter re  
potassium channel  
potassium channel  
potassium channel  
calcium-transporti  
hypothetical prote  
genome polyprotein  
hydroxymethylgluta  
nitric-oxide synth  
genome polyprotein  
genome polyprotein  
molybdopterin lmp  
translation initia  
probable chltr t2  
T2 protein - Chlam  
hypothetical prote  
hypothetical prote  
hydroxymyristoyl-  
hypothetical prote

85.3 29 30  
85.3 29 31  
82.4 28 32  
82.4 28 33  
82.4 28 34  
82.4 28 35  
82.4 28 36  
82.4 28 37  
82.4 28 38  
82.4 28 39  
79.4 40  
79.4 41  
79.4 42  
79.4 43  
79.4 44  
79.4 45  
79.4 46  
79.4 47  
79.4 48  
79.4 49  
79.4 50  
79.4 51  
79.4 52  
79.4 53  
79.4 54  
76.5 55  
76.5 56  
76.5 57  
76.5 58  
76.5 59  
76.5 60  
76.5 61  
76.5 62  
76.5 63  
76.5 64  
76.5 65  
76.5 66  
76.5 67  
76.5 68  
76.5 69  
76.5 70  
76.5 71  
76.5 72  
76.5 73  
76.5 74  
76.5 75  
76.5 76  
76.5 77  
76.5 78  
76.5 79  
76.5 80  
76.5 81  
76.5 82  
76.5 83  
76.5 84  
76.5 85  
76.5 86  
76.5 87  
76.5 88  
76.5 89  
76.5 90  
76.5 91  
76.5 92  
76.5 93  
76.5 94  
73.5 95  
73.5 96  
73.5 97  
73.5 98  
73.5 99  
73.5 100  
73.5 101  
73.5 102

B96666 2  
S30236 2  
F90736 1016 2  
A82251 81 2  
G85586 81 2  
H64814 81 2  
D86866 306 2  
H71729 321 2  
G96643 346 2  
C84979 473 2  
S67962 32 2  
T35807 182 2  
T26245 214 2  
T26247 300 2  
H75505 329 2  
A64383 330 2  
T26247 341 2  
H64251 437 2  
T04463 531 2  
G97000 571 2  
AD3409 646 2  
T31691 655 2  
D70425 1054 2  
T34558 1273 2  
T07200 49 2  
AG3408 85 2  
H82370 91 2  
B95049 140 2  
H97919 140 2  
A86722 144 2  
WMR219 186 1  
JC4784 186 2  
F64505 230 2  
AD2307 256 2  
T05661 273 2  
AC1342 300 2  
A11712 300 2  
T20562 334 2  
MMB5 340 1  
AH2097 352 2  
D84280 356 2  
T15120 408 2  
T39683 442 2  
H81402 442 2  
F71039 447 2  
T34366 455 2  
D69852 459 2  
G70175 476 2  
FWPUIB 480 1  
G86390 527 2  
AC1414 574 2  
AB1790 574 2  
H69274 601 2  
JH0595 802 2  
CHRTD1 853 1  
I56529 857 2  
S31761 858 2  
H69877 890 2  
T00588 902 2  
JQ0498 1016 2  
B30239 1045 2  
A43271 1144 1  
JQ1661 3066 1  
JQ1662 3066 1  
AG0142 81 2  
A05035 96 2  
C71560 98 2  
I40737 106 2  
T31765 113 2  
E70334 133 2  
G84116 140 2  
AC2533 159 2

103	25	73.5	166	2	A70024	conserved hypotet	176	25	73.5	500	2	S56489	hypothetical 54.3K
104	25	73.5	170	2	G81375	hypothetical prote	177	25	73.5	501	2	E89786	hypothetical prote
105	25	73.5	181	2	E69900	hypothetical prote	178	25	73.5	510	2	E71695	hypothetical prote
106	25	73.5	208	2	D71258	probable glpG prot	179	25	73.5	513	2	A80021	conserved hypotet
107	25	73.5	215	2	S74602	hypothetical prote	180	25	73.5	516	2	A87260	conserved hypotet
108	25	73.5	224	1	WMVZR1	26.3K late gene tr	181	25	73.5	533	2	F70551	hypothetical prote
109	25	73.5	224	2	G36848	A2L protein - vari	182	25	73.5	540	2	T48619	tRNA synthase-like
110	25	73.5	224	2	G72163	A2L protein - vari	183	25	73.5	545	2	F64579	site-specific DNA-
111	25	73.5	224	2	T28543	hypothetical prote	184	25	73.5	545	2	F71932	type II DNA modifi
112	25	73.5	228	2	T30706	probable transacti	185	25	73.5	546	2	S48932	hypothetical prote
113	25	73.5	233	2	T10198	hypothetical prote	186	25	73.5	557	2	F69481	probable acid-CoA
114	25	73.5	264	2	B71448	hypothetical prote	187	25	73.5	559	2	G71327	probable apolipopr
115	25	73.5	268	2	AH2122	branched-chain ami	188	25	73.5	586	1	RNEGB1	DNA-directed RNA p
116	25	73.5	274	2	H83707	bacitracin resista	189	25	73.5	589	2	D70031	ABC transporter (A
117	25	73.5	278	2	A83840	undecaprenol kinas	190	25	73.5	592	2	T15413	hypothetical prote
118	25	73.5	280	2	A12704	conserved hypotet	191	25	73.5	594	2	T40808	probable DNA polym
119	25	73.5	285	2	A97487	probable iron-sulf	192	25	73.5	602	2	T37254	acetylcholinestera
120	25	73.5	296	2	B75426	hypothetical prote	193	25	73.5	609	2	T11774	NADH2 dehydrogenas
121	25	73.5	296	2	S53960	CTK3 protein - yea	194	25	73.5	610	2	T11544	NADH2 dehydrogenas
122	25	73.5	296	2	A36966	probable dTDP-rham	195	25	73.5	624	2	H90071	hypothetical prote
123	25	73.5	301	2	A81066	transcription regu	196	25	73.5	627	2	A82714	hypothetical prote
124	25	73.5	303	2	T23583	hypothetical prote	197	25	73.5	632	2	A25784	hypothetical 70K p
125	25	73.5	305	2	T33578	hypothetical prote	198	25	73.5	637	2	B97496	hypothetical ABC t
126	25	73.5	305	2	E69946	hypothetical prote	199	25	73.5	655	2	G96524	protein T1N15.9 li
127	25	73.5	308	2	D95321	NodB1 transcriptio	200	25	73.5	675	2	S53831	NADH2 dehydrogenas
128	25	73.5	311	1	Z2R2DM	nodulation protein	201	25	73.5	680	2	T27078	hypothetical prote
129	25	73.5	311	2	A83746	transposase (16) B	202	25	73.5	721	2	T08956	AIM1 protein - Ara
130	25	73.5	315	2	T09165	probable peroxidas	203	25	73.5	740	2	S81568	probable membrane
131	25	73.5	316	2	F71338	probable ribose/ga	204	25	73.5	758	2	T25751	hypothetical prote
132	25	73.5	318	2	G69596	cephalosporin-C de	205	25	73.5	783	1	JDEC22	DNA-directed DNA p
133	25	73.5	318	2	E87637	hypothetical prote	206	25	73.5	783	2	AE0514	DNA polymerase II
134	25	73.5	331	2	T26871	hypothetical prote	207	25	73.5	783	2	H85487	DNA polymerase II
135	25	73.5	334	2	B72301	endoglucanase - Th	208	25	73.5	813	2	C97292	ATPases with chape
136	25	73.5	336	2	C84964	hypothetical prote	209	25	73.5	831	2	T49721	hypothetical prote
137	25	73.5	342	2	G84025	polysugar degradin	210	25	73.5	841	2	T48508	beta-adaptin-like
138	25	73.5	343	1	C70418	probable alcohol d	211	25	73.5	845	2	T07039	Hcr9-0 protein - t
139	25	73.5	345	2	T28026	hypothetical prote	212	25	73.5	853	2	T17461	disease resistance
140	25	73.5	346	2	D81288	probable fucose sy	213	25	73.5	855	2	T17460	disease resistance
141	25	73.5	347	2	A75537	hypothetical prote	214	25	73.5	860	2	T27084	hypothetical prote
142	25	73.5	347	2	T20618	hypothetical prote	215	25	73.5	946	2	D96503	protein F9C16.9 li
143	25	73.5	358	2	AE2425	hypothetical prote	216	25	73.5	987	2	S62752	probable DNA-direc
144	25	73.5	359	2	C84983	hypothetical prote	217	25	73.5	1058	2	T47525	kinesin-related pr
145	25	73.5	359	2	T21840	hypothetical prote	218	25	73.5	1078	2	T30879	glucan synthase -
146	25	73.5	364	2	AB0418	probable membrane	219	25	73.5	1090	2	T30576	hypothetical prote
147	25	73.5	371	2	C83736	transposase (15) B	220	25	73.5	1253	2	F86436	hypothetical prote
148	25	73.5	372	2	A64176	hypothetical prote	221	25	73.5	1304	2	T19397	hypothetical prote
149	25	73.5	380	2	F70399	hydrogenase expres	222	25	73.5	1333	1	XOHUDH	xanthine dehydroge
150	25	73.5	384	2	AE1636	N-acetylornithine	223	25	73.5	1339	2	T38991	conserved hypotet
151	25	73.5	385	2	S54103	beta-lactamase (8C	224	25	73.5	1469	2	T24216	chromosome condens
152	25	73.5	386	2	G75079	hypothetical prote	225	25	73.5	1513	2	T23681	hypothetical prote
153	25	73.5	388	2	B71066	hypothetical prote	226	25	73.5	1520	2	B82274	conserved hypotet
154	25	73.5	388	2	B89777	capsular polysacch	227	25	73.5	1622	2	T45240	hypothetical prote
155	25	73.5	406	2	AC2267	hypothetical prote	228	25	73.5	1817	2	AD2165	two-component hybr
156	25	73.5	408	2	C96984	probable Mn transp	229	25	73.5	1821	2	AG2335	hypothetical prote
157	25	73.5	413	2	A86814	phosphoribosylamin	230	25	73.5	1867	2	T38348	probable 1,3-beta-
158	25	73.5	416	2	D47116	trifoliotoxin synth	231	25	73.5	1955	2	T41170	hypothetical prote
159	25	73.5	420	2	A96535	unknown protein, 1	232	25	73.5	2526	2	T20531	hypothetical prote
160	25	73.5	433	2	T17654	hypothetical prote	233	25	73.5	2722	2	T20532	hypothetical prote
161	25	73.5	443	2	T45574	anthranilate N-hyd	234	25	73.5	2738	2	B88320	protein F07A11.6 l
162	25	73.5	446	2	C64205	signal recognition	235	25	73.5	20	2	JU0330	hypothetical prote
163	25	73.5	449	2	A64053	glutamate dehydrog	236	24	70.6	20	2	A99091	hypothetical prote
164	25	73.5	453	2	F75206	maltose-binding pe	237	24	70.6	62	2	B34514	MHC class II histo
165	25	73.5	460	2	T43224	hypothetical prote	238	24	70.6	66	2	AE3608	hypothetical prote
166	25	73.5	466	2	T02324	hypothetical prote	239	24	70.6	74	2	E84214	hypothetical prote
167	25	73.5	470	2	A13442	glycolate oxidase	240	24	70.6	80	2	F96787	protein T4012.7 li
168	25	73.5	471	2	T21102	hypothetical prote	241	24	70.6	94	2	D71284	hypothetical prote
169	25	73.5	472	1	S55379	cytochrome P450 Cy	242	24	70.6	109	2	B72213	conserved hypotet
170	25	73.5	479	2	AE2117	hypothetical prote	243	24	70.6	112	2	A69268	hypothetical prote
171	25	73.5	479	2	F86285	F9L1.11 protein -	244	24	70.6	115	2	AD0414	probable exported
172	25	73.5	492	2	B83020	hypothetical prote	245	24	70.6	133	2	S78156	H+-transporting tw
173	25	73.5	497	2	T32090	hypothetical prote	246	24	70.6	142	2	T23519	hypothetical prote
174	25	73.5	500	2	H91283	hypothetical prote	247	24	70.6	145	2	AG1588	hypothetical prote
175	25	73.5	500	2	B86125	hypothetical prote	248	24	70.6				



249 24 70.6 145 2 AD1651  
 250 24 70.6 147 1 S75650  
 251 24 70.6 147 2 S65579  
 252 24 70.6 147 2 T24057  
 253 24 70.6 155 2 T04304  
 254 24 70.6 156 2 H95252  
 255 24 70.6 156 2 F98117  
 256 24 70.6 156 2 JQ1377  
 257 24 70.6 166 2 E71040  
 258 24 70.6 176 1 I64161  
 259 24 70.6 177 2 C83495  
 260 24 70.6 178 2 T16280  
 261 24 70.6 178 2 D81269  
 262 24 70.6 187 2 H96593  
 263 24 70.6 190 2 A95895  
 264 24 70.6 191 2 T22302  
 265 24 70.6 193 2 B90157  
 266 24 70.6 194 2 T24491  
 267 24 70.6 194 2 B97211  
 268 24 70.6 198 2 AF1569  
 269 24 70.6 200 2 C86528  
 270 24 70.6 200 2 C72094  
 271 24 70.6 201 2 JH0617  
 272 24 70.6 201 2 S76151  
 273 24 70.6 203 2 T30317  
 274 24 70.6 206 2 B81221  
 275 24 70.6 207 2 B81256  
 276 24 70.6 209 2 D95186  
 277 24 70.6 209 2 B98053  
 278 24 70.6 211 2 S14920  
 279 24 70.6 216 2 F69166  
 280 24 70.6 221 2 T43159  
 281 24 70.6 221 2 T17997  
 282 24 70.6 223 2 H83462  
 283 24 70.6 224 2 T03205  
 284 24 70.6 224 2 T32655  
 285 24 70.6 227 2 T37499  
 286 24 70.6 227 2 T50899  
 287 24 70.6 227 2 H90109  
 288 24 70.6 228 2 B81214  
 289 24 70.6 228 2 H81789  
 290 24 70.6 231 2 S76372  
 291 24 70.6 233 2 AF3222  
 292 24 70.6 234 2 D95021  
 293 24 70.6 234 2 A97893  
 294 24 70.6 236 2 D72355  
 295 24 70.6 238 2 S78263  
 296 24 70.6 238 2 D82405  
 297 24 70.6 257 2 C69862  
 298 24 70.6 258 2 AG0459  
 299 24 70.6 258 2 H81321  
 300 24 70.6 261 2 D64166

## ALIGNMENTS

RESULT 1  
 S23094  
 beta-amyloid protein precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
 C:Accession: S23094  
 R:Kojima, S.; Omori, M.  
 FEBS Lett. 304, 57-60, 1992  
 A>Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
 A:Reference number: S23094; MUID:92316198; PMID:1618299  
 A:Accession: S23094  
 A:Molecule type: protein  
 A:Residues: 1-33 <KOJ>  
 A:Cross-references: UNIPARC:UPI00001777FB  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 91.2%; Score 31; DB 2; Length 33;  
 Best Local Similarity 85.7%; Pred. No. 1.5; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 |||||:  
 DB 21 KLVFFAE 27  
 RESULT 2  
 PN0512  
 beta-amyloid protein - guinea pig (fragment)  
 C:Species: Cavia porcellus (guinea pig)  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C:Accession: PN0512  
 R:Shinochigashi, Y.; Matsumoto, H.; Takano, Y.; Salto, R.; Iwata, T.; Kamiya, H.; Ohno, T.;  
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
 A>Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragm  
 A:Reference number: PN0512; MUID:93290653; PMID:7685598  
 A:Accession: PN0512  
 A:Molecule type: protein  
 A:Residues: 1-42 <SHI>  
 A:Cross-references: UNIPROT:Q7M088; UNIPARC:UPI0000031588  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid  
 Query Match 91.2%; Score 31; DB 2; Length 42;  
 Best Local Similarity 85.7%; Pred. No. 1.9; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 |||||:  
 DB 16 KLVFFAE 22  
 RESULT 3  
 A60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
 C:Accession: A60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog  
 A:Reference number: A60045; MUID:92017079; PMID:1656157  
 A:Accession: A60045  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <JOH>  
 A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56125  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain  
 Query Match 91.2%; Score 31; DB 2; Length 57;  
 Best Local Similarity 85.7%; Pred. No. 2.5; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFAQ 7  
 |||||:  
 DB 21 KLVFFAE 27  
 RESULT 4  
 F60045  
 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
 C:Accession: F60045  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog  
 A:Reference number: A60045; MUID:92017079; PMID:1656157  
 A:Accession: F60045  
 A:Molecule type: mRNA



A;Residues: 1-57 <JOH>  
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;  
Best Local Similarity 85.7%; Pred. No. 2.5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 21 KLVFFAE 27

RESULT 5  
D60045  
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C;Accession: D60045  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A;Reference number: A60045; MUID:92017079; PMID:1656157  
A;Accession: D60045  
A;Molecule type: mRNA  
A;Residues: 1-57 <JOH>  
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56124  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;  
Best Local Similarity 85.7%; Pred. No. 2.5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 21 KLVFFAE 27

RESULT 6  
E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C;Species: Ovis sp. (sheep)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C;Accession: E60045  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A;Reference number: A60045; MUID:92017079; PMID:1656157  
A;Accession: E60045  
A;Molecule type: mRNA  
A;Residues: 1-57 <JOH>  
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56130  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;  
Best Local Similarity 85.7%; Pred. No. 2.5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 21 KLVFFAE 27

RESULT 7  
G60045  
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
C;Species: Cavia porcellus (guinea pig)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C;Accession: G60045  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A;Reference number: A60045; MUID:92017079; PMID:1656157  
A;Accession: G60045  
A;Molecule type: mRNA  
A;Residues: 1-57 <JOH>  
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56126  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;  
Best Local Similarity 85.7%; Pred. No. 2.5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 21 KLVFFAE 27

RESULT 8  
B60045  
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C;Species: Ursus maritimus (polar bear)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C;Accession: B60045  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A;Reference number: A60045; MUID:92017079; PMID:1656157  
A;Accession: B60045  
A;Molecule type: mRNA  
A;Residues: 1-57 <JOH>  
A;Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:g2165; PIDN:  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;  
Best Local Similarity 85.7%; Pred. No. 2.5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7  
|||||:  
Db 21 KLVFFAE 27

RESULT 9  
PQ0438  
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995  
C;Accession: PQ0438; C60045  
R;Davidson, J.S.; West, R.L.; Korikalapudi, P.; Maroun, L.E.  
Biochem. Biophys. Res. Commun. 188, 905-911, 1992  
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor  
A;Reference number: PQ0438; MUID:93075180; PMID:1445331  
A;Accession: PQ0438  
A;Molecule type: DNA  
A;Residues: 1-82 <DAV>  
A;Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A;Reference number: A60045; MUID:92017079; PMID:1656157  
A;Accession: C60045  
A;Molecule type: mRNA  
A;Residues: 12-68 <JOH>  
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56129  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 91.2%; Score 31; DB 2; Length 82;  
Best Local Similarity 85.7%; Pred. No. 3.6;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7  
 |||||:  
 Db 32 KLVFFPAE 38

## RESULT 10

A49795  
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C;Species: Macaca fascicularis (crab-eating macaque)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: A49795  
 R;Podlany, M.B.; Tolan, D.R.; Selkoe, D.J.  
 Am. J. Pathol. 138, 1423-1435, 1991  
 A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a hypothesis of the amyloid beta protein precursor in Alzheimer's disease  
 A;Reference number: A49795; MUID:91273117; PMID:1905108  
 A;Accession: A49795  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-695 <POD>  
 A;Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:G342062; PIDN:AAA36829.1; PIDN:AAA36829.1; PIDN:AAA36829.1  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor  
 C;Keywords: alternative splicing

Query Match 91.2%; Score 31; DB 1; Length 695;  
 Best Local Similarity 85.7%; Pred. No. 28;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7  
 |||||:  
 Db 612 KLVFFPAE 618

## RESULT 11

A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N;Alternate names: proteinase nexin II  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
 C;Accession: A27485; UN19727; I49485  
 R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor  
 A;Reference number: A27485; MUID:88106489; PMID:3322280  
 A;Accession: A27485  
 A;Molecule type: mRNA  
 A;Residues: 1-695 <YAM>  
 A;Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:G191568; PIDN:G191568  
 A;Experimental source: brain  
 R;de Strooper, B.; van Leuven, F.; van den Berghe, H.  
 Biochim. Biophys. Acta 1129, 141-143, 1991  
 A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer to the human amyloid beta protein precursor than to the human amyloid beta protein precursor

A;Reference number: S19727; MUID:92096458; PMID:1756177  
 A;Accession: S19727  
 A;Molecule type: mRNA  
 A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
 A;Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379  
 R;Izumi, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
 Gene 112, 189-195, 1992  
 A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid beta protein precursor  
 A;Reference number: I49485; MUID:92203998; PMID:1555768  
 A;Accession: I49485  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-19 <RES>  
 A;Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:G220328; PIDN:BAA01456.1; PIDN:BAA01456.1  
 C;Genetics:

A;Map position: 16C3  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor  
 C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 91.2%; Score 31; DB 2; Length 695;  
 Best Local Similarity 85.7%; Pred. No. 28;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KLVFFPAQ 7  
 |||||:  
 Db 612 KLVFFPAE 618

## RESULT 12

S00550  
 Alzheimer's disease amyloid beta protein precursor - rat  
 N;Alternate names: beta-A4 amyloid protein  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
 C;Accession: S00550; A41245; A39820; S46251  
 R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
 EMBO J. 7, 1365-1370, 1988  
 A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
 A;Reference number: S00550; MUID:88312583; PMID:2900758  
 A;Accession: S00550  
 A;Molecule type: mRNA  
 A;Residues: 1-695 <SHI>  
 A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2PB; EMBL:X07648; NID:G55616; PIDN:X07648  
 R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.

Science 241, 223-226, 1988  
 A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein  
 A;Reference number: A41245; MUID:88264430; PMID:2968652  
 A;Accession: A41245  
 A;Molecule type: protein  
 A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
 A;Cross-references: UNIPARC:UPI00001777FD  
 A;Note: evidence for heparan sulfate attachment  
 R;Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.  
 FEBS Lett. 349, 109-116, 1994

A;Title: The beta-A4 amyloid precursor protein binding to copper.  
 A;Reference number: S46251; MUID:94320627; PMID:7913895  
 A;Contents: annotation; copper binding sites  
 A;Note: rat peptides were isolated but not sequenced  
 R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
 J. Biol. Chem. 266, 8464-8469, 1991  
 A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
 A;Reference number: A39820; MUID:91217087; PMID:1673681

A;Accession: A39820  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 18-32 <POT>  
 A;Cross-references: UNIPARC:UPI00001777FE  
 A;Experimental source: brain  
 C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor  
 C;Superfamily: Alzheimer's disease amyloid beta protein; glycoprotein; transmembrane protein  
 C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
 F;625-648/Domain: transmembrane #status predicted <TMW>

Query Match 91.2%; Score 31; DB 2; Length 695;  
 Best Local Similarity 85.7%; Pred. No. 28;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7  
 |||||:  
 Db 612 KLVFFPAE 618

## RESULT 13

JH0773  
 Alzheimer's disease amyloid beta protein precursor - African clawed frog  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
 C;Accession: JH0773  
 R;Okado, H.; Okamoto, H.  
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental expression  
 A;Reference number: JH0773; MUID:93129227; PMID:1282805  
 A;Accession: JH0773  
 A;Molecule type: mRNA

A;Residues: 1-747 <OKA>  
A;Cross-references: UNIPARC:UPI00000FC980; GB:SS2417; NID:G263150; PIDN:AAB24853.1; PID:  
A;Experimental source: larva  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase I  
C;Keywords: alternative splicing; amyloid  
P:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
  
Query Match 91.2%; Score 31; DB 2; Length 747;  
Best Local Similarity 85.7%; Pred. No. 30;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVFFPAQ 7  
|||:||||:  
DB 664 KLVFFPAE 670  
  
RESULT 14  
T06249  
protoporphyrin IX magnesium chelatase (EC 4.99.1.-) D chain - garden pea  
C;Species: Pisum sativum (garden pea)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T06249  
R;Luo, M.; Weinstein, J.D.  
submitted to the EMBL Data Library, July 1997  
A;Reference number: Z15566  
A;Accession: T06249  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Residues: 1-754 <LUO>  
A;Cross-references: UNIPROT:O22437; UNIPARC:UPI0000035C61; EMBL:AF014399; NID:G2318116;  
A;Experimental source: cv. Spring  
C;Genetics:  
A;Gene: Chld  
C;Function:  
A;Description: catalyzes the magnesium insertion step in chlorophyll biosynthesis  
C;Superfamily: magnesium chelatase, subunit Chld  
C;Keywords: lyase  
  
Query Match 91.2%; Score 31; DB 2; Length 754;  
Best Local Similarity 85.7%; Pred. No. 30;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVFFPAQ 7  
|||:||||:  
DB 462 KLVFFPAQ 468  
  
RESULT 15  
T02925  
protoporphyrin IX magnesium chelatase (EC 4.99.1.-) chain chld - common tobacco  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T02925  
R;Papenbrock, J.; Kruse, E.; Graefe, S.; Haenel, F.; Grimm, B.  
submitted to the EMBL Data Library, December 1996  
A;Description: Identification of a plant Chld cDNA sequence homologous to a bacterial ge  
A;Reference number: Z14773  
A;Accession: T02925  
A;Status: translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Residues: 1-758 <PAP>  
A;Cross-references: UNIPROT:O24133; UNIPARC:UPI0000127862; EMBL:Y10022; NID:e1013894; PI  
C;Genetics:  
A;Gene: chld  
C;Superfamily: magnesium chelatase, subunit Chld  
C;Keywords: lyase  
  
Query Match 91.2%; Score 31; DB 2; Length 758;  
Best Local Similarity 85.7%; Pred. No. 30;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVFFPAQ 7  
|||:||||:

DB 467 KLVFFPAQ 473  
  
RESULT 16  
Q8HUA4  
Alzheimer's disease amyloid beta protein precursor [validated] - human  
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi  
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
protein precursor splice form APP(770)  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44  
4668; A28583; A29302; A60805; J06038; S06121; A60355; A59011; A38384; S29076; S38252; S3  
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey  
Nucleic Acids Res. 17, 517-522, 1989  
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
A;Reference number: S02260; MUID:89128427; PMID:2783775  
A;Accession: S02260  
A;Molecule type: DNA  
A;Residues: 1-288,'V',365-770 <LEML>  
A;Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466  
A;Note: alternative splice form APP(695)  
R;Lemaire, H.G.  
submitted to the EMBL Data Library, November 1988  
A;Reference number: S05194  
A;Accession: S05194  
A;Molecule type: DNA  
A;Residues: 1-14,'VM',17-288,'V',365-770 <LEM2>  
A;Cross-references: UNIPARC:UPI000016AEFC; EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:  
A;Note: alternative splice form APP(695)  
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote  
A;Reference number: A32277; MUID:89165870; PMID:2538123  
A;Accession: A32277  
A;Molecule type: DNA  
A;Residues: 1-75 <LAF>  
A;Cross-references: UNIPARC:UPI000016A57D; GB:M24546; NID:G341202; PIDN:AAC13  
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit  
A;Reference number: A33260; MUID:89392030; PMID:2675837  
A;Accession: A33260  
A;Molecule type: DNA  
A;Residues: 656-737 <JOH>  
A;Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:G178863; PIDN:AAA51768.1; PID:  
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
A;Reference number: A35486; MUID:90321244; PMID:2196878  
A;Accession: A35486  
A;Molecule type: DNA  
A;Residues: 672-710 <PRE1>  
A;Cross-references: UNIPARC:UPI0000148176  
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
Gene 87, 257-263, 1990  
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.  
A;Reference number: I39451  
A;Accession: I39451  
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME  
A;Molecule type: DNA  
A;Residues: 1-770 <YOS1>  
A;Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:  
A;Accession: I39451  
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME  
A;Molecule type: DNA  
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>  
A;Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:  
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
Gene 102, 291-292, 1991  
A;Reference number: A59020; MUID:91340168; PMID:1908403  
A;Contents: annotation; erratum

A;Note: revised physical map for reference I39451  
 R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.U.; Power, M.D.; Lieberburg, I.; van Duine  
 Science 248, 1124-1126, 1990  
 A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh  
 A;Reference number: I39453; MUID:90260663; PMID:2111584  
 A;Accession: I39453  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 656-737 <LEV>  
 A;Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:g178618; PIDN:AAAS1727.1; PID:  
 A;Note: a mutation with 693-Gln is presented  
 R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer  
 A;Reference number: I59562; MUID:92022553; PMID:1925564  
 A;Accession: I59562  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 689-716, 'F', 718-737 <MUR>  
 A;Cross-references: UNIPARC:UPI000011P7EA; GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:  
 R;Kamino, K.; Ort, H.T.; Payami, H.; Wijeman, E.M.; Alonso, M.E.; Pulat, S.M.; Anderson,  
 arakis, S.B.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,  
 Am. J. Hum. Genet. 53, 998-1014, 1992  
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the  
 A;Reference number: A44017; MUID:93035397; PMID:1415269  
 A;Accession: A44017  
 A;Molecule type: DNA  
 A;Residues: 687-692, 'G', 694-718 <KAMI>  
 A;Cross-references: UNIPARC:UPI000011P7EB; GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:  
 A;Experimental source: familial Alzheimer disease family SB  
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)  
 A;Accession: B4017  
 A;Molecule type: DNA  
 A;Residues: 687-718 <KAM2>  
 A;Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:  
 A;Experimental source: familial Alzheimer disease family LIT  
 A;Note: sequence extracted from NCBI backbone (NCBIP:115376)  
 A;Note: this sequence has a silent mutation  
 R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
 Nature 325, 733-736, 1987  
 A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfad  
 A;Reference number: A03134; MUID:87144572; PMID:2881207  
 A;Accession: A03134  
 A;Molecule type: mRNA  
 A;Residues: 1-288, 'V', 365-770 <KAN>  
 A;Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g  
 A;Note: alternative splice form APP(695)  
 R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a  
 A;Reference number: A29030; MUID:87231971; PMID:3035574  
 A;Accession: A29030  
 A;Molecule type: mRNA  
 A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A;Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:g178539; PIDN:AAAS1722.1; PID:  
 A;Note: the authors translated the codon GAG for residue 647 as Asp  
 R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
 Science 235, 877-880, 1987  
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
 A;Reference number: A47584; MUID:87120328; PMID:3810169  
 A;Accession: A47584  
 A;Molecule type: mRNA  
 A;Residues: 674-756, 'S', 758-770 <GOL>  
 A;Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:  
 A;Experimental source: brain  
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
 Science 235, 880-884, 1987  
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
 A;Reference number: A47585; MUID:87120329; PMID:2949367  
 A;Accession: A47585  
 A;Molecule type: mRNA  
 A;Residues: 674-703 <TANI>  
 A;Cross-references: UNIPARC:UPI000016A46P; GB:M15532; NID:g177957; PIDN:AAAS1564.1; PID:

R;Dyrke, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muell  
 EMBO J. 7, 949-957, 1988  
 A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre  
 A;Reference number: S02638; MUID:88296437; PMID:2900137  
 A;Accession: S02638  
 A;Molecule type: mRNA  
 A;Residues: 672-678 <DYR>  
 A;Cross-references: UNIPARC:UPI0000035AB0  
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Nev  
 Nature 331, 528-530, 1988  
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associa  
 A;Reference number: S00707; MUID:88122640; PMID:2893290  
 A;Accession: S00707  
 A;Molecule type: mRNA  
 A;Residues: 286-344, 'I', 365-366 <TAN2>  
 A;Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PI  
 A;Experimental source: promyelocytic leukemia cell line HL60  
 A;Note: alternative splice form APP(751)  
 R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hau, D.; Greenberg, B.; D  
 Nature 331, 525-527, 1988  
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi  
 A;Reference number: S00925; MUID:88122639; PMID:2893289  
 A;Accession: S00925  
 A;Molecule type: mRNA  
 A;Residues: 1-344, 'I', 365-770 <PO2>  
 A;Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA  
 A;Note: alternative splice form APP(751)  
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito  
 A;Reference number: A38949; MUID:88122641; PMID:2893291  
 A;Accession: A38949  
 A;Molecule type: mRNA  
 A;Residues: 287-367 <KIT>  
 A;Cross-references: UNIPARC:UPI000014533B; GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:  
 A;Experimental source: glioblastoma cell line  
 A;Note: alternative splice form APP(770)  
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Asht  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three  
 A;Reference number: A30320  
 A;Accession: A30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 284-288, 'V', 365-770 <VIT1>  
 A;Cross-references: UNIPARC:UPI0000174094  
 A;Accession: B30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 122-288, 'V', 365-770 <VIT2>  
 A;Cross-references: UNIPARC:UPI0000174094  
 A;Accession: C30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 606-770 <VIT3>  
 A;Cross-references: UNIPARC:UPI0000174094  
 R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b  
 A;Reference number: A31087; MUID:88124954; PMID:2893379  
 A;Accession: A31087  
 A;Molecule type: mRNA

Query Match 91.2%; Score 31; DB 1; Length 770;  
 Best Local Similarity 85.7%; Pred. No. 31;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
 |||||  
 Db 687 KLVFFAE 693

RESULT 17

B86218  
 protein T27G7.20 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-May-2004  
 A:Accession: B86218  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Mafti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: B86218  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-778 <STO>  
 A:Cross-references: UNIPARC:UPI000016D8B1; GB:AE005172; NID:g6664313; PIDN:AAF22895.1; C:Genetics:  
 A:Map position: 1  
 A:Superfamily: magnesium chelatase, subunit ChlD  
 Query Match 91.2%; Score 31; DB 2; Length 778;  
 Best Local Similarity 85.7%; Pred. No. 31;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFPAQ 7  
 ||:||||  
 Db 485 KLVFFPAQ 491  
 RESULT 18  
 AE0523  
 conserved hypothetical protein STY0189 [imported] - Salmonella enterica subsp. enterica  
 C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AE0523  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A:Reference number: AB0502; MUID:21534947; PMID:11677608  
 A:Accession: AE0523  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-115 <PAR>  
 A:Cross-references: UNIPARC:UPI0000059A0B; GB:AL513382; PIDN:CAD01325.1; PID:g16501453; C:Genetics:  
 A:Gene: STY0189  
 Query Match 85.3%; Score 29; DB 2; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LVFFPAQ 7  
 ||:||||  
 Db 59 LVFFPAQ 64  
 RESULT 19  
 T06645  
 hypothetical protein T20K18.220 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: T06645  
 R:Sevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew

submitted to the Protein Sequence Database, April 1999  
 A:Reference number: Z15790  
 A:Accession: T06645  
 A:Molecule type: DNA  
 A:Residues: 1-152 <BEV>  
 A:Cross-references: UNIPROT:Q9STZ9; UNIPARC:UPI00000A0722; EMBL:AL049640; GSPDB:GNO00062; A:Experimental source: cultivar Columbia; BAC clone T20K18  
 C:Genetics:  
 A:Gene: ATSP:T20K18.220  
 A:Map position: 4  
 A:Introns: 87/3; 109/3  
 C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100  
 Query Match 85.3%; Score 29; DB 2; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFPA 6  
 ||:||||  
 Db 9 KLVFFPA 14  
 RESULT 20  
 B64735  
 yacC protein - Escherichia coli (strain K-12)  
 C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
 C:Accession: B64735; A33863; S45199  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co; .A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: B64735  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-156 <BLAT>  
 A:Cross-references: UNIPROT:Q8X949; UNIPARC:UPI00000D0877; GB:AE000121; GB:U00096; NID:9 R:Xie, Q.W.; Tabor, C.W.; Tabor, H.  
 J. Bacteriol. 171, 4457-4465, 1989  
 A:Title: Spermidine biosynthesis in Escherichia coli: promoter and termination regions o A:Reference number: A33863; MUID:89327165; PMID:2666401  
 A:Accession: A33863  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 42-156 <XIE>  
 A:Cross-references: UNIPARC:UPI000013A023; GB:J02804; NID:g147850; PIDN:AAA24642.1; PID: R:Fujita, N.  
 submitted to the EMBL Data Library, January 1994  
 A:Reference number: S45181  
 A:Accession: S45199  
 A:Molecule type: DNA  
 A:Residues: 42-156 <FUJ>  
 A:Cross-references: UNIPARC:UPI000013A023; EMBL:D26562; NID:g473770; PIDN:BAA05578.1; PI A:Experimental source: strain K-12 substrain W3110  
 C:Genetics:  
 A:Gene: yacC  
 Query Match 85.3%; Score 29; DB 2; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LVFFPAQ 7  
 ||:||||  
 Db 100 LVFFPAQ 105  
 RESULT 21  
 P85495  
 hypothetical protein yacC [imported] - Escherichia coli (strain O157:H7, substrain EDJ93 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C;Accession: F85495  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: F85495  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-156 <STO>  
A;Cross-references: UNIPROT:Q8X949; UNIPARC:UPI000000D0877; GB:AE005174; NID:g12512834; F  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: yacC

Query Match 85.3%; Score 29; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFAQ 7  
| | | | |  
Db 100 LVFFAQ 105

## RESULT 22

F90644  
hypothetical protein ECs0126 [imported] - Escherichia coli (strain O157:H7, substrain R1  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: F90644

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: F90644  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-156 <HAY>  
A;Cross-references: UNIPROT:Q8X949; UNIPARC:UPI000000D0877; GB:BA000007; PIDN:BA033549.1;  
A;Experimental source: strain O157:H7, substrain R1MD 050952  
C;Genetics:  
A;Gene: ECs0126

Query Match 85.3%; Score 29; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFAQ 7  
| | | | |  
Db 100 LVFFAQ 105

## RESULT 23

H85138  
hypothetical protein AT4g12800 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: H85138

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A;Reference number: A85001; MUID:20083488; PMID:10617198  
A;Accession: H85138  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-231 <STO>  
A;Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI000000A7E0E; GB:NC\_001268; NID:g7267992; F

C;Genetics:  
A;Gene: AT4g12900  
A;Map position: 4  
C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 85.3%; Score 29; DB 2; Length 231;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFA 6  
| | | | |  
Db 12 KLVFFFA 17

## RESULT 24

T32514  
hypothetical protein C44B12.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Dec-2004  
C;Accession: T32514

R;Tin-Wollam, A.  
submitted to the EMBL Data Library, December 1997  
A;Description: The sequence of C. elegans cosmid C44B12.  
A;Reference number: Z21183  
A;Accession: T32514  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-247 <TIN>  
A;Cross-references: UNIPROT:O44145; UNIPARC:UPI00001793B3; EMBL:AF036692; PIDN:AAB88324  
A;Experimental source: strain Bristol N2; clone C44B12  
C;Genetics:  
A;Gene: CESP:C44B12.1  
A;Map position: 4  
A;Introns: 28/3; 82/1; 164/1; 192/1

Query Match 85.3%; Score 29; DB 2; Length 247;  
Best Local Similarity 71.4%; Pred. No. 30;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
| | | | |  
Db 224 KLVFFSQ 230

## RESULT 25

T48903  
wax synthase [imported] - Simmondsia chinensis

C;Species: Simmondsia chinensis  
C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C;Accession: T48903

R;Lardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W.  
Plant Physiol. 122, 645-655, 2000  
A;Title: Purification of a jojoba embryo wax synthase, cloning of its cDNA and producti  
A;Reference number: Z25002

A;Accession: T48903  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-352 <LAR>  
A;Cross-references: UNIPROT:Q9XGY6; UNIPARC:UPI000000A1C81; EMBL:AF149919; PIDN:AAD38041

Query Match 85.3%; Score 29; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFA 6  
| | | | |  
Db 135 KLVFFFA 140

## RESULT 26

T48008  
hypothetical protein T17J13.120 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 31-Dec-2004  
C;Accession: T48008

R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,  
submitted to the Protein Sequence Database, February 2000  
A;Reference number: Z24482



A:Accession: T48008  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-428 <RIE>  
A:Cross-references: UNIPROT:Q9MIQ8; UNIPARC:UPI00000488B7; EMBL:AL138651  
A:Experimental source: cultivar Columbia; BAC clone TI7J13  
C:Genetics:  
A:Map position: 3  
A:Introns: 137/3  
A>Note: TI7J13.120  
C:Superfamily: N-hydroxycinnamoyl/benzoyl transferase

Query Match 85.3%; Score 29; DB 2; Length 428;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFA 6  
|||||  
DB 271 KLVFFFA 276

RESULT 27  
C91268  
transcription activator of cad operon [imported] - Escherichia coli (strain O157:H7, sub  
C:Species: Escherichia coli  
C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: C91268  
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: C91268  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-512 <HAY>  
A:Cross-references: UNIPROT:Q8XDS2; UNIPARC:UPI00000D031B; GB:BA000007; PIDN:BA838538.1;  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs5115

Query Match 85.3%; Score 29; DB 2; Length 512;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFFAQ 7  
|||||  
DB 37 LVFFFAQ 42

RESULT 28  
A86109  
transcription activator of cad operon [imported] - Escherichia coli (strain O157:H7, sub  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: A86109  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A86109  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-512 <STO>  
A:Cross-references: UNIPROT:Q8XDS2; UNIPARC:UPI00000D031B; GB:AE005174; NID:gl2519113; F  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: cadC

Query Match 85.3%; Score 29; DB 2; Length 512;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFFAQ 7  
|||||  
DB 37 LVFFFAQ 42

RESULT 29  
C41968  
transcription activator cadC - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: C41968; S56362; D65223  
R:Watson, N.; Duniyak, D.S.; Rosey, E.L.; Slonczewski, J.L.; Olson, E.R.  
J. Bacteriol. 174, 530-540, 1992  
A>Title: Identification of elements involved in transcriptional regulation of the Escher  
A:Reference number: A41968; MUID:92105022; PMID:1370290  
A:Accession: C41968  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-512 <WAT>  
A:Cross-references: UNIPROT:P23890; UNIPARC:UPI0000126DA9; GB:M67452; NID:gl45451; PIDN  
A>Note: sequence extracted from NCBI backbone (NCBIN:75631, NCBIP:75632)  
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.  
Nucleic Acids Res. 23, 2105-2119, 1995  
A>Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.  
A:Reference number: S56314; MUID:95334362; PMID:7610040  
A:Accession: S56362  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-512 <BUR>  
A:Cross-references: UNIPARC:UPI0000126DA9; EMBL:U14003; NID:gl263172; PIDN:AAA37033.1; P  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.: Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A>Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: D65223  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-512 <BLAT>  
A:Cross-references: UNIPARC:UPI0000126DA9; GB:AE000486; GB:U000096; NID:gl790574; PIDN:AA  
A:Experimental source: strain K-12, substrain MGI655  
C:Genetics:  
A:Gene: cadC  
C:Keywords: DNA binding; transcription regulation; transmembrane protein

Query Match 85.3%; Score 29; DB 2; Length 512;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFFAQ 7  
|||||  
DB 37 LVFFFAQ 42

RESULT 30  
B96666  
protein P22c12.6 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: B96666  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: B96666  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-776 <STO>  
 A;Cross-references: UNIPROT:Q9SH68; UNIPARC:UPI00000A55E3; GB:AE005173; NID:g6692116; PID:125  
 C;Genetics:  
 A;Gene: F22C12.6  
 A;Map position: 1

Query Match 85.3%; Score 29; DB 2; Length 776;  
 Best Local Similarity 71.4%; Pred. No. 91;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7  
 :|:|||||  
 Db 129 QLIFPAQ 135

## RESULT 31

S30236  
 genome polypotein - zucchini yellow mosaic virus (strain Singapore) (fragment)  
 N;Contains: coat protein; nuclear inclusion protein a; RNA-directed RNA polymerase (EC 2.7.7.48)  
 C;Species: zucchini yellow mosaic virus, ZYMV  
 A;Variety: strain Singapore  
 C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
 C;Accession: S30236  
 R;Wu, M.; Yeong, C.Y.; Lee, S.C.; Wong, S.M.  
 Nucleic Acids Res. 21, 1317, 1993  
 A;Title: Nucleotide sequence of the 3' half of zucchini yellow mosaic virus (Singapore isolate)  
 A;Reference number: S30236; MUID:93219099; PMID:8464715  
 A;Accession: S30236  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-1016 <WUM>  
 A;Cross-references: UNIPROT:Q05912; UNIPARC:UPI00000ECC69; EMBL:X68509; NID:g288233; PID:125  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992  
 C;Superfamily: tobacco etch virus genome polypotein  
 C;Keywords: coat protein; genome-linked protein; nucleotidyltransferase; phosphoprotein;  
 F;9-61/Product: VPg protein #status predicted <VPG>  
 F;62-494/Product: nuclear inclusion protein a #status predicted <NIA>  
 F;495-1010/Product: RNA-directed RNA polymerase #status predicted <POL>  
 F;1011-1016/Product: coat protein (fragment) #status predicted <COP>  
 F;125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 85.3%; Score 29; DB 2; Length 1016;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPA 6  
 :|:|||||  
 Db 837 KLVFFPA 842

## RESULT 32

F90736  
 molybdopterin biosynthesis protein D chain [imported] - Escherichia coli (strain O157:H7)  
 C;Species: Escherichia coli  
 C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 16-Aug-2004  
 C;Accession: F90736  
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands  
 A;Reference number: A99629; MUID:21156231; PMID:11258796  
 A;Accession: F90736  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-81 <HAY>  
 A;Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000D09BF; GB:BA000007; PIDN:BA034285.1; NID:g12513773;  
 A;Experimental source: strain O157:H7, substrain RMD 0509952  
 C;Genetics:  
 A;Gene: ECs0862  
 C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 82.4%; Score 28; DB 2; Length 81;  
 Best Local Similarity 71.4%; Pred. No. 18;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7  
 :|:|||||  
 Db 3 KVLFFPAQ 9

## RESULT 33

A82251  
 molybdenum cofactor biosynthesis protein D VC1027 [imported] - Vibrio cholerae (strain 18-Aug-2000)  
 C;Species: Vibrio cholerae  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 16-Aug-2004  
 C;Accession: A82251  
 R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J.L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A;Reference number: A82035; MUID:20406833; PMID:10952301  
 A;Accession: A82251  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-81 <HEI>  
 A;Cross-references: UNIPROT:Q9KT78; UNIPARC:UPI00000C2E58; GB:AE004184; GB:AE003852; NID:g12513773;  
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC1027

A;Map position: 1

C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

F;81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 82.4%; Score 28; DB 2; Length 81;  
 Best Local Similarity 71.4%; Pred. No. 18;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7  
 :|:|||||  
 Db 3 KVLFFPAQ 9

## RESULT 34

G85586  
 molybdopterin biosynthesis [imported] - Escherichia coli (strain O157:H7, substrain EDL)  
 C;Species: Escherichia coli  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
 C;Accession: G85586  
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca, Nature 409, 529-533, 2001  
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A;Reference number: A85480; MUID:21074935; PMID:11206551  
 A;Accession: G85586  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-81 <STO>  
 A;Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000D09BF; GB:AE005174; NID:g12513773;  
 A;Experimental source: strain O157:H7, substrain EDL933  
 C;Genetics:  
 A;Gene: moaD  
 C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 82.4%; Score 28; DB 2; Length 81;  
 Best Local Similarity 71.4%; Pred. No. 18;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7  
 :|:|||||  
 Db 3 KVLFFPAQ 9



```

RESULT 35
H64814
molybdopterin biosynthesis protein D chain [validated] - Escherichia coli (strain K-12)
N:Alternate names: moaD protein; molybdopterin-converting factor 10K chain; molybdopterin
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: H64814; S35001; A46585; S31882
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen
A.; Rose, D.J.; Mau, B.; Shaoh, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64814
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-81 <BLAT>
A:Cross-references: UNIPROT:P30748; UNIPARC:UPI00001116DF; GB:AE000096; NID:9
A:Experimental source: strain K-12, substrain MG1655
R:Rivers, S.B.; McNaairn, E.; Blasco, F.; Giordano, G.; Boxer, D.H.
Mol. Microbiol. 8, 1071-1081, 1993
A:Title: Molecular genetic analysis of the moa operon of Escherichia coli K-12 required
A:Reference number: S34998; MUID:93368423; PMID:8361352
A:Accession: S35001
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-44, 'R', 46-81 <RIV>
A:Cross-references: UNIPARC:UPI000016F2FD; EMBL:X70420; NID:G42007; PIDN:CMA49864.1; PID
A:Experimental source: strain K12
R:Pitterle, D.M.; Rajagopalan, K.V.
J. Biol. Chem. 268, 13499-13505, 1993
A:Title: The biosynthesis of molybdopterin in Escherichia coli. Purification and charact
A:Reference number: A46585; MUID:93293873; PMID:8514782
A:Accession: A46585
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8, 'E', 10-15 <PIT>
A:Cross-references: UNIPARC:UPI0000178EC3
A:Note: sequence extracted from NCBI backbone (NCBIP:134491)
C:Genetics:
A:Gene: moaD
A:Map position: 17.7 min
A:Complex: heterodimer with D chain (PTR:S31883) [validated, MUID:93293873]
C:Function:
A:Description: required for the addition of the Mo-binding dithiolene group to a molybdo
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein
C:Keywords: heterodimer; molybdopterin biosynthesis
F:81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 82.4%; Score 28; DB 2; Length 81;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 3 KVLFFPAQ 9

RESULT 36
D86866
prophage p83 protein 01 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
A:Accession: D86866
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86866
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <STO>
A:Cross-references: UNIPROT:Q9CEB2; UNIPARC:UPI00000C6B67; GB:AE0005176; PID:g12724972; F
A:Experimental source: strain IL1403

```

## C:Genetics:

A:Gene: ps301

Query Match 82.4%; Score 28; DB 2; Length 306;  
 Best Local Similarity 71.4%; Pred. No. 64;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 Db 182 KLVYPAQ 188

## RESULT 37

H71729

hypothetical protein RP189 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004

C:Accession: H71729

R:Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Sichert-Ponten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: H71729

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-321 &lt;AND&gt;

A:Cross-references: UNIPROT:Q92DX5; UNIPARC:UPI0000139421; GB:AJ235270; NID:9325269; MUI

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: RP189

C:Superfamily: Rickettsia prowazekii hypothetical protein RP189

Query Match 82.4%; Score 28; DB 2; Length 321;  
 Best Local Similarity 83.3%; Pred. No. 67;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPA 6

Db 178 KLIFFPA 183

## RESULT 38

G96643

hypothetical protein T13M11.15 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: G96643

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: G96643

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-346 &lt;STO&gt;

A:Cross-references: UNIPROT:Q9SYB5; UNIPARC:UPI00000A936E; GB:AE005173; NID:g4508079; P

C:Genetics:

A:Gene: T13M11.15

A:Map position: 1

Query Match 82.4%; Score 28; DB 2; Length 346;  
 Best Local Similarity 85.7%; Pred. No. 72;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7

Db 178 KLIFFPA 183

Db 261 KLVPFFQ 267

## RESULT 39

C84979  
hypothetical protein cysG [imported] - Buchnera sp. (strain APS)  
C;Species: Buchnera sp.  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 18-Aug-2003  
C;Accession: C84979  
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000  
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.  
A;Reference number: A84930; MUID:20445173; PMID:10993077  
A;Accession: C84979  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-473 <STO>  
A;Cross-references: UNIPARC:UPI0000058596; GB:AP0000398; GSPDB:GN00144  
A;Experimental source: strain APS  
C;Genetics:  
A;Gene: cysG; BU425  
C;Superfamily: siroheme synthase

Query Match 82.4%; Score 28; DB 2; Length 473;  
Best Local Similarity 83.3%; Pred. No. 97;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFPAQ 7  
:|||||  
Db 285 LVFFPAQ 290

## RESULT 40

S67962  
valine-tRNA ligase (EC 6.1.1.9) - brine shrimp (fragments)  
C;Species: Artemia sp. (brine shrimp)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 03-Jun-2002  
C;Accession: S67962  
R;Brandsma, M.; Kerjan, P.; Dijk, J.; Janssen, G.M.C.; Moeller, W.  
Eur. J. Biochem. 233, 277-282, 1995  
A;Title: Valyl-tRNA synthetase from Artemia. Purification and association with elongation factor Tu  
A;Reference number: S67962; MUID:96061959; PMID:7588756  
A;Accession: S67962  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-17;18-32 <BRA>  
A;Cross-references: UNIPARC:UPI000007DF94; UNIPARC:UPI000007B488  
C;Keywords: ligase

Query Match 79.4%; Score 27; DB 2; Length 32;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFPAQ 7  
:|||||  
Db 18 MVFFPAQ 23

## RESULT 41

T35807  
hypothetical protein SC8D9.03 SC8D9.03 - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C;Accession: T35807  
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, February 1999  
A;Reference number: Z21589  
A;Accession: T35807  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-182 <MUR>  
A;Cross-references: UNIPROT:Q9Z588; UNIPARC:UPI00000DAEDF; EMBL:AL035569; PIDN:CAB37567.  
A;Experimental source: strain A3(2)

## C;Genetics:

A;Gene: SC8DB:SC8D9.03  
C;Superfamily: yeast conserved hypothetical protein YJL055w

Query Match 79.4%; Score 27; DB 2; Length 182;  
Best Local Similarity 71.4%; Pred. No. 66;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7  
:|||||  
Db 160 ELVFFAE 166

## RESULT 42

T47892  
hypothetical protein T4C21.220 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T47892  
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.;  
.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24479  
A;Accession: T47892  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-214 <CHO>  
A;Cross-references: UNIPROT:Q9LZY2; UNIPARC:UPI000009DAB0; EMBL:AL162295  
A;Experimental source: cultivar Columbia; BAC clone T4C21  
C;Genetics:  
A;Map position: 3  
A;Introns: 46/2; 65/2; 106/2; 128/3; 159/3; 197/3  
A;Note: T4C21.220

Query Match 79.4%; Score 27; DB 2; Length 214;  
Best Local Similarity 71.4%; Pred. No. 77;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7  
:|||||  
Db 19 KLVPFYAR 25

## RESULT 43

T26245  
hypothetical protein W06G6.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T26245  
R;McMurray, A.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z20180  
A;Accession: T26245  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-300 <WIL>  
A;Cross-references: UNIPROT:Q9XU61; UNIPARC:UPI0000061208; EMBL:Z83129; PIDN:CAB05641.1  
A;Experimental source: clone W06G6  
C;Genetics:  
A;Gene: CESP.W06G6.6  
A;Map position: 5  
A;Introns: 171/2; 204/2

Query Match 79.4%; Score 27; DB 2; Length 300;  
Best Local Similarity 83.3%; Pred. No. 11e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFA 6  
:|||||  
Db 281 KMVFFA 286

## RESULT 44

B46678  
 endoglycosidase F3 (EC 3.2.-.-) precursor - Flavobacterium meningosepticum  
 C:Species: Flavobacterium meningosepticum  
 C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
 C:Accession: B46678  
 R:Tarentino, A.L.; Quinones, G.; Changchien, L.M.; Plummer Jr., T.H.  
 J. Biol. Chem. 268, 9702-9708, 1993  
 A>Title: Multiple endoglycosidase F activities expressed by Flavobacterium meningosepticum  
 A:Reference number: A46678; MUID:93252846; PMID:8486657  
 A:Accession: B46678  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-329 <FAR>  
 A:Cross-references: UNIPROT:P36913; UNIPARC:UPI0000129B37; GB:L06332; NID:gi48695; PIDN:  
 C:Keywords: glycosidase; hydrolase

Query Match 79.4%; Score 27; DB 2; Length 329;  
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 |:|:|:|  
 Db 2 KKIFFPAQ 8

RESULT 45  
 H75505  
 tryptophanyl-tRNA synthetase - Deinococcus radiodurans (strain R1)  
 C:Species: Deinococcus radiodurans  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: H75505  
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A:Reference number: A75250; MUID:20036896; PMID:10567266  
 A:Accession: H75505  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-330 <WHI>  
 A:Cross-references: UNIPROT:Q9RWV7; UNIPARC:UPI0000136720; GB:AE001913; GB:AE000513; NID  
 A:Experimental source: strain R1  
 C:Genetics:  
 A:Gene: DR0558  
 A:Map position: 1  
 C:Superfamily: tryptophan-tRNA ligase

Query Match 79.4%; Score 27; DB 2; Length 330;  
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 |:|:|:|  
 Db 78 KVVFFVQ 84

RESULT 46  
 A64383  
 hypothetical protein M70665 - Methanococcus jannaschii  
 C:Species: Methanococcus jannaschii  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 05-Oct-2004  
 C:Accession: A64383  
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
 Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
 raon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
 Science 273, 1058-1073, 1996  
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,  
 A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
 A:Reference number: A64300; MUID:96337999; PMID:8688087  
 A:Accession: A64383  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA

A:Residues: 1-341 <BUL>  
 A:Cross-references: UNIPROT:Q58079; UNIPARC:UPI0000139BA4; GB:U67513; GB:L77117; NID:gi48  
 C:Genetics:  
 A:Map position: REV591204-590179  
 A:Start codon: GTG  
 C:Superfamily: uncharacterized conserved protein

Query Match 79.4%; Score 27; DB 2; Length 341;  
 Best Local Similarity 57.1%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
 |:|:|:|  
 Db 67 KLIFPAE 73

RESULT 47  
 T26247  
 hypothetical protein W0636.8 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T26247  
 R:McMurray, A.  
 submitted to the EMBL Data Library, November 1996  
 A:Reference number: Z20180  
 A:Accession: T26247  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-349 <WIL>  
 A:Cross-references: UNIPROT:Q9XU59; UNIPARC:UPI0000061209; EMBL:283129; PIDN:CAB05643.1;  
 A:Experimental source: clone W0656  
 C:Genetics:  
 A:Gene: CESP:W06G6.8  
 A:Map position: 5  
 A:Introns: 172/2; 210/3; 247/2

Query Match 79.4%; Score 27; DB 2; Length 349;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPA 6  
 |:|:|:|  
 Db 324 KRVFFPA 329

RESULT 48  
 H64251  
 replication initiation protein dnaA - Mycoplasma genitalium  
 C:Species: Mycoplasma genitalium  
 C>Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: H64251  
 R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;  
 M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
 C.A.; Venter, J.C.  
 Science 270, 397-403, 1995  
 A>Title: The minimal gene complement of Mycoplasma genitalium.  
 A:Reference number: A64200; MUID:96026346; PMID:7569993  
 A:Accession: H64251  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-437 <TIGR>  
 A:Cross-references: UNIPROT:P35888; UNIPARC:UPI000012952C; GB:U39734; GB:L43967; NID:gi38  
 A:Experimental source: strain G-37  
 C:Genetics:  
 A:Genetic code: SGC3  
 C:Superfamily: replication initiation protein dnaA  
 C:Keywords: ATP; nucleotide binding; P-loop  
 F:141-148/Region: nucleotide-binding motif A (P-loop)  
 F:202-206/Region: nucleotide-binding motif B

Query Match 79.4%; Score 27; DB 2; Length 437;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|:|:|:  
Db 315 KLVFFPAK 321

## RESULT 49

T04463  
hypothetical protein F4D11.170 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: T04463  
R/Bavan, M.; Bense, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Hoheisel, J.; Mewes, H.W.  
submitted to the Protein Sequence Database, April 1998  
A/Reference number: 215360  
A/Accession: T04463  
A/Molecule type: DNA  
A/Residues: 1-531 <BEV>  
A/Cross-references: UNIPROT:O65536; UNIPARC:UPI000009EC78; EMBL:AL022537  
A/Experimental source: cultivar Columbia; BAC clone F4D11  
C/Genetics:  
A/Map position: 4  
A/Introns: 39/2; 60/1; 89/2; 118/3; 256/3; 396/3; 437/3; 466/3  
A/Note: F4D11.170

Query Match 79.4%; Score 27; DB 2; Length 531;  
Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|:|:|:|:  
Db 79 KLVHFAQ 85

## RESULT 50

G97000  
diguanylate cyclase/phosphodiesterase domain (GGDEF) containing protein [imported] - Clo  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: G97000  
R/Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4836, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: G97000  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-571 <KUR>  
A/Cross-references: UNIPROT:Q97KU8; UNIPARC:UPI00000C3FBF; GB:AE001437; PIDN:AAK78794.1;  
A/Experimental source: Clostridium acetobutylicum ATCC824  
C/Genetics:  
A/Gene: CAC0818

Query Match 79.4%; Score 27; DB 2; Length 571;  
Best Local Similarity 71.4%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|:|:|:|:  
Db 314 KVMFFPAQ 320

## RESULT 51

AD3409  
ABC transporter ATP-binding protein BME11258 [imported] - Brucella melitensis (strain 16  
C/Species: Brucella melitensis  
C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 31-Dec-2004  
C/Accession: AD3409  
R/DelVecchio, V.G.; Kaprat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
M.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitens

A/Reference number: AD3252; PMID:11756688

A/Accession: AD3409  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-646 <KUR>  
A/Cross-references: UNIPROT:Q8YGA2; UNIPARC:UPI0000057FD3; GB:AE008917; PIDN:AAU52439.1

A/Experimental source: strain 16M

C/Genetics:

A/Gene: BME11258

A/Map position: 1

Query Match 79.4%; Score 27; DB 2; Length 646;

Best Local Similarity 71.4%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|:|:|:|:  
Db 388 KVAFPAQ 394

## RESULT 52

T31691  
hypothetical protein F27E11.2 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Dec-2004  
C/Accession: T31691  
R/Wamsley, P.; Keppler, D.  
submitted to the EMBL Data Library, July 1997  
A/Description: The sequence of C. elegans cosmid F27E11.  
A/Reference number: Z21069  
A/Accession: T31691  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-655 <WAM>  
A/Cross-references: UNIPROT:Q16191; UNIPARC:UPI0000178DE0; EMBL:AF016413; PIDN:AAAB65255

A/Experimental source: strain Bristol N2; clone F27E11

C/Genetics:

A/Gene: CESP:F27E11.2

A/Map position: 5

A/Introns: 62/2; 78/3; 104/1; 144/1; 202/2; 249/3; 450/3; 540/2; 570/3; 631/1

Query Match 79.4%; Score 27; DB 2; Length 655;

Best Local Similarity 71.4%; Pred. No. 2.3e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7  
|:|:|:|:  
Db 39 KLVFFLQ 45

## RESULT 53

D70425

conserved hypothetical protein aq\_1442 - Aquifex aeolicus

C/Species: Aquifex aeolicus

C/Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 16-Aug-2004

C/Accession: D70425

R/Dackert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C

V.

Nature 392, 353-358, 1998

A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A/Reference number: A70300; MUID:98196686; PMID:9537320

A/Accession: D70425

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-1054 <AQP>

A/Cross-references: UNIPROT:O67430; UNIPARC:UPI000005660F; GB:AE000740; NID:q2983826; P

A/Experimental source: strain VF5

C/Genetics:

A/Gene: aq\_1442

C/Superfamily: Sensor diguanylate cyclase/c-di-GMP phosphodiesterase

Query Match 79.4%; Score 27; DB 2; Length 1054;

Best Local Similarity 83.3%; Pred. No. 3.6e+02;

```

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      2  LVFFAQ 7
      :|||||
Db      997 IVFFAQ 1002

RESULT 54
T34558
hypothetical protein DKFPz434H2450.1 - human (fragments)
C:Species: Homo sapiens (man)
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34558
R:Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, October 1999
A:Reference number: Z21540
A:Accession: T34558
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-947;948-1273 <POU>
A:Cross-references: UNIPROT:Q9UFH2; UNIPARC:UPI00001775C3; UNIPARC:UPI00001775C4; EMBL:A
A:Experimental source: adult testis; clone DKFPz434H2450
A>Note: the cDNA sequence contains a +1 frameshift near codon 947
C:Genetics:
A>Note: DKFPz434H2450.1
C:Superfamily: dynein heavy chain, ciliary

Query Match      79.4%; Score 27; DB 2; Length 1273;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches      5;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  KLVFFAQ 7
      :|:|:|
Db      538 KLIFLAQ 544

RESULT 55
T07200
hypothetical protein 49a - Chlorella vulgaris chloroplast
C:Species: chloroplast Chlorella vulgaris
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07200
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakae
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A>Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo
A:Reference number: Z15985; MUID:97303241; PMID:9159184
A:Accession: T07200
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-49 <WAK>
A:Cross-references: UNIPARC:UPI000011E446; EMBL:AB001684; NID:g2224352; PIDN:BAA57847.1;
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match      76.5%; Score 26; DB 2; Length 49;
Best Local Similarity 57.1%; Pred. No. 32;
Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1  KLVFFAQ 7
      :|:|:|:|
Db      19 KLIFFSQ 25

RESULT 56
AG3408
molybdopterin (mpt) converting factor, chain 1 [imported] - Brucella melitensis (strain
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 16-Aug-2004
C:Accession: AG3408
R;DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Loeb, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

```

```

A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AB3252; PMID:11756688
A:Accession: AG3408
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-85 <KUR>
A:Cross-references: UNIPROT:Q8YGA7; UNIPROT:Q8G1L7; UNIPARC:UPI0000057FCE; GB:AE008917;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11253
A:Map position: 1
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match      76.5%; Score 26; DB 2; Length 85;
Best Local Similarity 83.3%; Pred. No. 55;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1  KLVFFA 6
      :|:|:|
Db      4  KLVVFA 9

RESULT 57
H82370
conserved hypothetical protein VC0057 [imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82370
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P.
1, R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82370
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <HEI>
A:Cross-references: UNIPROT:Q9KVT2; UNIPARC:UPI00000C2BAC; GB:AE004096; GB:AE003852; NID
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0057
A:Map position: 1

Query Match      76.5%; Score 26; DB 2; Length 91;
Best Local Similarity 83.3%; Pred. No. 58;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      2  LVFFAQ 7
      :|:|:|
Db      20 VVFFAQ 25

RESULT 58
B95049
hypothetical protein SP0424 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95049
R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: B95049
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <KUR>
A:Cross-references: UNIPROT:P59201; UNIPARC:UPI0000051423; GB:AE005672; PIDN:AAK74587.1,
A:Experimental source: strain TIGR4
C:Genetics:

```



```

RESULT 63
F64505
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: F64505
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
erson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: F64505
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-230 <BUL>
A:Cross-references: UNIPROT:Q59042; UNIPARC:UPI0000132B59; GB:U67605; GB:L77117; MID:g15
C:Genetics:
A:Map position: FOR1629578-1630270
C:Superfamily: phosphoribosylformylglycinamide synthase component I
C:Keywords: ligase

Query Match 76.5%; Score 26; DB 2; Length 230;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVEPFAQ 7
|:|:|:|
Db 29 ELVFFTQ 35

RESULT 64
AD2307
hypothetical protein alr4011 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2307
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2307
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <KUR>
A:Cross-references: UNIPROT:Q8YQ25; UNIPARC:UPI00000CE9AC; GB:BA000019; PIDN:BA075710.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr4011

Query Match 76.5%; Score 26; DB 2; Length 256;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVEPFAQ 7
|:|:|:|
Db 235 KLLEFLFLQ 241

RESULT 65
T06661
hypothetical protein T6G15.140 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C:Accession: T06661
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15791
A:Accession: T06661

```

```

A:Molecule type: DNA
A:Residues: 1-273 <BEV>
A:Cross-references: UNIPROT:Q9T0H9; UNIPARC:UPI00000AA99C; EMBL:AL049656; GSPDB:GN000062;
A:Experimental source: cultivar Columbia; BAC clone T6G15
C:Genetics:
A:Gene: ATSP:T6G15.140
A:Map position: 4
A:Superfamily: uncharacterized conserved protein
C:Introns: 48/1; 95/3; 111/3; 144/1; 220/3; 237/3
A:Authors: uncharacterized conserved protein
A:Reference number: AB1077; MUID:21537279; PMID:11679669

Query Match 76.5%; Score 26; DB 2; Length 273;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVVFFAQ 7
|:|:|:|
Db 216 LVVFFAE 221

RESULT 66
AC1342
ABC transporter (ATP-binding protein) homolog lmo21139 [imported] - Listeria monocytogene
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C:Accession: AC1342
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1342
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <GLA>
A:Cross-references: UNIPROT:Q8Y5C6; UNIPARC:UPI00000CF1DD; GB:NC_003210; PIDN:CAD00217.1
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2139

Query Match 76.5%; Score 26; DB 2; Length 300;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XLVFFAQ 7
|:|:|:|
Db 92 QLIFFAE 98

RESULT 67
A11712
ABC transporter (ATP-binding protein) homolog lin2244 [imported] - Listeria innocua (str
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C:Accession: A11712
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11712
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <GLA>
A:Cross-references: UNIPROT:Q929N0; UNIPARC:UPI00000CC7D4; GB:AL592022; PIDN:CAC97473.1;
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2244

```



Query Match 76.5%; Score 26; DB 2; Length 300;  
Best Local Similarity 57.1%; Pred. No. 1.8e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 92 QLIFFAE 98  
:|:|:|:

RESULT 68  
T20562  
hypothetical protein F07H5.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T20562  
R;Steward, C.  
submitted to the EMBL Data Library, December 1995  
A;Reference number: Z19292  
A;Accession: T20562  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-334 <WIL>  
A;Cross-references: UNIPROT:Q19185; UNIPARC:UPI000007C780; EMBL:Z68314; PIDN:CAA92663.1  
A;Experimental source: clone F07H5  
C;Genetics:  
A;Gene: CESP:F07H5.2  
A;Map position: 2  
A;Introns: 72/2; 146/3; 217/1; 280/3

Query Match 76.5%; Score 26; DB 2; Length 334;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
Db 196 KLIFFA 201  
||:|:|

RESULT 69  
MMBES  
cell fusion protein precursor - human herpesvirus 3  
C;Species: human herpesvirus 3, varicella-zoster virus  
C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 09-Jul-2004  
C;Accession: E27212  
R;Davison, A.J.; Scott, J.E.  
J. Gen. Virol. 67, 1759-1816, 1986  
A;Title: The complete DNA sequence of varicella-zoster virus.  
A;Reference number: A27345; MUID:86306657; PMID:3018124  
A;Accession: E27212  
A;Molecule type: DNA  
A;Residues: 1-340 <DAV>  
A;Cross-references: UNIPROT:P09261; UNIPARC:UPI000000175A; EMBL:X04370; NID:g59989; PIDN:  
C;Genetics:  
A;Gene: 5  
C;Superfamily: herpesvirus cell fusion protein  
C;Keywords: membrane fusion; transmembrane protein  
F;1-31/Domain: signal sequence #status predicted <SIG>  
F;32-340/Product: cell fusion protein #status predicted <CFP>  
F;115-137/Domain: transmembrane #status predicted <TM1>  
F;220-238/Domain: transmembrane #status predicted <TM3>  
F;251-269/Domain: transmembrane #status predicted <TM4>  
F;307-322/Domain: transmembrane #status predicted <TM5>

Query Match 76.5%; Score 26; DB 1; Length 340;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
Db 122 KMIFFA 127  
||:|:|

RESULT 70  
AH2097  
sorbitol dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AH2097  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguich  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AH2097  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-352 <KUR>  
A;Cross-references: UNIPROT:Q8YUK9; UNIPARC:UPI00000CE3D5; GB:BA000019; PIDN:BA874034.1  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr2335  
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 76.5%; Score 26; DB 2; Length 352;  
Best Local Similarity 57.1%; Pred. No. 2.1e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7  
Db 262 KILFFAE 268  
||:|:|

RESULT 71  
D84280  
hypothetical protein Vng1249c [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: D84280  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,  
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabi  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: D84280  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-356 <STO>  
A;Cross-references: UNIPROT:Q9HQA7; UNIPARC:UPI000006383C; GB:AE004437; NID:gl0580776;  
C;Genetics:  
A;Gene: VNG1249C

Query Match 76.5%; Score 26; DB 2; Length 356;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
Db 209 KLIFFA 214  
||:|:|

RESULT 72  
T15120  
hypothetical protein T23C6.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Dec-2004  
C;Accession: T15120  
R;Du, Z.  
submitted to the EMBL Data Library, April 1997  
A;Description: The sequence of C. elegans cosmid T23C6.  
A;Reference number: Z18295  
A;Accession: T15120  
A;Status: preliminary; translated from GB/EMBL/DBJ



A:Molecule type: DNA  
A:Residues: 1-408 <DUZ>  
A:Cross-references: UNIPROT:O02043; UNIPARC:UPI00000781F4; EMBL:AF000191; NID:g1946976;  
A:Experimental source: strain Bristol N2; clone T23C6  
C:Genetics:  
A:Gene: CESP:T23C6.5  
A:Map position: X  
A:Introns: 30/1; 56/3; 107/3; 143/1; 214/3; 240/2; 295/3; 328/1; 377/3

Query Match 76.5%; Score 26; DB 2; Length 408;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFAQ 7  
Db 36 LVFFSQ 41

RESULT 73  
T39683  
zootin-like protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C:Accession: T39683; T40195  
R:Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrel, B.G.  
submitted to the EMBL Data Library, March 1998  
A:Reference number: Z21869  
A:Accession: T39683  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-124 <OLI>  
A:Cross-references: UNIPROT:O9Y718; UNIPARC:UPI0000697C4; EMBL:AL049489; PIDN:CAB39796.  
A:Experimental source: strain 972h-1; cosmid c1778  
R:Wood, V.; Rajandream, M.A.; Barrel, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.  
submitted to the EMBL Data Library, February 1998  
A:Reference number: Z21910  
A:Accession: T40195  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 89-442 <WOO>  
A:Cross-references: UNIPARC:UPI000006AD4A; EMBL:Z97992; PIDN:CAB10796.1; GSPDB:GN000067;  
A:Experimental source: strain 972h-1; cosmid c30D10  
C:Genetics:  
A:Gene: SPDB:SPBC1778.01c; SPDB:SPBC30D10.01  
A:Map position: 2

Query Match 76.5%; Score 26; DB 2; Length 442;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFAQ 7  
Db 437 VVFFAQ 442

RESULT 74  
H81402  
probable integral membrane protein Cj0560 [imported] - Campylobacter jejuni (strain NCTC)  
C:Species: Campylobacter jejuni  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: H81402  
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel  
Nature 403, 665-668, 2000  
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A:Reference number: A81250; MUID:20150912; PMID:10688204  
A:Accession: H81402  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-442 <PAR>  
A:Cross-references: UNIPROT:Q9PHV5; UNIPARC:UPI00000C217E; GB:AL1139075; GB:AL1111168; NID  
A:Experimental source: serotype O2, strain NCTC 11168  
C:Genetics:

A:Gene: Cj0560

Query Match 76.5%; Score 26; DB 2; Length 442;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
Db 313 KLVFFA 318

RESULT 75  
F71039  
hypothetical protein PH1606 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 05-Oct-2004  
C:Accession: F71039  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: F71039  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-447 <KAW>  
A:Cross-references: UNIPROT:O59243; UNIPARC:UPI00000630DE; GB:AP000006; NID:g3236133; PI  
A:Experimental source: strain OT3  
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C:Genetics:  
A:Gene: PH1606  
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1142

Query Match 76.5%; Score 26; DB 2; Length 447;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
Db 207 KLVFFA 212

Search completed: December 29, 2005, 17:49:23  
Job time : 18.129 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds  
(without alignments)  
37.818 Million cell updates/sec

Title: US-10-009-122-4  
Perfect score: 31  
Sequence: 1 KPVFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues  
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Published Applications AA.Main:  
1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	6	3	US-09-867-847-13
2	31	100.0	6	3	US-09-867-847-21
3	31	100.0	6	3	US-09-915-092-3
4	31	100.0	6	3	US-09-915-092-11
5	31	100.0	6	3	US-09-747-408-4
6	31	100.0	6	3	US-09-747-408-12
7	31	100.0	6	5	US-10-728-028-3
8	31	100.0	6	5	US-10-728-028-11
9	31	100.0	6	5	US-10-825-958-11
10	31	100.0	6	5	US-10-825-958-19
11	31	100.0	59	4	US-10-424-599-174685
12	31	100.0	64	4	US-10-424-599-164908
13	31	100.0	102	4	US-10-424-599-203722
14	31	100.0	175	4	US-10-437-963-118848
15	31	100.0	372	4	US-10-437-963-118846
16	31	100.0	373	4	US-10-437-963-118916
17	30	96.8	420	4	US-10-437-963-118773
18	28	90.3	54	4	US-10-424-599-266901
19	28	90.3	115	4	US-10-425-115-327241
20	28	90.3	126	4	US-10-425-115-280464
21	28	90.3	159	4	US-10-425-115-193086
22	28	90.3	240	4	US-10-767-701-37567
23	28	90.3	452	4	US-10-369-493-6279
24	28	90.3	490	5	US-10-994-726-438
25	28	90.3	506	3	US-09-877-476-2
26	28	90.3	506	3	US-09-877-476-28
27	28	90.3	506	3	US-09-877-476-30

28	90.3	506	3	US-09-877-476-36	Sequence 36, Appl
28	90.3	506	4	US-10-276-977-7	Sequence 7, Appl
28	90.3	506	4	US-10-758-524-2	Sequence 2, Appl
28	90.3	506	4	US-10-758-524-28	Sequence 28, Appl
28	90.3	506	4	US-10-758-524-30	Sequence 30, Appl
28	90.3	506	4	US-10-758-524-36	Sequence 36, Appl
28	90.3	508	4	US-10-282-122A-47052	Sequence 47052, A
28	90.3	508	5	US-10-994-726-437	Sequence 437, App
28	90.3	509	5	US-10-732-923-18725	Sequence 18725, A
28	90.3	509	5	US-10-732-923-18726	Sequence 18726, A
28	90.3	509	5	US-10-732-923-18737	Sequence 18737, A
28	90.3	571	4	US-10-282-122A-51929	Sequence 51929, A
28	90.3	1089	4	US-10-369-493-2154	Sequence 2154, Ap
27	87.1	34	4	US-10-425-115-236339	Sequence 236339
27	87.1	46	4	US-10-425-115-200545	Sequence 200545,
27	87.1	47	4	US-10-424-599-232761	Sequence 232761,
27	87.1	48	4	US-10-425-115-206883	Sequence 206883,
27	87.1	56	4	US-10-437-963-176215	Sequence 176215,
27	87.1	57	4	US-10-425-114-38807	Sequence 38807, A
27	87.1	62	3	US-09-764-877-1136	Sequence 1136, Ap
27	87.1	62	4	US-10-242-515-1136	Sequence 1136, Ap
27	87.1	63	4	US-10-424-599-146372	Sequence 146372,
27	87.1	72	4	US-10-425-115-248149	Sequence 248149,
27	87.1	73	4	US-10-425-115-229605	Sequence 229605,
27	87.1	80	4	US-10-425-115-259222	Sequence 259222,
27	87.1	81	4	US-10-425-115-215979	Sequence 215979,
27	87.1	82	4	US-10-424-599-195261	Sequence 195261,
27	87.1	82	5	US-10-450-763-44156	Sequence 44156, A
27	87.1	83	4	US-10-425-115-275005	Sequence 275005,
27	87.1	88	4	US-10-424-599-259257	Sequence 259257,
27	87.1	92	4	US-10-424-599-246138	Sequence 246138,
27	87.1	96	4	US-10-424-599-207674	Sequence 207674,
27	87.1	99	4	US-10-425-115-221194	Sequence 221194,
27	87.1	103	4	US-10-424-599-182454	Sequence 182454,
27	87.1	103	4	US-10-437-963-201763	Sequence 201763,
27	87.1	104	3	US-09-823-153-4	Sequence 4, Appl
27	87.1	104	4	US-10-713-981-4	Sequence 4, Appl
27	87.1	106	4	US-10-425-115-215097	Sequence 215097,
27	87.1	107	4	US-10-424-599-207673	Sequence 207673,
27	87.1	107	4	US-10-437-963-146282	Sequence 146282,
27	87.1	125	4	US-10-425-115-289631	Sequence 289631,
27	87.1	131	4	US-10-424-599-208184	Sequence 208184,
27	87.1	131	4	US-10-424-599-221174	Sequence 221174,
27	87.1	144	5	US-10-450-763-56921	Sequence 56921, A
27	87.1	146	4	US-10-424-599-214877	Sequence 214877,
27	87.1	153	4	US-10-424-599-243854	Sequence 243854,
27	87.1	158	4	US-10-424-599-169140	Sequence 169140,
27	87.1	173	4	US-10-408-765A-1782	Sequence 1782, Ap
27	87.1	173	5	US-10-220-335-207	Sequence 207, App
27	87.1	189	4	US-10-432-198-4	Sequence 4, Appl
27	87.1	189	4	US-10-432-198-5	Sequence 5, Appl
27	87.1	189	4	US-10-432-198-6	Sequence 6, Appl
27	87.1	189	4	US-10-432-198-7	Sequence 7, Appl
27	87.1	206	4	US-10-238-075-489	Sequence 489, App
27	87.1	211	4	US-10-425-115-359320	Sequence 359320,
27	87.1	211	4	US-10-425-115-359323	Sequence 359323,
27	87.1	212	4	US-10-424-599-211252	Sequence 211252,
27	87.1	218	4	US-10-276-72A-7	Sequence 7, Appl
27	87.1	221	5	US-10-450-763-37353	Sequence 37353, A
27	87.1	221	5	US-10-450-763-53342	Sequence 53342, A
27	87.1	240	4	US-10-724-972A-7100	Sequence 7100, Ap
27	87.1	249	4	US-10-437-963-183912	Sequence 183912,
27	87.1	285	4	US-10-425-115-246512	Sequence 246512,
27	87.1	297	3	US-09-864-921-180	Sequence 180, App
27	87.1	297	5	US-10-766-682-180	Sequence 180, App
27	87.1	332	4	US-10-424-599-247557	Sequence 247557,
27	87.1	335	4	US-10-425-115-359332	Sequence 359332,
27	87.1	335	5	US-10-739-930-8473	Sequence 8473, Ap

101	27	87.1	347	4	US-10-425-114-47805	Sequence 47805, A	174	26	83.9	60	6	US-11-093-088-44	Sequence 44, Appl
102	27	87.1	351	4	US-10-275-595A-28	Sequence 28, Appl	175	26	83.9	61	4	US-10-424-599-279574	Sequence 279574, A
103	27	87.1	356	4	US-10-425-115-359329	Sequence 359329, A	176	26	83.9	61	4	US-10-767-701-48124	Sequence 48124, A
104	27	87.1	381	4	US-10-276-272A-10	Sequence 10, Appl	177	26	83.9	61	4	US-10-425-115-294863	Sequence 294863, A
105	27	87.1	388	4	US-10-437-963-102898	Sequence 102898, A	178	26	83.9	61	4	US-10-425-115-323415	Sequence 323415, A
106	27	87.1	389	4	US-10-276-272A-4	Sequence 4, Appl	179	26	83.9	62	4	US-10-424-599-148416	Sequence 148416, A
107	27	87.1	393	5	US-10-739-930-6015	Sequence 6015, Ap	180	26	83.9	65	6	US-10-125-258-43	Sequence 43, Appl
108	27	87.1	401	4	US-10-094-240-20	Sequence 20, Appl	181	26	83.9	65	6	US-11-092-429-43	Sequence 43, Appl
109	27	87.1	401	4	US-10-056-405-20	Sequence 20, Appl	182	26	83.9	65	6	US-11-092-430-43	Sequence 43, Appl
110	27	87.1	407	4	US-10-767-701-47158	Sequence 47158, A	183	26	83.9	65	6	US-11-093-225-43	Sequence 43, Appl
111	27	87.1	407	4	US-10-425-115-283373	Sequence 283373, A	184	26	83.9	65	6	US-11-092-027-43	Sequence 43, Appl
112	27	87.1	408	4	US-10-437-963-173765	Sequence 173765, A	185	26	83.9	65	6	US-11-092-427-43	Sequence 43, Appl
113	27	87.1	422	4	US-10-424-599-277445	Sequence 277445, A	186	26	83.9	65	6	US-11-093-088-43	Sequence 43, Appl
114	27	87.1	422	5	US-10-739-930-9013	Sequence 9013, Ap	187	26	83.9	68	4	US-10-424-599-190908	Sequence 190908, A
115	27	87.1	425	4	US-10-424-599-191171	Sequence 191171, A	188	26	83.9	71	4	US-10-424-599-218467	Sequence 218467, A
116	27	87.1	425	4	US-10-276-272A-6	Sequence 6, Appl	189	26	83.9	71	4	US-10-424-599-234678	Sequence 234678, A
117	27	87.1	428	4	US-10-425-115-295015	Sequence 6, Appl	190	26	83.9	71	4	US-10-425-115-211132	Sequence 211132, A
118	27	87.1	444	4	US-10-437-963-102909	Sequence 295015, A	191	26	83.9	72	5	US-10-450-763-52260	Sequence 52260, A
119	27	87.1	454	5	US-10-437-963-173765	Sequence 173765, A	192	26	83.9	75	4	US-10-425-115-185420	Sequence 185420, A
120	27	87.1	471	6	US-11-021-951-185	Sequence 2882, Ap	193	26	83.9	76	4	US-10-425-115-337684	Sequence 337684, A
121	27	87.1	478	5	US-10-486-781A-6	Sequence 185, Ap	194	26	83.9	76	4	US-10-425-115-259075	Sequence 259075, A
122	27	87.1	478	5	US-10-954-778-13	Sequence 6, Appl	195	26	83.9	82	4	US-10-425-115-350964	Sequence 350964, A
123	27	87.1	498	5	US-10-486-781A-11	Sequence 11, Appl	196	26	83.9	82	4	US-10-425-115-350964	Sequence 350964, A
124	27	87.1	581	4	US-10-282-122A-65905	Sequence 65905, A	197	26	83.9	93	4	US-10-425-115-367965	Sequence 367965, A
125	27	87.1	582	3	US-09-916-658-4	Sequence 2882, Ap	198	26	83.9	93	4	US-10-424-599-286485	Sequence 286485, A
126	27	87.1	582	3	US-09-391-104-28	Sequence 4, Appl	199	26	83.9	93	4	US-10-437-963-178420	Sequence 178420, A
127	27	87.1	582	3	US-09-801-196-27	Sequence 28, Appl	200	26	83.9	96	4	US-10-425-115-349216	Sequence 349216, A
128	27	87.1	582	3	US-09-919-497-84	Sequence 84, Appl	201	26	83.9	97	4	US-10-424-599-182131	Sequence 182131, A
129	27	87.1	582	3	US-09-916-849A-2	Sequence 27, Appl	202	26	83.9	98	4	US-10-437-963-109168	Sequence 109168, A
130	27	87.1	582	4	US-10-133-797-6	Sequence 2, Appl	203	26	83.9	99	4	US-10-424-599-289978	Sequence 289978, A
131	27	87.1	582	4	US-10-131-985-43	Sequence 6, Appl	204	26	83.9	101	4	US-10-425-114-57111	Sequence 57111, A
132	27	87.1	582	4	US-10-411-010-26	Sequence 43, Appl	205	26	83.9	105	4	US-10-424-599-210257	Sequence 210257, A
133	27	87.1	582	4	US-10-447-315-9	Sequence 26, Appl	206	26	83.9	106	4	US-10-424-599-254314	Sequence 254314, A
134	27	87.1	582	4	US-10-276-272A-19	Sequence 19, Appl	207	26	83.9	109	4	US-10-425-115-215142	Sequence 215142, A
135	27	87.1	582	5	US-10-901-417-43	Sequence 19, Appl	208	26	83.9	111	3	US-09-933-767-303	Sequence 303, App
136	27	87.1	582	5	US-10-353-264-26	Sequence 43, Appl	209	26	83.9	111	4	US-10-004-860-303	Sequence 303, App
137	27	87.1	582	5	US-10-773-446-100	Sequence 26, Appl	210	26	83.9	111	4	US-10-023-282-303	Sequence 303, App
138	27	87.1	590	4	US-10-276-272A-2	Sequence 100, App	211	26	83.9	114	4	US-10-424-599-235618	Sequence 235618, A
139	27	87.1	592	4	US-10-282-122A-65055	Sequence 2, Appl	212	26	83.9	114	4	US-10-437-963-170598	Sequence 170598, A
140	27	87.1	592	4	US-10-276-272A-12	Sequence 12, Appl	213	26	83.9	117	4	US-10-424-599-280839	Sequence 280839, A
141	27	87.1	626	4	US-10-369-493-11939	Sequence 12, Appl	214	26	83.9	118	4	US-10-047-676A-17	Sequence 17, Appl
142	27	87.1	729	4	US-10-276-272A-15	Sequence 11939, A	215	26	83.9	118	4	US-10-424-599-212612	Sequence 212612, A
143	27	87.1	738	4	US-10-221-097-48	Sequence 15, Appl	216	26	83.9	120	5	US-10-790-914-17	Sequence 17, Appl
144	27	87.1	814	4	US-10-425-115-214562	Sequence 48, Appl	217	26	83.9	120	4	US-10-425-115-257063	Sequence 257063, A
145	27	87.1	833	4	US-10-041-018-255	Sequence 214562, A	218	26	83.9	130	4	US-10-425-115-245327	Sequence 245327, A
146	27	87.1	856	4	US-10-041-018-204	Sequence 255, App	219	26	83.9	134	4	US-10-425-115-327283	Sequence 327283, A
147	27	87.1	856	4	US-10-041-018-240	Sequence 204, App	220	26	83.9	137	4	US-10-424-599-236305	Sequence 236305, A
148	27	87.1	856	4	US-10-041-018-340	Sequence 240, App	221	26	83.9	143	4	US-10-425-115-33247	Sequence 33247, A
149	27	87.1	930	4	US-10-276-272A-13	Sequence 340, App	222	26	83.9	152	4	US-10-425-115-240443	Sequence 240443, A
150	27	87.1	1034	3	US-09-841-739-2	Sequence 13, Appl	223	26	83.9	159	4	US-10-437-963-106452	Sequence 106452, A
151	27	87.1	1034	3	US-09-864-921-97	Sequence 2, Appl	224	26	83.9	176	4	US-10-424-599-222299	Sequence 222299, A
152	27	87.1	1024	4	US-10-156-733-2	Sequence 97, Appl	225	26	83.9	190	4	US-10-424-599-144945	Sequence 144945, A
153	27	87.1	1024	4	US-10-449-315-2	Sequence 2, Appl	226	26	83.9	191	3	US-09-738-626-6093	Sequence 6093, Ap
154	27	87.1	1024	5	US-10-766-682-97	Sequence 2, Appl	227	26	83.9	225	4	US-10-425-115-208680	Sequence 208680, A
155	27	87.1	1070	4	US-10-421-097-49	Sequence 97, Appl	228	26	83.9	243	4	US-10-369-493-6935	Sequence 6935, Ap
156	27	87.1	1204	3	US-09-841-739-5	Sequence 49, Appl	229	26	83.9	293	4	US-10-652-857-4	Sequence 4, Appl
157	27	87.1	1204	4	US-10-449-315-5	Sequence 5, Appl	230	26	83.9	295	4	US-10-282-122A-65569	Sequence 65569, A
158	27	87.1	2697	3	US-09-961-527A-5	Sequence 5, Appl	231	26	83.9	310	5	US-10-774-355A-1555	Sequence 1555, Ap
159	26	83.9	28	4	US-10-767-701-48268	Sequence 5, Appl	232	26	83.9	314	5	US-10-774-355A-2197	Sequence 2197, Ap
160	26	83.9	36	4	US-10-424-599-208993	Sequence 48268, A	233	26	83.9	321	5	US-10-499-065A-564	Sequence 564, App
161	26	83.9	37	4	US-10-425-115-343187	Sequence 208993, A	234	26	83.9	343	4	US-10-156-761-9520	Sequence 9520, Ap
162	26	83.9	45	5	US-10-472-928-4052	Sequence 343187, A	235	26	83.9	344	4	US-10-210-173-42	Sequence 42, Appl
163	26	83.9	51	4	US-10-437-963-142406	Sequence 142406, Ap	236	26	83.9	363	4	US-10-437-963-176802	Sequence 176802, A
164	26	83.9	53	4	US-10-424-599-197895	Sequence 197895, A	237	26	83.9	373	4	US-10-437-963-125070	Sequence 125070, A
165	26	83.9	53	4	US-10-425-114-49675	Sequence 49675, A	238	26	83.9	384	5	US-10-501-282-6210	Sequence 6210, Ap
166	26	83.9	55	4	US-10-437-963-164041	Sequence 164041, A	239	26	83.9	390	4	US-10-369-493-6541	Sequence 6541, Ap
167	26	83.9	59	4	US-10-425-115-366583	Sequence 366583, A	240	26	83.9	390	5	US-10-732-923-7871	Sequence 7871, Ap
168	26	83.9	60	6	US-10-125-258-44	Sequence 44, Appl	241	26	83.9	393	4	US-10-369-493-13098	Sequence 13098, A
169	26	83.9	60	6	US-11-092-429-44	Sequence 44, Appl	242	26	83.9	397	4	US-10-017-161-2220	Sequence 2220, Ap
170	26	83.9	60	6	US-11-092-430-44	Sequence 44, Appl	243	26	83.9	397	4	US-10-292-798-1866	Sequence 1866, Ap
171	26	83.9	60	6	US-11-093-225-44	Sequence 44, Appl	244	26	83.9	400	5	US-10-739-930-8089	Sequence 8089, Ap
172	26	83.9	60	6	US-11-092-027-44	Sequence 44, Appl	245	26	83.9	404	4	US-10-369-493-15092	Sequence 15092, A
173	26	83.9	60	6	US-11-092-427-44	Sequence 44, Appl	246	26	83.9	414	4	US-10-369-493-11566	Sequence 11566, A
										414	4	US-10-282-122A-48315	Sequence 48315, A

```

247 26 83.9 426 3 US-09-738-626-6036
248 26 83.9 426 4 US-10-627-476-424
249 26 83.9 431 5 US-10-495-148-21
250 26 83.9 431 5 US-10-732-923-11170
251 26 83.9 437 5 US-10-501-282-5896
252 26 83.9 442 4 US-10-437-963-145134
253 26 83.9 444 4 US-10-369-493-9766
254 26 83.9 446 5 US-10-732-923-23883
255 26 83.9 459 4 US-10-369-493-18271
256 26 83.9 459 5 US-10-732-923-23570
257 26 83.9 465 4 US-10-424-599-254007
258 26 83.9 466 5 US-10-732-923-11191
259 26 83.9 470 4 US-10-437-963-155526
260 26 83.9 483 4 US-10-369-493-5486
261 26 83.9 483 4 US-10-369-493-5487
262 26 83.9 504 6 US-11-097-143-21684
263 26 83.9 518 4 US-10-032-585-7864
264 26 83.9 526 4 US-10-369-493-3924
265 26 83.9 536 4 US-10-424-599-212613
266 26 83.9 548 4 US-10-282-122A-63246
267 26 83.9 581 6 US-11-097-143-15831
268 26 83.9 618 5 US-10-450-763-56476
269 26 83.9 641 5 US-10-450-763-55856
270 26 83.9 661 4 US-10-425-115-330488
271 26 83.9 681 4 US-10-335-977-5995
272 26 83.9 690 4 US-10-425-114-61393
273 26 83.9 698 4 US-10-437-963-132561
274 26 83.9 712 4 US-10-335-977-5996
275 26 83.9 717 4 US-10-335-977-5997
276 26 83.9 749 4 US-10-369-493-22359
277 26 83.9 754 6 US-11-097-143-23787
278 26 83.9 860 6 US-11-097-143-21294
279 26 83.9 888 4 US-10-282-122A-63048
280 26 83.9 891 6 US-11-097-143-26673
281 26 83.9 919 5 US-10-200-545-95
282 26 83.9 960 4 US-10-437-963-129061
283 26 83.9 976 5 US-10-732-923-1219
284 26 83.9 994 4 US-10-437-963-129064
285 26 83.9 1082 4 US-10-282-122A-49664
286 25 80.6 6 3 US-09-867-847-7
287 25 80.6 6 3 US-09-867-847-11
288 25 80.6 6 3 US-09-867-847-19
289 25 80.6 6 3 US-09-867-847-20
290 25 80.6 6 3 US-09-972-475-9
291 25 80.6 6 3 US-09-915-092-1
292 25 80.6 6 3 US-09-915-092-9
293 25 80.6 6 3 US-09-915-092-10
294 25 80.6 6 3 US-09-915-092-28
295 25 80.6 6 3 US-09-956-625-25
296 25 80.6 6 3 US-09-747-408-1
297 25 80.6 6 3 US-09-747-408-3
298 25 80.6 6 3 US-09-747-408-10
299 25 80.6 6 3 US-09-747-408-11
300 25 80.6 6 4 US-10-463-729-9

```

# ALIGNMENTS

```

RESULT 1
US-09-867-847-13
; Sequence 13, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

```

```

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-13

```

```

Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KPVFFA 6
Db 1 KPVFFA 6

```

## RESULT 2

```

US-09-867-847-21
; Sequence 21, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-21

```

```

Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KPVFFA 6
Db 1 KPVFFA 6

```

## RESULT 3

```

US-09-915-092-3
; Sequence 3, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert

```

```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-3

Query Match      100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6

RESULT 4
US-09-915-092-11
; Sequence 11, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-11

Query Match      100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6

RESULT 5
US-09-747-408-4
; Sequence 4, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-4

Query Match      100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6

RESULT 6
US-09-747-408-12
; Sequence 12, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-12

Query Match      100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6

RESULT 7
US-10-728-028-3
; Sequence 3, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-728-028-3

Query Match      100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6
```

; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-728-028-3

Query Match 100.0%; Score 31; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
| | | | |  
Db 1 KPVFFA 6

## RESULT 8

US-10-728-028-11  
; Sequence 11, Application US/10728028  
; Publication No. US20050048000A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: KONG, Xianqi  
; APPLICANT: CHALIFOUR, Robert  
; APPLICANT: MIGNEAULT, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: NEI-139CP  
; CURRENT APPLICATION NUMBER: US/10/728,028  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: 60/443291  
; PRIOR FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: 09/915092  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct

## US-10-728-028-11

Query Match 100.0%; Score 31; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
| | | | |  
Db 1 KPVFFA 6

## RESULT 9

US-10-825-958-11  
; Sequence 11, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11

; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-10-825-958-11

Query Match 100.0%; Score 31; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
| | | | |  
Db 1 KPVFFA 6

## RESULT 10

US-10-825-958-19  
; Sequence 19, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (6)  
; OTHER INFORMATION: AMIDATION  
US-10-825-958-19

Query Match 100.0%; Score 31; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
| | | | |  
Db 1 KPVFFA 6

## RESULT 11

US-10-424-599-174685  
; Sequence 174685, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 174685  
; LENGTH: 59  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_12875C.1.pep  
US-10-424-599-174685

Query Match 100.0%; Score 31; DB 4; Length 59;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
|||  
Db 11 KVFVFA 16

## RESULT 12

US-10-424-599-164908  
; Sequence 164908, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 164908  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_11992C.1.pep  
US-10-424-599-164908

Query Match 100.0%; Score 31; DB 4; Length 64;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
|||  
Db 34 KVFVFA 39

## RESULT 13

US-10-424-599-203722  
; Sequence 203722, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 203722  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_25988C.1.pep  
US-10-424-599-203722

Query Match 100.0%; Score 31; DB 4; Length 102;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
|||  
Db 5 KVFVFA 10

## RESULT 14

US-10-437-963-118848  
; Sequence 118848, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 118848  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_22120C.1.pep  
US-10-437-963-118848

Query Match 100.0%; Score 31; DB 4; Length 175;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
|||  
Db 80 KVFVFA 85

## RESULT 15

US-10-437-963-118846  
; Sequence 118846, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 118846  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(372)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT4530\_22119C.1.pep  
US-10-437-963-118846

Query Match 100.0%; Score 31; DB 4; Length 372;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
Db 121 KVFVFA 126

## RESULT 16

US-10-437-963-138916

Sequence 138916, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barabuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 138916

LENGTH: 373

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT4530\_4025C.1.pep

US-10-437-963-138916

Query Match 100.0%; Score 31; DB 4; Length 373;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
Db 80 KVFVFA 85

## RESULT 17

US-10-437-963-118773

Sequence 118773, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barabuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 118773

LENGTH: 420

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT4530\_22052C.1.pep

US-10-437-963-118773

Query Match 96.8%; Score 30; DB 4; Length 420;

Best Local Similarity 83.3%; Pred. No. 5.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
Db 355 KVFVFA 360

## RESULT 18

US-10-424-599-266901

Sequence 266901, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 266901

LENGTH: 54

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(54)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_83031C.1.pep

US-10-424-599-266901

Query Match 90.3%; Score 28; DB 4; Length 54;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
Db 18 KVFVFA 23

## RESULT 19

US-10-425-115-327241

Sequence 327241, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 327241

LENGTH: 115

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577\_61513C.1.pep

US-10-425-115-327241

Query Match 90.3%; Score 28; DB 4; Length 115;

Best Local Similarity 83.3%; Pred. No. 3.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



QY 1 KFVFFA 6  
|||||:  
Db 72 KFVFFS 77

## RESULT 20

US-10-425-115-290464  
; Sequence 290464, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 290464  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_27992C.1.pep  
US-10-425-115-290464

Query Match 90.3%; Score 28; DB 4; Length 126;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
|||||:  
Db 99 KFLFFA 104

## RESULT 21

US-10-425-115-193086  
; Sequence 193086, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 193086  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(159)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_10767C.1.pep  
US-10-425-115-193086

Query Match 90.3%; Score 28; DB 4; Length 159;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
|||||:  
Db 89 RFVFFA 94

## RESULT 22

US-10-767-701-37567  
; Sequence 37567, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 37567  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C3123\_1.pep  
US-10-767-701-37567

Query Match 90.3%; Score 28; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
|||||:  
Db 155 KFVFFS 160

## RESULT 23

US-10-369-493-6279  
; Sequence 6279, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 6279  
; LENGTH: 452  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-6279

Query Match 90.3%; Score 28; DB 4; Length 452;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
|||||:  
Db 291 RFVFFA 296

## RESULT 24

US-10-994-726-438  
; Sequence 438, Application US/10994726  
; Publication No. US20050147999A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: Lyme Disease Vaccines  
; FILE REFERENCE: PB481DI

```

; CURRENT APPLICATION NUMBER: US/10/994,726
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 09/830,230
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 438
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-994-726-438

```

```

Query Match          90.3%; Score 28; DB 5; Length 490;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVFVFA 6
Db      23 RFVFFA 28

```

```

RESULT 25
US-09-877-476-2
; Sequence 2, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-877-476-2

```

```

Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVFVFA 6
Db      356 KFLFFA 361

```

```

RESULT 26
US-09-877-476-28
; Sequence 28, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476

```

```

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ
; OTHER INFORMATION: ID NO:4) and 3' 330 amino acids from A. thaliana
; OTHER INFORMATION: FAE1 (SEQ ID NO:2); designated Bn176
US-09-877-476-28

```

```

Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVFVFA 6
Db      356 KFLFFA 361

```

```

RESULT 27
US-09-877-476-30
; Sequence 30, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 399 amino acids from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:2) and 3' 107 amino acids from B. napus
; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399
; NAME/KEY: VARIANT
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa = Pro or Gln
US-09-877-476-30

```

```

Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVFVFA 6
Db      356 KFLFFA 361

```

```

RESULT 28
US-09-877-476-36
; Sequence 36, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476

```

```
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 506 amino acids from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
; OTHER INFORMATION: At K92R; hypothetical
US-09-877-476-36

Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361

RESULT 29
US-10-276-977-7
; Sequence 7, Application US/10276977
; Publication No. US20040049806A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
; APPLICANT: KUNST, LUBKA
; APPLICANT: SMITH, MARK A.
; APPLICANT: MOON, HANGSIK
; TITLE OF INVENTION: NUCLEIC ACID ENCODING A PLANT VERY LONG CHAIN
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/276,977
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/IB01/01140
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,789
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-276-977-7

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361

RESULT 30
US-10-758-524-2
; Sequence 2, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758,524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-758-524-2
```

```
; PRIOR APPLICATION NUMBER: 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-758-524-2

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361

RESULT 31
US-10-758-524-28
; Sequence 28, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758,524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ
; OTHER INFORMATION: ID NO:4) and 3' 330 amino acids from A. thaliana
; OTHER INFORMATION: FAE1 (SEQ ID NO:2); designated Bn176
US-10-758-524-28

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361

RESULT 32
US-10-758-524-30
; Sequence 30, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758,524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
```

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 399 amino acids from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:2) and 3' 107 amino acids from B. napus
; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa = Pro or Gln
US-10-758-524-30

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFFA 6
Db      356 KFLFFA 361
      ||:||||
      ||:||||

RESULT 33
US-10-758-524-36
; Sequence 36, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758.524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 506 amino acids from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
; OTHER INFORMATION: At K92R; hypothetical
US-10-758-524-36

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFFA 6
Db      356 KFLFFA 361
      ||:||||
      ||:||||

RESULT 34
US-10-282-122A-47052
; Sequence 47052, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

```

```

; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 47052
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-282-122A-47052

Query Match          90.3%; Score 28; DB 4; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFFA 6
Db      41 RFVFFA 46
      ||:||||
      ||:||||

RESULT 35
US-10-994-726-437
; Sequence 437, Application US/10994726
; Publication No. US20050147999A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481D1
; CURRENT APPLICATION NUMBER: US/10/994,726
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 09/830,230
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 437
; LENGTH: 508

```

```
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-994-726-437

Query Match          90.3%; Score 28; DB 5; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      :|||||
Db      41 RFVFFA 46

RESULT 36
US-10-732-923-18725
; Sequence 18725, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18725
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica juncea
US-10-732-923-18725

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      :|||||
Db      359 KFLFFA 364

RESULT 37
US-10-732-923-18726
; Sequence 18726, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18726
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica juncea
US-10-732-923-18726

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      :|||||
Db      358 KFLFFA 363

RESULT 38
US-10-732-923-18737
; Sequence 18737, Application US/10732923
; Publication No. US20050108791A1
```

---

```
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18737
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica rapa
US-10-732-923-18737

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      :|||||
Db      358 KFLFFA 363

RESULT 39
US-10-282-122A-51929
; Sequence 51929, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51929
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51929
```

```
Query Match      90.3%; Score 28; DB 4; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
Db      314 KFMFFA 319

RESULT 40
US-10-369-493-2154
; Sequence 2154, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2154
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1089)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2154

Query Match      90.3%; Score 28; DB 4; Length 1089;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
Db      13 KVFVFS 18

RESULT 41
US-10-425-115-236339
; Sequence 236339, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 236339
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_147123C.1.pep
US-10-425-115-236339

Query Match      87.1%; Score 27; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KVFVFP 5
Db      23 KVFVFP 27

RESULT 42
US-10-425-115-200545
; Sequence 200545, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 200545
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_114485C.1.pep
US-10-425-115-200545

Query Match      87.1%; Score 27; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFP 5
Db      25 KVFVFP 29

RESULT 43
US-10-424-599-232761
; Sequence 232761, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 232761
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52207C.1.pep
US-10-424-599-232761

Query Match      87.1%; Score 27; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFP 5
Db      11 KVFVFP 15

RESULT 44
US-10-425-115-206883
; Sequence 206883, Application US/10425115
```

```
; Publication No. US200400214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 206893
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_120267C.1.pap
US-10-425-115-206893

Query Match      87.1%; Score 27; DB 4; Length 48;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 15 KFAFFA 20

RESULT 45
US-10-437-963-176215
; Publication 176215, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176215
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73986C.1.pap
US-10-437-963-176215

Query Match      87.1%; Score 27; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
Db 13 KVFVFF 17

RESULT 46
US-10-425-114-38807
; Sequence 38807, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 38807
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700684806_FLI.pap
US-10-425-114-38807

Query Match      87.1%; Score 27; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
Db 29 KVFVFF 33

RESULT 47
US-09-764-877-1136
; Sequence 1136, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1136
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1136

Query Match      87.1%; Score 27; DB 3; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
Db 31 KVFVFF 35

RESULT 48
US-10-242-515-1136
; Sequence 1136, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
```

```
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1136
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (55)-
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (60)-
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-515-1136

Query Match      87.1%; Score 27; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFVFF 5
        |||||
Db      31 KFVFF 35

RESULT 49
US-10-424-599-146372
; Sequence 146372, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 146372
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_103191C.1.pep
US-10-424-599-146372

Query Match      87.1%; Score 27; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFVFF 5
        |||||
```

```
Db      18 KFVFF 22

RESULT 50
US-10-425-115-248149
; Sequence 248149, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 248149
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_157899C.1.pep
US-10-425-115-248149

Query Match      87.1%; Score 27; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFVFF 5
        |||||
Db      67 KFVFF 71

RESULT 51
US-10-425-115-229605
; Sequence 229605, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 229605
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_140993C.1.pep
US-10-425-115-229605

Query Match      87.1%; Score 27; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFVFF 5
        |||||
Db      1 KFVFF 5

RESULT 52
US-10-425-115-259222
```



```
; Sequence 259222, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 259222
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_167996C.1.pep
US-10-425-115-259222

Query Match      87.1%; Score 27; DB 4; Length 80;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFF 6
Db      66 KTFVFF 71

RESULT 53
US-10-425-115-215979
; Sequence 215979, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215979
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_128569C.1.pep
US-10-425-115-215979

Query Match      87.1%; Score 27; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
Db      30 KVFVFF 34

RESULT 54
US-10-424-599-195261
; Sequence 195261, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 275005
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Zea mays
```

```
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 195261
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_18348C.1.pep
US-10-424-599-195261

Query Match      87.1%; Score 27; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
Db      66 KVFVFF 70

RESULT 55
US-10-450-763-44156
; Sequence 44156, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44156
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-44156

Query Match      87.1%; Score 27; DB 5; Length 82;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 6
Db      11 EFVFFA 16

RESULT 56
US-10-425-115-275005
; Sequence 275005, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 275005
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Zea mays
```

; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_182395C.1.pep  
US-10-425-115-275005

Query Match 87.1%; Score 27; DB 4; Length 83;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 49 KVFVF 53

RESULT 57  
US-10-424-599-259257  
; Sequence 259257, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 259257  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_76133C.1.pep  
US-10-424-599-259257

Query Match 87.1%; Score 27; DB 4; Length 88;  
Best Local Similarity 66.7%; Pred. No. 4.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
Db 13 RFIFFA 18

RESULT 58  
US-10-424-599-246138  
; Sequence 246138, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 246138  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(92)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_64294C.1.pep  
US-10-424-599-246138

Query Match 87.1%; Score 27; DB 4; Length 92;

Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 71 KVFVF 75

RESULT 59  
US-10-424-599-207674  
; Sequence 207674, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 207674  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_29556C.1.pep  
US-10-424-599-207674

Query Match 87.1%; Score 27; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 5 KVFVF 9

RESULT 60  
US-10-425-115-221194  
; Sequence 221194, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 221194  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_133318C.1.pep  
US-10-425-115-221194

Query Match 87.1%; Score 27; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 20 KVFVF 24

RESULT 61

US-10-424-599-182454  
; Sequence 182454, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 182454  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_135769C.1.pep  
US-10-424-599-182454

Query Match 87.1%; Score 27; DB 4; Length 103;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5  
|||  
Db 30 KVFVF 34

RESULT 62  
US-10-437-963-201763  
; Sequence 201763, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 201763  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_97105C.1.pep  
US-10-437-963-201763

Query Match 87.1%; Score 27; DB 4; Length 103;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5  
|||  
Db 43 KVFVF 47

RESULT 63  
US-09-823-153-4  
; Sequence 4, Application US/09823153  
; Patent No. US20020025540A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company

; APPLICANT: Roberts, Susan  
; APPLICANT: Pak, Roger  
; APPLICANT: Lewis, Martin  
; APPLICANT: Smith, David  
; APPLICANT: Hendrick, Joseph  
; APPLICANT: Vinitsky, Alexander  
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX  
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF  
; FILE REFERENCE: D0004  
; CURRENT APPLICATION NUMBER: US/09/823,153  
; CURRENT FILING DATE: 2001-07-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 104  
; TYPE: PRT  
; ORGANISM: Human Beta App  
US-09-823-153-4

Query Match 87.1%; Score 27; DB 3; Length 104;  
Best Local Similarity 83.3%; Pred. No. 5.4e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
:||||  
Db 21 EFVFFA 26

RESULT 64  
US-10-713-981-4  
; Sequence 4, Application US/10713981  
; Publication No. US20040121411A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; APPLICANT: Roberts, Susan  
; APPLICANT: Pak, Roger  
; APPLICANT: Lewis, Martin  
; APPLICANT: Smith, David  
; APPLICANT: Hendrick, Joseph  
; APPLICANT: Vinitsky, Alexander  
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX  
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF  
; FILE REFERENCE: D0004 DIV  
; CURRENT APPLICATION NUMBER: US/10/713,981  
; CURRENT FILING DATE: 2003-11-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 104  
; TYPE: PRT  
; ORGANISM: Human Beta App  
US-10-713-981-4

Query Match 87.1%; Score 27; DB 4; Length 104;  
Best Local Similarity 83.3%; Pred. No. 5.4e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
:||||  
Db 21 EFVFFA 26

RESULT 65  
US-10-425-115-215097  
; Sequence 215097, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 215097  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_127767C.1.pep  
US-10-425-115-215097

Query Match 87.1%; Score 27; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 97 KVFVF 101

RESULT 66  
US-10-424-599-207673  
; Sequence 207673, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 207673  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_29555C.1.pep  
US-10-424-599-207673

Query Match 87.1%; Score 27; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 16 KVFVF 20

RESULT 67  
US-10-437-963-146282  
; Sequence 146282, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 146282

; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_46920C.1.pep  
US-10-437-963-146282

Query Match 87.1%; Score 27; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 18 KVFVF 22

RESULT 68  
US-10-424-599-278159  
; Sequence 278159, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 278159  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_93200C.1.pep  
US-10-424-599-278159

Query Match 87.1%; Score 27; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 5 KVFVF 9

RESULT 69  
US-10-425-115-208261  
; Sequence 208261, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 208261  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_121527C.1.pep  
US-10-425-115-208261

Query Match 87.1%; Score 27; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFF 5
Db 33 KPVFF 37

RESULT 70
US-10-425-115-286779
; Sequence 286779, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286779
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(110)
; OTHER INFORMATION: unsure at all Xaa locations
;
; OTHER INFORMATION: Clone ID: MRT4577_24637C.1.pep
US-10-425-115-286779

Query Match 87.1%; Score 27; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFF 5
Db 96 KPVFF 100

RESULT 71
US-09-864-408A-4214
; Sequence 4214, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4214
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-4214

Query Match 87.1%; Score 27; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFF 5

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFF 5
Db 67 KPVFF 71

RESULT 72
US-10-425-115-256025
; Sequence 256025, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 256025
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165087C.1.pep
US-10-425-115-256025

Query Match 87.1%; Score 27; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFF 5
Db 47 KPVFF 51

RESULT 73
US-10-425-115-289631
; Sequence 289631, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 289631
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_27231C.1.pep
US-10-425-115-289631

Query Match 87.1%; Score 27; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFF 5
Db 26 KPVFF 30

RESULT 74
US-10-424-599-208184
; Sequence 208184, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
```

; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 208184  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_30014C.1.pep  
US-10-424-599-208184

Query Match 87.1%; Score 27; DB 4; Length 131;  
Best Local Similarity 66.7%; Pred. No. 6.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
|||:  
Db 118 KPIFFS 123

RESULT 75  
US-10-424-599-221174  
; Sequence 221174, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 221174  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_41750C.1.pep  
US-10-424-599-221174

Query Match 87.1%; Score 27; DB 4; Length 131;  
Best Local Similarity 83.3%; Pred. No. 6.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
|||:  
Db 83 KPAFFA 88

Search completed: December 29, 2005, 18:49:39  
Job time : 70.2903 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds  
(without alignments)  
24.763 Million cell updates/sec

Title: US-10-009-122-4

Perfect score: 31

Sequence: 1 KVFVFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: /cgm2\_6/ptodata/1/iaa/5 COMB.pap:\*\*
- 2: /cgm2\_6/ptodata/1/iaa/6 COMB.pap:\*\*
- 3: /cgm2\_6/ptodata/1/iaa/H COMB.pap:\*\*
- 4: /cgm2\_6/ptodata/1/iaa/PCRUS COMB.pap:\*\*
- 5: /cgm2\_6/ptodata/1/iaa/RE COMB.pap:\*\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles1.pap:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	6	2	US-09-747-408-4
2	31	100.0	6	2	US-09-747-408-12
3	30	96.8	1283	2	US-09-248-796A-18091
4	28	90.3	490	2	US-09-830-230A-438
5	28	90.3	506	2	US-08-888-998-2
6	28	90.3	506	2	US-09-362-633-2
7	28	90.3	506	2	US-09-877-476-2
8	28	90.3	506	2	US-09-877-476-28
9	28	90.3	506	2	US-09-877-476-30
10	28	90.3	506	2	US-09-877-476-36
11	28	90.3	508	2	US-09-830-230A-437
12	27	87.1	67	2	US-09-248-796A-26311
13	27	87.1	82	2	US-09-513-999C-4859
14	27	87.1	98	2	US-09-270-767-40694
15	27	87.1	98	2	US-09-270-767-55910
16	27	87.1	104	2	US-09-823-153-4
17	27	87.1	116	2	US-09-270-767-57813
18	27	87.1	238	2	US-09-902-540-10859
19	27	87.1	240	2	US-09-134-001C-5445
20	27	87.1	266	2	US-09-270-767-42516
21	27	87.1	320	2	US-09-248-796A-19539
22	27	87.1	340	2	US-09-270-767-40453
23	27	87.1	340	2	US-09-270-767-55669
24	27	87.1	475	2	US-09-270-767-45548
25	27	87.1	525	2	US-09-270-767-34763
26	27	87.1	525	2	US-09-270-767-49980
27	27	87.1	579	2	US-08-704-711A-1

28	87.1	579	2	US-09-521-220-1	Sequence 1, Appli
29	87.1	582	2	US-08-704-711A-2	Sequence 2, Appli
30	87.1	582	2	US-08-448-489-1	Sequence 1, Appli
31	87.1	582	2	US-09-211-704A-9	Sequence 9, Appli
32	87.1	582	2	US-09-521-220-2	Sequence 2, Appli
33	87.1	582	2	US-09-391-104-28	Sequence 28, Appli
34	87.1	582	2	US-09-919-497-84	Sequence 84, Appli
35	87.1	582	2	US-09-689-730-1	Sequence 1, Appli
36	87.1	1024	2	US-10-449-315-2	Sequence 2, Appli
37	87.1	1204	2	US-10-449-315-5	Sequence 5, Appli
38	83.9	45	2	US-09-270-767-37091	Sequence 37091, A
39	83.9	45	2	US-09-270-767-52308	Sequence 52308, A
40	83.9	46	2	US-09-798-635A-41	Sequence 41, Appli
41	83.9	60	2	US-10-125-258-44	Sequence 44, Appli
42	83.9	61	2	US-09-583-110-4885	Sequence 4885, Ap
43	83.9	65	2	US-10-125-258-43	Sequence 43, Appli
44	83.9	84	2	US-09-270-767-60733	Sequence 60733, A
45	83.9	104	2	US-09-621-976-6739	Sequence 6739, Ap
46	83.9	111	2	US-09-205-258-303	Sequence 303, App
47	83.9	111	2	US-10-004-860-303	Sequence 303, App
48	83.9	118	2	US-09-627-376-17	Sequence 17, Appli
49	83.9	118	2	US-10-047-676B-17	Sequence 17, Appli
50	83.9	156	2	US-09-270-767-45241	Sequence 45241, A
51	83.9	177	2	US-09-270-767-35390	Sequence 35390, A
52	83.9	177	2	US-09-270-767-50607	Sequence 50607, A
53	83.9	186	2	US-09-251-645-4	Sequence 4, Appli
54	83.9	201	2	US-09-270-767-33463	Sequence 33463, A
55	83.9	201	2	US-09-270-767-48680	Sequence 48680, A
56	83.9	249	2	US-09-270-767-38186	Sequence 38186, A
57	83.9	249	2	US-09-270-767-53403	Sequence 53403, A
58	83.9	249	2	US-09-248-796A-27128	Sequence 27128, A
59	83.9	320	2	US-09-830-910-2	Sequence 2, Appli
60	83.9	328	2	US-09-248-796A-15301	Sequence 15301, A
61	83.9	394	2	US-09-270-767-41366	Sequence 41366, A
62	83.9	394	2	US-09-270-767-56582	Sequence 56582, A
63	83.9	402	2	US-09-252-991A-25289	Sequence 25289, A
64	83.9	414	2	US-09-902-540-11308	Sequence 11308, A
65	83.9	426	2	US-09-602-787A-424	Sequence 424, App
66	83.9	437	2	US-09-489-039A-8958	Sequence 8958, Ap
67	83.9	446	2	US-09-252-991A-17185	Sequence 17185, A
68	83.9	453	2	US-09-489-039A-8303	Sequence 8303, Ap
69	83.9	493	2	US-09-252-991A-28992	Sequence 28992, A
70	83.9	557	2	US-09-540-236-2206	Sequence 2206, Ap
71	83.9	573	2	US-09-489-039A-11884	Sequence 11884, A
72	83.9	597	2	US-09-252-991A-22560	Sequence 22560, A
73	83.9	745	2	US-09-902-540-10275	Sequence 10275, A
74	83.9	892	2	US-09-540-236-2074	Sequence 2074, Ap
75	80.6	6	1	US-08-612-785B-9	Sequence 9, Appli
76	80.6	6	2	US-08-703-675C-32	Sequence 32, Appli
77	80.6	6	2	US-08-617-267C-9	Sequence 9, Appli
78	80.6	6	2	US-09-747-408-1	Sequence 1, Appli
79	80.6	6	2	US-09-747-408-3	Sequence 3, Appli
80	80.6	6	2	US-09-747-408-10	Sequence 10, Appli
81	80.6	6	2	US-09-747-408-11	Sequence 11, Appli
82	80.6	7	1	US-08-127-904-14	Sequence 14, Appli
83	80.6	7	1	US-08-612-785B-7	Sequence 7, Appli
84	80.6	7	1	US-08-703-675C-30	Sequence 30, Appli
85	80.6	7	2	US-08-617-267C-7	Sequence 7, Appli
86	80.6	7	2	US-09-264-709A-13	Sequence 13, Appli
87	80.6	7	2	US-09-747-408-2	Sequence 2, Appli
88	80.6	7	2	US-09-747-408-18	Sequence 18, Appli
89	80.6	7	2	US-09-747-408-19	Sequence 19, Appli
90	80.6	7	4	FCT-US94-10475-14	Sequence 14, Appli
91	80.6	8	1	US-08-612-785B-5	Sequence 5, Appli
92	80.6	8	1	US-08-630-645-1	Sequence 1, Appli
93	80.6	8	2	US-08-703-675C-28	Sequence 28, Appli
94	80.6	8	2	US-08-617-267C-5	Sequence 5, Appli
95	80.6	8	2	US-09-095-106A-44	Sequence 44, Appli
96	80.6	8	2	US-08-766-596A-1	Sequence 1, Appli
97	80.6	8	4	US-09-668-314C-73	Sequence 73, Appli
98	80.6	8	4	PCT-US96-10220-1	Sequence 1, Appli
99	80.6	9	2	US-08-766-596A-64	Sequence 64, Appli
100	80.6	9	2	US-09-747-408-20	Sequence 20, Appli



101	25	80.6	10	2	US-08-970-833-3	Sequence 3, Appli	174	25	80.6	28	1	US-08-293-284A-4	Sequence 4, Appli
102	25	80.6	10	2	US-09-724-961-20	Sequence 20, Appli	175	25	80.6	28	1	US-08-461-216-2	Sequence 2, Appli
103	25	80.6	10	2	US-09-724-961-21	Sequence 21, Appli	176	25	80.6	28	2	US-09-388-890-2	Sequence 3, Appli
104	25	80.6	10	2	US-09-724-961-22	Sequence 22, Appli	177	25	80.6	28	2	US-09-388-890-3	Sequence 3, Appli
105	25	80.6	10	2	US-09-724-961-23	Sequence 23, Appli	178	25	80.6	28	2	US-09-388-890-4	Sequence 4, Appli
106	25	80.6	10	2	US-09-724-961-24	Sequence 24, Appli	179	25	80.6	28	2	US-09-388-890-5	Sequence 5, Appli
107	25	80.6	10	2	US-09-580-018-20	Sequence 20, Appli	180	25	80.6	28	2	US-09-388-890-6	Sequence 6, Appli
108	25	80.6	10	2	US-09-580-018-21	Sequence 21, Appli	181	25	80.6	28	2	US-09-388-890-7	Sequence 7, Appli
109	25	80.6	10	2	US-09-580-018-22	Sequence 22, Appli	182	25	80.6	28	2	US-09-388-890-8	Sequence 8, Appli
110	25	80.6	10	2	US-09-580-018-23	Sequence 23, Appli	183	25	80.6	28	2	US-09-388-890-9	Sequence 9, Appli
111	25	80.6	10	2	US-09-580-018-24	Sequence 24, Appli	184	25	80.6	28	2	US-09-388-890-10	Sequence 10, Appli
112	25	80.6	10	2	US-09-724-551-20	Sequence 20, Appli	185	25	80.6	28	2	US-09-388-890-11	Sequence 11, Appli
113	25	80.6	10	2	US-09-724-551-21	Sequence 21, Appli	186	25	80.6	28	2	US-09-388-890-12	Sequence 12, Appli
114	25	80.6	10	2	US-09-724-551-22	Sequence 22, Appli	187	25	80.6	28	2	US-09-388-890-13	Sequence 13, Appli
115	25	80.6	10	2	US-09-724-551-23	Sequence 23, Appli	188	25	80.6	28	2	US-09-388-890-14	Sequence 14, Appli
116	25	80.6	10	2	US-09-724-551-24	Sequence 24, Appli	189	25	80.6	28	2	US-08-723-661B-1	Sequence 1, Appli
117	25	80.6	10	2	US-09-724-940-20	Sequence 20, Appli	190	25	80.6	28	2	US-08-723-661B-2	Sequence 2, Appli
118	25	80.6	10	2	US-09-724-940-21	Sequence 21, Appli	191	25	80.6	28	2	US-09-660-954-2	Sequence 3, Appli
119	25	80.6	10	2	US-09-724-940-22	Sequence 22, Appli	192	25	80.6	28	2	US-09-660-954-3	Sequence 4, Appli
120	25	80.6	10	2	US-09-724-940-23	Sequence 23, Appli	193	25	80.6	28	2	US-09-660-954-4	Sequence 5, Appli
121	25	80.6	10	2	US-09-724-940-24	Sequence 24, Appli	194	25	80.6	28	2	US-09-660-954-5	Sequence 6, Appli
122	25	80.6	11	1	US-08-630-645-14	Sequence 14, Appli	195	25	80.6	28	2	US-09-660-954-6	Sequence 7, Appli
123	25	80.6	11	1	US-08-766-596A-14	Sequence 14, Appli	196	25	80.6	28	2	US-09-660-954-7	Sequence 8, Appli
124	25	80.6	11	2	US-09-988-842-9	Sequence 9, Appli	197	25	80.6	28	2	US-09-660-954-8	Sequence 9, Appli
125	25	80.6	11	2	US-09-988-842-25	Sequence 25, Appli	198	25	80.6	28	2	US-09-660-954-9	Sequence 10, Appli
126	25	80.6	11	4	PCT-US96-10220-14	Sequence 14, Appli	199	25	80.6	28	2	US-09-660-954-10	Sequence 11, Appli
127	25	80.6	14	2	US-09-594-366-5	Sequence 5, Appli	200	25	80.6	28	2	US-09-660-954-11	Sequence 12, Appli
128	25	80.6	14	2	US-09-992-800-5	Sequence 5, Appli	201	25	80.6	28	2	US-09-660-954-12	Sequence 13, Appli
129	25	80.6	15	1	US-08-612-785B-14	Sequence 14, Appli	202	25	80.6	28	2	US-09-660-954-13	Sequence 14, Appli
130	25	80.6	15	1	US-08-612-785B-37	Sequence 37, Appli	203	25	80.6	28	2	US-08-898-300-4	Sequence 4, Appli
131	25	80.6	15	2	US-08-612-785B-37	Sequence 37, Appli	204	25	80.6	28	2	US-08-824-513-4	Sequence 4, Appli
132	25	80.6	15	2	US-08-766-596A-56	Sequence 56, Appli	205	25	80.6	28	2	US-09-623-548A-959	Sequence 959, App
133	25	80.6	15	2	US-08-766-596A-57	Sequence 57, Appli	206	25	80.6	28	2	US-09-623-548A-965	Sequence 965, App
134	25	80.6	15	2	US-08-766-596A-58	Sequence 58, Appli	207	25	80.6	28	2	US-09-623-548A-976	Sequence 976, App
135	25	80.6	15	2	US-08-766-596A-60	Sequence 60, Appli	208	25	80.6	28	2	US-09-623-548A-992	Sequence 992, App
136	25	80.6	15	2	US-08-766-596A-61	Sequence 61, Appli	209	25	80.6	28	2	US-09-623-548A-1003	Sequence 1003, App
137	25	80.6	15	2	US-08-766-596A-63	Sequence 63, Appli	210	25	80.6	28	2	US-09-657-276-959	Sequence 959, App
138	25	80.6	15	2	US-08-766-596A-65	Sequence 65, Appli	211	25	80.6	28	2	US-09-657-276-965	Sequence 965, App
139	25	80.6	17	2	US-09-264-709A-2	Sequence 2, Appli	212	25	80.6	28	2	US-09-657-276-976	Sequence 976, App
140	25	80.6	17	2	US-09-594-366-3	Sequence 3, Appli	213	25	80.6	28	2	US-09-657-276-992	Sequence 992, App
141	25	80.6	17	2	US-09-623-548A-950	Sequence 950, App	214	25	80.6	28	2	US-09-657-276-1003	Sequence 1003, App
142	25	80.6	17	2	US-09-623-548A-983	Sequence 983, App	215	25	80.6	30	1	US-09-865-294A-66	Sequence 66, Appli
143	25	80.6	17	2	US-09-992-800-3	Sequence 3, Appli	216	25	80.6	30	1	US-08-609-090-3	Sequence 3, Appli
144	25	80.6	17	2	US-09-657-276-950	Sequence 950, App	217	25	80.6	33	1	US-09-861-847A-1	Sequence 1, Appli
145	25	80.6	17	2	US-09-657-276-983	Sequence 983, App	218	25	80.6	33	1	US-08-609-090-4	Sequence 4, Appli
146	25	80.6	19	2	US-08-970-833-11	Sequence 11, Appli	219	25	80.6	35	1	US-08-475-579A-4	Sequence 4, Appli
147	25	80.6	19	2	US-09-723-384-5	Sequence 5, Appli	220	25	80.6	35	1	US-08-304-585-6	Sequence 6, Appli
148	25	80.6	19	2	US-09-724-961-75	Sequence 75, Appli	221	25	80.6	35	1	US-08-612-785B-16	Sequence 16, Appli
149	25	80.6	19	2	US-09-724-552-5	Sequence 5, Appli	222	25	80.6	35	1	US-08-612-785B-36	Sequence 36, Appli
150	25	80.6	19	2	US-09-580-018-75	Sequence 75, Appli	223	25	80.6	35	1	US-08-612-785B-38	Sequence 38, Appli
151	25	80.6	19	2	US-09-723-927-5	Sequence 5, Appli	224	25	80.6	35	1	US-08-612-785B-40	Sequence 40, Appli
152	25	80.6	19	2	US-09-724-489-5	Sequence 5, Appli	225	25	80.6	35	2	US-08-617-267C-16	Sequence 16, Appli
153	25	80.6	19	2	US-09-724-477-5	Sequence 5, Appli	226	25	80.6	35	2	US-09-623-548A-979	Sequence 979, App
154	25	80.6	19	2	US-09-723-762-5	Sequence 5, Appli	227	25	80.6	35	2	US-09-623-548A-1006	Sequence 1006, App
155	25	80.6	19	2	US-09-201-430-5	Sequence 5, Appli	228	25	80.6	35	2	US-09-657-276-979	Sequence 979, App
156	25	80.6	19	2	US-09-724-551-75	Sequence 75, Appli	229	25	80.6	36	1	US-09-657-276-1006	Sequence 1006, App
157	25	80.6	19	2	US-10-815-353-5	Sequence 5, Appli	230	25	80.6	36	1	US-08-609-090-6	Sequence 6, Appli
158	25	80.6	19	2	US-10-816-529-5	Sequence 5, Appli	231	25	80.6	36	2	US-09-861-847A-6	Sequence 6, Appli
159	25	80.6	19	2	US-10-815-391-5	Sequence 5, Appli	232	25	80.6	36	2	US-09-861-847A-11	Sequence 11, Appli
160	25	80.6	19	2	US-10-816-022-5	Sequence 5, Appli	233	25	80.6	38	1	US-08-302-808-1	Sequence 1, Appli
161	25	80.6	19	2	US-09-724-940-75	Sequence 75, Appli	234	25	80.6	38	1	US-07-737-371E-68	Sequence 68, Appli
162	25	80.6	19	2	US-10-934-609-5	Sequence 5, Appli	235	25	80.6	38	2	US-08-986-948-1	Sequence 1, Appli
163	25	80.6	19	2	US-10-884-892-5	Sequence 5, Appli	236	25	80.6	38	2	US-09-623-548A-975	Sequence 975, App
164	25	80.6	20	2	US-08-970-833-10	Sequence 10, Appli	237	25	80.6	38	2	US-09-623-548A-1002	Sequence 1002, App
165	25	80.6	20	2	US-09-724-953-33	Sequence 33, Appli	238	25	80.6	38	2	US-09-657-276-975	Sequence 975, App
166	25	80.6	20	2	US-09-724-567-33	Sequence 33, Appli	239	25	80.6	39	1	US-09-657-276-1002	Sequence 1002, App
167	25	80.6	20	2	US-09-579-952-33	Sequence 33, Appli	240	25	80.6	39	1	US-08-304-585-5	Sequence 5, Appli
168	25	80.6	26	1	US-09-585-817-33	Sequence 33, Appli	241	25	80.6	39	1	US-08-302-808-2	Sequence 2, Appli
169	25	80.6	26	1	US-08-304-585-7	Sequence 7, Appli	242	25	80.6	39	1	US-08-609-090-7	Sequence 7, Appli
170	25	80.6	28	1	US-08-346-849-4	Sequence 4, Appli	243	25	80.6	39	1	US-08-682-245A-1	Sequence 1, Appli
171	25	80.6	28	1	US-08-302-808-7	Sequence 7, Appli	244	25	80.6	40	1	US-08-986-948-2	Sequence 2, Appli
172	25	80.6	28	1	US-08-609-090-2	Sequence 2, Appli	245	25	80.6	40	1	US-07-744-767A-1	Sequence 1, Appli
173	25	80.6	28	1	US-08-986-948-7	Sequence 7, Appli	246	25	80.6	40	1	US-08-235-400-2	Sequence 2, Appli
												US-08-476-464A-2	Sequence 2, Appli

```

247 25 80.6 40 1 US-08-304-585-1
248 25 80.6 40 1 US-08-304-585-8
249 25 80.6 40 1 US-08-302-808-3
250 25 80.6 40 1 US-08-433-734-1
251 25 80.6 40 1 US-08-609-090-8
252 25 80.6 40 1 US-07-737-371B-69
253 25 80.6 40 1 US-08-682-245A-2
254 25 80.6 40 1 US-08-986-948-3
255 25 80.6 40 1 US-08-461-216-1
256 25 80.6 40 2 US-08-959-148-1
257 25 80.6 40 2 US-09-242-724-22
258 25 80.6 40 2 US-08-723-661B-1
259 25 80.6 40 2 US-09-082-365-3
260 25 80.6 40 2 US-09-133-866-1
261 25 80.6 40 2 US-09-861-847A-7
262 25 80.6 40 2 US-09-861-847A-8
263 25 80.6 40 2 US-09-988-842-3
264 25 80.6 40 2 US-10-455-218-1
265 25 80.6 40 2 US-10-151-614-1
266 25 80.6 40 2 US-09-623-548A-956
267 25 80.6 40 2 US-09-623-548A-962
268 25 80.6 40 2 US-09-623-548A-968
269 25 80.6 40 2 US-09-623-548A-978
270 25 80.6 40 2 US-09-623-548A-989
271 25 80.6 40 2 US-09-623-548A-995
272 25 80.6 40 2 US-09-623-548A-1005
273 25 80.6 40 2 US-09-657-276-956
274 25 80.6 40 2 US-09-657-276-962
275 25 80.6 40 2 US-09-657-276-968
276 25 80.6 40 2 US-09-657-276-978
277 25 80.6 40 2 US-09-657-276-989
278 25 80.6 40 2 US-09-657-276-995
279 25 80.6 40 2 US-09-657-276-1005
280 25 80.6 40 2 US-09-962-955D-36
281 25 80.6 40 4 PCT-US92-06700-1
282 25 80.6 41 1 US-07-819-361-1
283 25 80.6 41 1 US-08-302-808-4
284 25 80.6 41 1 US-08-682-245A-3
285 25 80.6 41 1 US-08-986-948-4
286 25 80.6 42 1 US-07-744-767A-2
287 25 80.6 42 1 US-08-179-574-1
288 25 80.6 42 1 US-08-271-162-5
289 25 80.6 42 1 US-08-347-144-1
290 25 80.6 42 1 US-08-462-859A-19
291 25 80.6 42 1 US-08-123-659A-19
292 25 80.6 42 1 US-08-464-247A-19
293 25 80.6 42 1 US-08-464-248A-19
294 25 80.6 42 1 US-08-476-464A-1
295 25 80.6 42 1 US-08-304-585-2
296 25 80.6 42 1 US-08-302-808-5
297 25 80.6 42 1 US-08-268-348A-1
298 25 80.6 42 1 US-08-268-348A-2
299 25 80.6 42 1 US-08-268-348A-3
300 25 80.6 42 1 US-08-268-348A-4

```

# ALIGNMENTS

```

RESULT 1
US-09-747-408-4
; Sequence 4, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

```

```

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-4

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 1 KVFVFA 6

RESULT 2
US-09-747-408-12
; Sequence 12, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-12

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 1 KVFVFA 6

RESULT 3
US-09-248-796A-18091
; Sequence 18091, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18091
; LENGTH: 1283
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18091

Query Match 96.8%; Score 30; DB 2; Length 1283;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      1 KVFVFA 6
Db      259 KTFVFA 264

RESULT 4
US-09-830-230A-438
; Sequence 438, Application US/09830230A
; Patent No. 6902893
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; FILE REFERENCE: PB481US
; CURRENT APPLICATION NUMBER: US/09/830,230A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 438
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-230A-438

Query Match      90.3%; Score 28; DB 2; Length 490;
Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      23 RFVFFA 28

RESULT 5
US-08-888-998-2
; Sequence 2, Application US/08888998
; Patent No. 6124524
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAEL GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,998
; FILING DATE: 07-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,603
; FILING DATE: 26-OCT-1994

ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 12176-004300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..506
; OTHER INFORMATION: /note="Amino acid sequence of FAEL
; protein."
US-08-888-998-2

Query Match      90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 5.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      356 KFLVFA 361

RESULT 6
US-09-362-633-2
; Sequence 2, Application US/09362633
; Patent No. 6184355
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAEL GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,633
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,998
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 12176-004300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
```

MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..506  
 OTHER INFORMATION: /note= "Amino acid sequence of PAE1  
 OTHER INFORMATION: protein."  
 US-09-362-633-2

Query Match 90.3%; Score 28; DB 2; Length 506;  
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
 ||:||||  
 Db 356 KFLPFA 361

RESULT 7  
 US-09-877-476-2  
 ; Sequence 2, Application US/09877476  
 ; Patent No. 6713664  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jaworski, Jan G.  
 ; APPLICANT: Blacklock, Brenda J.  
 ; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA  
 ; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES  
 ; FILE REFERENCE: 07148-108001  
 ; CURRENT APPLICATION NUMBER: US/09/877,476  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR FILING DATE: 2000-06-08  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 506  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 US-09-877-476-2

Query Match 90.3%; Score 28; DB 2; Length 506;  
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
 ||:||||  
 Db 356 KFLPFA 361

RESULT 8  
 US-09-877-476-28  
 ; Sequence 28, Application US/09877476  
 ; Patent No. 6713664  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jaworski, Jan G.  
 ; APPLICANT: Blacklock, Brenda J.  
 ; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA  
 ; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES  
 ; FILE REFERENCE: 07148-108001  
 ; CURRENT APPLICATION NUMBER: US/09/877,476  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR FILING DATE: 2000-06-08  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 506  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ  
 ; OTHER INFORMATION: ID NO:4) and 3' 330 amino acids from A. thaliana  
 ; OTHER INFORMATION: PAE1 (SEQ ID NO:2); designated Bn176  
 US-09-877-476-28

Query Match 90.3%; Score 28; DB 2; Length 506;  
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
 ||:||||  
 Db 356 KFLPFA 361

RESULT 9  
 US-09-877-476-30  
 ; Sequence 30, Application US/09877476  
 ; Patent No. 6713664  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jaworski, Jan G.  
 ; APPLICANT: Blacklock, Brenda J.  
 ; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA  
 ; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES  
 ; FILE REFERENCE: 07148-108001  
 ; CURRENT APPLICATION NUMBER: US/09/877,476  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR FILING DATE: 2000-06-08  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 30  
 ; LENGTH: 506  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: 5' 399 amino acids from A. thaliana PAE1 (SEQ ID  
 ; OTHER INFORMATION: NO:2) and 3' 107 amino acids from B. napus  
 ; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399  
 ; NAME/KEY: VARIANT  
 ; LOCATION: (0)..(0)  
 ; OTHER INFORMATION: Xaa = Pro or Gln  
 US-09-877-476-30

Query Match 90.3%; Score 28; DB 2; Length 506;  
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
 ||:||||  
 Db 356 KFLPFA 361

RESULT 10  
 US-09-877-476-36  
 ; Sequence 36, Application US/09877476  
 ; Patent No. 6713664  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jaworski, Jan G.  
 ; APPLICANT: Blacklock, Brenda J.  
 ; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA  
 ; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES  
 ; FILE REFERENCE: 07148-108001  
 ; CURRENT APPLICATION NUMBER: US/09/877,476  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR FILING DATE: 2000-06-08  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 36  
 ; LENGTH: 506  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: 506 amino acids from A. thaliana PAE1 (SEQ ID  
 ; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated  
 ; OTHER INFORMATION: At K92R; hypothetical  
 US-09-877-476-36

```
Query Match          90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
DB      356 KLFVFA 361

RESULT 11
US-09-830-230A-437
; Sequence 437, Application US/09830230A
; Patent No. 6902893
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481US
; CURRENT APPLICATION NUMBER: US/09/830,230A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 437
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-230A-437

Query Match          90.3%; Score 28; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
DB      41 RFVFFA 46

RESULT 12
US-09-248-796A-26311
; Sequence 26311, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26311
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26311

Query Match          87.1%; Score 27; DB 2; Length 67;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
DB      16 KFIFYA 21

RESULT 13
US-09-513-999C-4859
; Sequence 4859, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4859
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-4859

Query Match          87.1%; Score 27; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
DB      32 KVFVFF 36

RESULT 14
US-09-270-767-40694
; Sequence 40694, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40694
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40694

Query Match          87.1%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
DB      84 KVFVFF 88

RESULT 15
US-09-270-767-55910
; Sequence 55910, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
```

; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55910  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-55910

Query Match 87.1%; Score 27; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5  
Db 84 KPVFF 88

RESULT 16  
US-09-823-153-4  
; Sequence 4, Application US/09823153  
; Patent No. 6713248  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; APPLICANT: Roberts, Susan  
; APPLICANT: Pak, Roger  
; APPLICANT: Lewis, Martin  
; APPLICANT: Smith, David  
; APPLICANT: Hendrick, Joseph  
; APPLICANT: Vinitzky, Alexander  
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX  
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF  
; FILE REFERENCE: D0004  
; CURRENT APPLICATION NUMBER: US/09/823,153  
; CURRENT FILING DATE: 2001-07-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 104  
; TYPE: PRT  
; ORGANISM: Human Beta App  
US-09-823-153-4

Query Match 87.1%; Score 27; DB 2; Length 104;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
Db 21 EFVFFA 26

RESULT 17  
US-09-270-767-57813  
; Sequence 57813, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57813  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-57813

Query Match 87.1%; Score 27; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5  
Db 62 KPVFF 66

RESULT 18  
US-09-902-540-10859  
; Sequence 10859, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 10859  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-10859

Query Match 87.1%; Score 27; DB 2; Length 238;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5  
Db 132 KPVFF 136

RESULT 19  
US-09-134-001C-5445  
; Sequence 5445, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5445  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5445

Query Match 87.1%; Score 27; DB 2; Length 240;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
Db 168 QVFFA 173

```
RESULT 20
US-09-270-767-42516
; Sequence 42516, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42516
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42516
Query Match      87.1%; Score 27; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVF 5
Db 62 KVFVF 66

RESULT 21
US-09-248-796A-19539
; Sequence 19539, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19539
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19539
Query Match      87.1%; Score 27; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVF 5
Db 23 KVFVF 27

RESULT 22
US-09-270-767-40453
; Sequence 40453, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40453
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40453
Query Match      87.1%; Score 27; DB 2; Length 340;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFA 6
Db 310 KYVFFA 315

RESULT 23
US-09-270-767-55669
; Sequence 55669, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55669
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55669
Query Match      87.1%; Score 27; DB 2; Length 340;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFA 6
Db 310 KYVFFA 315

RESULT 24
US-09-270-767-45548
; Sequence 45548, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45548
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45548
Query Match      87.1%; Score 27; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVF 5
Db 49 KVFVF 53
```

```

RESULT 25
US-09-270-767-34763
; Sequence 34763, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34763
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34763

Query Match      87.1%; Score 27; DB 2; Length 525;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
Db      446 KYIIFA 451

RESULT 26
US-09-270-767-49980
; Sequence 49980, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 49980
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49980

Query Match      87.1%; Score 27; DB 2; Length 525;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
Db      446 KYIIFA 451

RESULT 27
US-08-704-711A-1
; Sequence 1, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007-5109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>

```

```

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-1

Query Match      87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
Db      375 KVFVF 379

RESULT 28
US-09-521-220-1
; Sequence 1, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007-5109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>

```



```
/ 21-OCT-1994
/ 17-MAR-1994
/ PRIOR APPLICATION DATA:
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: DE 4438838.1
/ FILING DATE: 21-OCT-1994
/ APPLICATION NUMBER: DE 4409663.1
/ FILING DATE: 17-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: GRANADOS, Patricia D.
/ REGISTRATION NUMBER: 33,683
/ REFERENCE/DOCKET NUMBER: 26083/124
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 579 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-521-220-1

Query Match      87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
DB      375 KVFVF 379

RESULT 29
US-08-704-711A-2
/ Sequence 2, Application US/08704711A
/ Patent No. 6114159
/ GENERAL INFORMATION:
/ APPLICANT: WILL, Horet
/ APPLICANT: HINZMANN, Bernd
/ TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
/ TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/704,711A
/ FILING DATE: 20-NOV-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/DE95/00357
/ FILING DATE: 17-MAR-1995
/ PRIOR APPLICATION DATA: DE 4438838.1
/ APPLICATION NUMBER: DE 4409663.1
/ FILING DATE: 17-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: GRANADOS, Patricia D.
/ REGISTRATION NUMBER: 33,683

/ 21-OCT-1994
/ 17-MAR-1994
/ REFERENCE/DOCKET NUMBER: 26083/124
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 582 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-704-711A-2

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
DB      378 KVFVF 382

RESULT 30
US-08-448-489-1
/ Sequence 1, Application US/08448489
/ Patent No. 6184022
/ GENERAL INFORMATION:
/ APPLICANT: SEIKI, Motoharu
/ APPLICANT: SATO, Hiroshi
/ APPLICANT: SHINAGAWA, Akira
/ TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
/ FILE REFERENCE: 55-290P
/ CURRENT APPLICATION NUMBER: US/08/448,489
/ CURRENT FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 582
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-08-448-489-1

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
DB      378 KVFVF 382

RESULT 31
US-09-211-704A-9
/ Sequence 9, Application US/09211704A
/ Patent No. 6271014
/ GENERAL INFORMATION:
/ APPLICANT: de Saint-Vis, Blandine Marie
/ APPLICANT: Fossiez, Francois
/ APPLICANT: Caux, Christophe
/ APPLICANT: Lebecque, Serge J.E.
/ TITLE OF INVENTION: Mammalian Proteases; Related Reagents
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DNAX Research Institute
/ STREET: 901 California Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304-1104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/211.704A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/005,263
; FILING DATE: 09-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SF0781K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-211-704A-9

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
Db      378 KVFVF 382

RESULT 32
US-09-521-220-2
; Sequence 2, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-521-220-2

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
Db      378 KVFVF 382

RESULT 33
US-09-391-104-28
; Sequence 28, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073 US P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-391-104-28

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
Db      378 KVFVF 382

RESULT 34
US-09-919-497-84
; Sequence 84, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 582
; TYPE: PRT
```

```

; ORGANISM: Homo sapiens
US-09-919-497-84

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
Db      378 KVFVF 382

RESULT 35
US-09-689-730-1
; Sequence 1, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-689-730-1

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
Db      378 KVFVF 382

RESULT 36
US-10-449-315-2
; Sequence 2, Application US/10449315
; Patent No. 6942984
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US /09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-2

Query Match      87.1%; Score 27; DB 2; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
          |||||

; ORGANISM: Homo sapiens
US-09-919-497-84

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
Db      378 KVFVF 382

RESULT 37
US-10-449-315-5
; Sequence 5, Application US/10449315
; Patent No. 6942984
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US /09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-5

Query Match      87.1%; Score 27; DB 2; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
          |||||
          |||||
Db      355 KVFVF 359

RESULT 38
US-09-270-767-37091
; Sequence 37091, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37091
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37091

Query Match      83.9%; Score 26; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
          |||||
          |||||
Db      16 FVFFA 20

RESULT 39
US-09-270-767-52308
; Sequence 52308, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
```

; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 52308  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-52308

Query Match 83.9%; Score 26; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6  
| | | | |  
Db 16 FVFFA 20

RESULT 40  
US-09-798-635A-41  
; Sequence 41, Application US/09798635A  
; Patent No. 6936432  
; GENERAL INFORMATION:  
; APPLICANT: Gopalan, Venkat  
; APPLICANT: Jovanovic, Milan  
; APPLICANT: Eder, Paul S.  
; APPLICANT: Giordano, Tony  
; APPLICANT: Powers, Gordon D.  
; APPLICANT: Xavier, K. Ashish  
; TITLE OF INVENTION: No. 6936432el Bacterial RNase P Proteins and  
; FILE REFERENCE: 50093/016002 Their Use in Identifying Antibacterial Compounds  
; CURRENT APPLICATION NUMBER: US/09/798,635A  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/516,061  
; PRIOR FILING DATE: 2000-03-01  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: Haemophilus influenzae  
US-09-798-635A-41

Query Match 83.9%; Score 26; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6  
| | | | |  
Db 39 FVFFA 43

RESULT 41  
US-10-125-258-44  
; Sequence 44, Application US/10125258  
; Patent No. 6891085  
; GENERAL INFORMATION:  
; APPLICANT: Altier, Daniel J.  
; APPLICANT: Herrmann, Rafael  
; APPLICANT: Lu, Albert L.  
; APPLICANT: McCutchen, Billy F.  
; APPLICANT: Presnail, James K.  
; APPLICANT: Weaver, Janine L.  
; APPLICANT: Wong, James F. H.  
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their  
; FILE REFERENCE: 35718/246215 Uses  
; CURRENT APPLICATION NUMBER: US/10/125,258  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: 60/285,355  
; PRIOR FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Ostrinia nubilalis  
US-10-125-258-44

Query Match 83.9%; Score 26; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6  
| | | | |  
Db 8 FVFFA 12

RESULT 42  
US-09-583-110-4885  
; Sequence 4885, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; FILE REFERENCE: PATH00-07A Pneumoniae for Diagnostics and Therapeutics  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 4885  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-4885

Query Match 83.9%; Score 26; DB 2; Length 61;  
Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
| | | | |  
Db 44 KFVF 48

RESULT 43  
US-10-125-258-43  
; Sequence 43, Application US/10125258  
; Patent No. 6891085  
; GENERAL INFORMATION:  
; APPLICANT: Altier, Daniel J.  
; APPLICANT: Herrmann, Rafael  
; APPLICANT: Lu, Albert L.  
; APPLICANT: McCutchen, Billy F.  
; APPLICANT: Presnail, James K.  
; APPLICANT: Weaver, Janine L.  
; APPLICANT: Wong, James F. H.  
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their  
; FILE REFERENCE: 35718/246215 Uses  
; CURRENT APPLICATION NUMBER: US/10/125,258  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: 60/285,355  
; PRIOR FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Ostrinia nubilalis

## US-10-125-258-43

Query Match 83.9%; Score 26; DB 2; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
 |||||  
 Db 8 FVFFA 12

## RESULT 44

US-09-270-767-60733  
 ; Sequence 60733, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 60733  
 ; LENGTH: 84  
 ; TYPE: PRT  
 ; ORGANISM: *Drosophila melanogaster*  
 US-09-270-767-60733

Query Match 83.9%; Score 26; DB 2; Length 84;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5  
 ||:|  
 Db 48 KFIFF 52

## RESULT 45

US-09-621-976-6739  
 ; Sequence 6739, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 6739  
 ; LENGTH: 104  
 ; TYPE: PRT  
 ; ORGANISM: *Homo sapiens*  
 US-09-621-976-6739

Query Match 83.9%; Score 26; DB 2; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
 |||||  
 Db 31 FVFFA 35

## RESULT 46

US-09-205-258-303  
 ; Sequence 303, Application US/09205258  
 ; Patent No. 6525174  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins  
 ; FILE REFERENCE: PZ007P1  
 ; CURRENT APPLICATION NUMBER: US/09/205,258  
 ; CURRENT FILING DATE: 1998-12-04  
 ; EARLIER APPLICATION NUMBER: PCT/US98/11422  
 ; EARLIER FILING DATE: 1998-06-04  
 ; EARLIER APPLICATION NUMBER: 60/048,885  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/049,375  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,881  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,880  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,896  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/049,020  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,876  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,895  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,884  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,894  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,971  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,964  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,882  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,899  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,893  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,900  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,901  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,892  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,915  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/049,019  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,970  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,972  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,916  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/049,373  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,875  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/049,374  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,917  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,949  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,974  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,883  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,897  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,898  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,962  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,963

```
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 303
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-303

Query Match      83.9%; Score 26; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFPA 6
DB      79 FVFPA 83

RESULT 47
US-10-004-860-303
; Sequence 303, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 303
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-004-860-303

Query Match      83.9%; Score 26; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFPA 6
DB      79 FVFPA 83

RESULT 48
US-09-627-376-17
; Sequence 17, Application US/09627376
; Patent No. 6342385
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17402/22
; CURRENT APPLICATION NUMBER: US/09/627,376
```

```
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-627-376-17

Query Match      83.9%; Score 26; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFPA 6
DB      39 FVFPA 43

RESULT 49
US-10-047-676B-17
; Sequence 17, Application US/10047676B
; Patent No. 6699970
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; APPLICANT: Caufield, Page W.
; APPLICANT: Chen, Ping
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17403/22
; CURRENT APPLICATION NUMBER: US/10/047,676B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 09/627,376
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-047-676B-17

Query Match      83.9%; Score 26; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFPA 6
DB      39 FVFPA 43

RESULT 50
US-09-270-767-45241
; Sequence 45241, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 45241
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45241

Query Match      83.9%; Score 26; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFP 5
DB      11
```

```
Db      120 KPIFF 124

RESULT 51
US-09-270-767-35390
; Sequence 35390, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35390
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35390

Query Match      83.9%; Score 26; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
Db      122 FVFFFA 126

RESULT 52
US-09-270-767-50607
; Sequence 50607, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50607
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50607

Query Match      83.9%; Score 26; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
Db      122 FVFFFA 126

RESULT 53
US-09-251-645-4
; Sequence 4, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CCG1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-251-645-4

Query Match      83.9%; Score 26; DB 2; Length 186;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFFA 6
Db      134 QFIFFA 139

RESULT 54
US-09-270-767-33463
; Sequence 33463, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33463
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33463

Query Match      83.9%; Score 26; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
Db      80 FVFFFA 84

RESULT 55
US-09-270-767-48680
; Sequence 48680, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48680
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48680

Query Match      83.9%; Score 26; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
Db      80 FVFFFA 84
```

Db 80 FVFFA 84

## RESULT 56

US-09-270-767-38186  
; Sequence 38186, Application US/09270767  
; Patent No. 6703491

## GENERAL INFORMATION:

; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 38186

LENGTH: 249

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-38186

Query Match 83.9%; Score 26; DB 2; Length 249;

Best Local Similarity 80.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5

Db 196 KFIFF 200

## RESULT 57

US-09-270-767-53403  
; Sequence 53403, Application US/09270767  
; Patent No. 6703491

## GENERAL INFORMATION:

; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 53403

LENGTH: 249

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-53403

Query Match 83.9%; Score 26; DB 2; Length 249;

Best Local Similarity 80.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5

Db 196 KFIFF 200

## RESULT 58

US-09-248-796A-27128  
; Sequence 27128, Application US/09248796A  
; Patent No. 6747137

## GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 27128

LENGTH: 249

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-27128

Query Match 83.9%; Score 26; DB 2; Length 249;

Best Local Similarity 80.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5

Db 108 KFIFF 112

## RESULT 59

US-09-830-910-2  
; Sequence 2, Application US/09830910  
; Patent No. 6482807

## GENERAL INFORMATION:

; APPLICANT: Van Der Ley, Peter Andre  
; APPLICANT: Hamstra, Hendrik Jan  
; APPLICANT: Steeghs, Liana Juliana Josephine Margriet  
; TITLE OF INVENTION: LPS with reduced toxicity from genetically modified  
; FILE REFERENCE: Gram-negative bacteria  
; FILE REFERENCE: LPS with reduced toxicity  
; CURRENT APPLICATION NUMBER: US/09/830,910  
; CURRENT FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: PCT/NL98/00633

PRIOR FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 310

TYPE: PRT

ORGANISM: Neisseria meningitidis

US-09-830-910-2

Query Match 83.9%; Score 26; DB 2; Length 310;

Best Local Similarity 80.0%; Pred. No. 8.1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5

Db 6 KFIFF 10

## RESULT 60

US-09-248-796A-15301  
; Sequence 15301, Application US/09248796A  
; Patent No. 6747137

## GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 15301  
; LENGTH: 328  
; TYPE: PRT  
; ORGANISM: Candida albicans  
; FEATURE:  
; NAME/KEY: UNSURE



```
; LOCATION: (4),(5)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-15301

Query Match      83.9%; Score 26; DB 2; Length 328;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|:|
Db 6 QFIFFA 11

RESULT 61
US-09-270-767-41366
; Sequence 41366, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41366
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41366

Query Match      83.9%; Score 26; DB 2; Length 394;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|:|
Db 267 KFWVFA 272

RESULT 62
US-09-270-767-56582
; Sequence 56582, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56582
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56582

Query Match      83.9%; Score 26; DB 2; Length 394;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|:|
Db 267 KFWVFA 272

RESULT 63
US-09-252-991A-25289
; Sequence 25289, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25289
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25289

Query Match      83.9%; Score 26; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFFA 6
   :|:|
Db 309 FVFFFA 313

RESULT 64
US-09-902-540-11308
; Sequence 11308, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11308
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11308

Query Match      83.9%; Score 26; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFFA 6
   :|:|
Db 185 FVFFFA 189

RESULT 65
US-09-602-787A-424
; Sequence 424, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kruger, Burkhard
; APPLICANT: Schuder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habehauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
```

```

; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03

```

```

; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 424
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-424

Query Match      83.9%; Score 26; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVEFFA 6
      |||||
Db      120 FVEFFA 124

RESULT 66
US-09-489-039A-8958
; Sequence 8958, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8958
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8958

Query Match      83.9%; Score 26; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVEFFA 6
      |||||
Db      36 FVEFFA 40

RESULT 67
US-09-252-991A-17185
; Sequence 17185, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17185
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17185

Query Match      83.9%; Score 26; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVEFFA 6
      |||||

```

Db 48 FVFFA 52

RESULT 68  
US-09-489-039A-8303  
; Sequence 8303, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 8303  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
; NAME/KEY: UNSURE  
; LOCATION: (133)  
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
US-09-489-039A-8303

Query Match 83.9%; Score 26; DB 2; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||  
Db 266 FVFFA 270

RESULT 69  
US-09-252-991A-28992  
; Sequence 28992, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 28992  
; LENGTH: 493  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28992

Query Match 83.9%; Score 26; DB 2; Length 493;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
|||  
Db 2 KRIFF 6

RESULT 70  
US-09-540-236-2206  
; Sequence 2206, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 2206  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: M.cattarrhalis  
US-09-540-236-2206

Query Match 83.9%; Score 26; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||  
Db 355 FVFFA 359

RESULT 71  
US-09-489-039A-11884  
; Sequence 11884, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 11884  
; LENGTH: 573  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-11884

Query Match 83.9%; Score 26; DB 2; Length 573;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||  
Db 511 FVFFA 515

RESULT 72  
US-09-252-991A-22560  
; Sequence 22560, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 22560  
; LENGTH: 597  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22560

Query Match 83.9%; Score 26; DB 2; Length 597;

Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6  
|  
|  
|  
|  
Db 90 FVFFA 94

## RESULT 73

US-09-540-540-10275  
; Sequence 10275, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 10275  
; LENGTH: 745  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-10275

Query Match 83.9%; Score 26; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6  
|  
|  
|  
|  
Db 185 FVFFA 189

## RESULT 74

US-09-540-236-2074  
; Sequence 2074, Application US/09540236  
; Patent No. 6673310  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 2074  
; LENGTH: 892  
; TYPE: PRT  
; ORGANISM: M.catarhalis  
US-09-540-236-2074

Query Match 83.9%; Score 26; DB 2; Length 892;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6  
|  
|  
|  
|  
Db 658 FVFFA 662

## RESULT 75

US-08-612-785B-9  
; Sequence 9, Application US/08612785B  
; Patent No. 5854204  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid

; TITLE OF INVENTION: Aggregation  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/612,785B  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-612-785B-9

Query Match 80.6%; Score 25; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 1;

Qy 1 KVFVFA 6  
|  
|  
|  
|  
Db 1 KLVFFA 6

Search completed: December 29, 2005, 17:52:34  
Job time : 22.1323 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds  
(without alignments)  
32.238 Million cell updates/sec

Title: US-10-009-122-4

Perfect score: 31

Sequence: 1 KVFPPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

A Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	6	4	AB48477 Antifibri
2	31	100.0	6	4	AB48485 Antifibri
3	31	100.0	6	4	AB82625 All-D pep
4	31	100.0	6	4	AB82633 All-D pep
5	31	100.0	6	5	AAU96813 Amyloid t
6	31	100.0	6	5	AAU96821 Amyloid t
7	31	100.0	6	5	AAU11659 Peptide #
8	31	100.0	6	5	AAU11651 Peptide #
9	31	100.0	6	6	AAE35447 Beta pep
10	31	100.0	6	6	AAE35440 Beta pep
11	31	100.0	6	8	ADQ37264 Vaccine a
12	31	100.0	6	8	ADQ37316 Antifibri
13	31	100.0	6	8	ADQ37324 Antifibri
14	31	100.0	6	8	ADQ37272 Vaccine a
15	31	100.0	6	9	ADY37931 Amyloid-t
16	31	100.0	6	9	ADY37923 Amyloid-t
17	31	100.0	336	7	ABM89186 Rice abio
18	30	96.8	202	5	ADK35620 Novel hum
19	28	90.3	75	4	ABB17989 Human ner
20	28	90.3	452	8	ADN23626 Bacterial
21	28	90.3	485	8	ADN46740 Thermococ
22	28	90.3	490	2	AAI19993 B. burgdo
23	28	90.3	506	2	AAE95594 Arabidops
24	28	90.3	506	5	AAE17850 Alternati

25	28	90.3	506	5	AAE17622	A. thalia
26	28	90.3	506	5	AAE17625	Arabidops
27	28	90.3	506	5	AAE17621	Brassica
28	28	90.3	506	5	AAE17608	Arabidops
29	28	90.3	506	2	AEA37517	Arabidops
30	28	90.3	508	2	AAI19992	B. burgdo
31	28	90.3	508	6	ABU19128	Protein e
32	28	90.3	571	6	ABU24005	Protein e
33	28	90.3	1089	8	ADN19501	Bacterial
34	27	87.1	52	3	AAE1668	Arabidops
35	27	87.1	57	8	ADX67964	Plant ful
36	27	87.1	62	4	ABBO3189	Human mus
37	27	87.1	62	6	ABU12483	Novel hum
38	27	87.1	62	8	ADJ28509	Human mus
39	27	87.1	82	3	AAO00778	Human sec
40	27	87.1	82	4	ABG13797	Novel hum
41	27	87.1	91	4	AAO12276	Human pol
42	27	87.1	99	4	AAO10108	Human pol
43	27	87.1	104	4	AAE12897	Human rec
44	27	87.1	114	4	AB93728	Human pro
45	27	87.1	115	5	ABP33134	Human iso
46	27	87.1	126	4	AAO02898	Human pol
47	27	87.1	132	4	AAO00490	Human pol
48	27	87.1	144	4	ABG26562	Novel hum
49	27	87.1	146	4	AAO07503	Human pol
50	27	87.1	148	8	ADQ66558	Novel hum
51	27	87.1	173	4	AAU27710	Human ful
52	27	87.1	173	5	AAU77842	Oestrogen
53	27	87.1	173	7	ADJ69976	Human hea
54	27	87.1	184	3	AAE47987	Arabidops
55	27	87.1	186	9	ABE38594	L. pneumo
56	27	87.1	189	5	AAU79255	Human mem
57	27	87.1	189	5	AAU79257	Rat membr
58	27	87.1	189	5	AAU79258	Rabbit me
59	27	87.1	189	5	AAU79256	Murine me
60	27	87.1	197	7	ABM73888	DNA clone
61	27	87.1	206	4	ABE52559	Escherich
62	27	87.1	221	4	ABG22983	Novel hum
63	27	87.1	221	4	ABG06994	Novel hum
64	27	87.1	227	8	ADH45453	Human mol
65	27	87.1	238	9	ABM91660	M. xanthu
66	27	87.1	240	5	ABP40600	Staphyloc
67	27	87.1	240	8	ADSO7805	Staphyloc
68	27	87.1	248	3	AAI10914	Arabidops
69	27	87.1	252	3	AAI10913	Arabidops
70	27	87.1	270	3	AAI10912	Arabidops
71	27	87.1	270	5	AAU80872	Human CLA
72	27	87.1	297	5	ABU81731	Human cas
73	27	87.1	312	8	ADP47907	Human CAT
74	27	87.1	313	3	AAE33404	Zea may
75	27	87.1	335	8	ADT58396	Plant pol
76	27	87.1	344	3	AAE28863	Arabidops
77	27	87.1	347	8	ADX78439	Plant ful
78	27	87.1	350	9	ADY15182	PRO polyp
79	27	87.1	350	9	ADY15180	PRO polyp
80	27	87.1	351	5	AAU74357	Human cyt
81	27	87.1	351	8	ABM80293	Tumour-as
82	27	87.1	393	8	ADT55938	Plant pol
83	27	87.1	401	5	ABP52840	Anopheles
84	27	87.1	401	7	ABR44483	Moquito
85	27	87.1	409	8	ADN74449	Thale cre
86	27	87.1	422	8	ADT58936	Plant pol
87	27	87.1	436	5	ABB91404	Herbicida
88	27	87.1	454	6	ADB08942	Alloioioc
89	27	87.1	478	6	ABP73100	Amino aci
90	27	87.1	478	7	ADT5262	African m
91	27	87.1	498	6	ABP73103	Amino aci
92	27	87.1	504	7	ADC60748	Termitomy
93	27	87.1	549	8	ADP29329	Human sec
94	27	87.1	579	2	AAE86406	Human mat
95	27	87.1	581	6	ABU37981	Protein e
96	27	87.1	581	9	ABE94410	Human MTL
97	27	87.1	582	2	AAE86407	Human mat

98	27	87.1	582	2	AAR75648	Aar75648 Human pla	171	26	83.9	223	8	ADE75401	Ade75401 Goat alph
99	27	87.1	582	2	AAW52134	Aaw52134 Rabbit me	172	26	83.9	243	8	ADN24282	Adn24282 Bacterial
100	27	87.1	582	4	AAE84616	Aae84616 Amino aci	173	26	83.9	289	3	AAV74724	Aay74724 Neisseria
101	27	87.1	582	4	AAE10423	Aae10423 Human mat	174	26	83.9	289	3	AAV74722	Aay74722 Neisseria
102	27	87.1	582	5	AAU84294	Aau84294 Human end	175	26	83.9	289	3	AAV74723	Aay74723 Neisseria
103	27	87.1	582	5	AAE21037	Aae21037 Human mem	176	26	83.9	291	5	AAAB60856	Aab60856 N. mening
104	27	87.1	582	5	AAW50865	Aaw50865 Matrix me	177	26	83.9	291	5	AAU85401	Aau85401 Neisseria
105	27	87.1	582	7	ADC15498	Adc15498 Human bas	178	26	83.9	293	3	AAV79683	Aay79683 Neisseria
106	27	87.1	582	7	ADBE64179	Adbe64179 Human Pro	179	26	83.9	293	3	AAV75339	Aay75339 Neisseria
107	27	87.1	582	7	ADBE64177	Adbe64177 Rat Prote	180	26	83.9	293	3	AAV75337	Aay75337 Neisseria
108	27	87.1	582	7	ADF13708	Adf13708 Tumour-As	181	26	83.9	293	3	AAV75338	Aay75338 Neisseria
109	27	87.1	582	7	ADN95889	Adn95889 Human BEC	182	26	83.9	293	8	ADR31670	Adr31670 N. mening
110	27	87.1	582	8	ADN07703	Adn07703 Human mat	183	26	83.9	295	6	ABU37645	Abu37645 Protein e
111	27	87.1	582	8	ABM81541	Abm81541 Tumour-as	184	26	83.9	299	6	ABP77830	Abp77830 N. gonorr
112	27	87.1	582	8	ADP23426	Adp23426 PRO polyP	185	26	83.9	317	6	ABP78259	Abp78259 N. gonorr
113	27	87.1	582	9	AE94378	Aeb94378 Human MTL	186	26	83.9	321	7	ADG90764	Adg90764 Hepatic s
114	27	87.1	582	6	ABP79179	Abp79179 N. gonorr	187	26	83.9	321	8	ADP04189	Adp04189 Human col
115	27	87.1	582	6	ABU37131	Abu37131 Protein e	188	26	83.9	322	4	AAU30371	Aau30371 Novel hum
116	27	87.1	582	8	ADJ22906	Adj22906 Bacterial	189	26	83.9	330	4	AAU49675	Aau49675 Propionib
117	27	87.1	738	4	AAAG67526	Aag67526 Amino aci	190	26	83.9	330	6	ABM46194	Abm46194 Propionib
118	27	87.1	833	4	ADM98835	Adm98835 HMW-CoA r	191	26	83.9	339	4	AAG72670	Aag72670 Murine OR
119	27	87.1	841	4	AAW23595	Aam23595 Murine BS	192	26	83.9	344	7	ADE40136	Ade40136 Human NOV
120	27	87.1	856	8	ADM98920	Adm98920 HMW-CoA r	193	26	83.9	346	7	ABE62833	Abe62833 Rat Prote
121	27	87.1	856	8	ADM98784	Adm98784 HMW-CoA r	194	26	83.9	369	3	AAV75249	Aay75249 Neisseria
122	27	87.1	856	8	ADM98820	Adm98820 HMW-CoA r	195	26	83.9	371	3	AAV75248	Aay75248 Neisseria
123	27	87.1	1024	4	AAU02880	Aau02880 Human cas	196	26	83.9	371	3	AAV75247	Aay75247 Neisseria
124	27	87.1	1024	5	ABU81720	Abu81720 Human CLA	197	26	83.9	380	8	ADB12503	Adb12503 Allolococ
125	27	87.1	1024	5	ABU81720	Abu81720 Human cas	198	26	83.9	390	8	ADN23888	Adn23888 Bacterial
126	27	87.1	1024	6	ABG72211	Abg72211 Human cas	199	26	83.9	393	8	ADS24065	Ads24065 Bacterial
127	27	87.1	1024	6	ABG99643	Abg99643 Amino aci	200	26	83.9	395	6	ABP77710	Abp77710 N. gonorr
128	27	87.1	1070	4	AAAG67527	Aag67527 Amino aci	201	26	83.9	397	5	ABB49314	Abb49314 Listeria
129	27	87.1	1204	4	AAU02881	Aau02881 Human cas	202	26	83.9	397	5	ADC87413	Adc87413 Human GPC
130	27	87.1	1204	6	ABG72212	Abg72212 Protein e	203	26	83.9	400	8	ADT58012	Adt58012 Plant pol
131	27	87.1	2697	6	AAO26550	Aao26550 Cochliobo	204	26	83.9	402	7	ABO76543	Abp76543 Pseudomon
132	26	83.9	45	6	ABU02448	Abu02448 S. pneumo	205	26	83.9	404	8	ADS26059	Ads26059 Bacterial
133	26	83.9	53	8	ADM80309	Adm80309 Plant ful	206	26	83.9	405	6	ABM67471	Abm67471 Photorhab
134	26	83.9	60	8	ABP55940	Abp55940 Oetrinia	207	26	83.9	414	8	ABU20391	Abu20391 Protein e
135	26	83.9	61	8	ADK48370	Adk48370 Streptoco	208	26	83.9	414	8	ADS22533	Ads22533 Bacterial
136	26	83.9	62	1	AAAP94262	Aap94262 Antibacte	209	26	83.9	414	9	ABM92109	Abm92109 M. xanthu
137	26	83.9	63	1	AAAP90000	Aap90000 Antibacte	210	26	83.9	416	3	AAAG41542	Aag41542 Arabidops
138	26	83.9	65	6	AAO13635	Aao13635 Human pol	211	26	83.9	418	6	ABP79629	Abp79629 N. gonorr
139	26	83.9	65	6	ABP55939	Abp55939 Oetrinia	212	26	83.9	426	4	AAAB76721	Aab76721 Corynebac
140	26	83.9	69	9	ABE41581	Aeb41581 L. pneumo	213	26	83.9	426	4	AAAG92282	Aag92282 C. glutam
141	26	83.9	72	4	ABG21901	Abg21901 Novel hum	214	26	83.9	426	7	ADL65521	Adl65521 C. glutam
142	26	83.9	72	5	ADK36142	Adk36142 Novel hum	215	26	83.9	431	7	ADD69592	Add69592 Human REM
143	26	83.9	72	9	AEA20997	Aea20997 Novel hum	216	26	83.9	437	6	ADB11164	Adb11164 Allolococ
144	26	83.9	74	3	AAAG10736	Aag10736 Arabidops	217	26	83.9	437	7	ABO62441	Abp62441 Klebsiell
145	26	83.9	84	3	AAAG61260	Aag61260 Arabidops	218	26	83.9	438	6	ADA48730	Ada48730 Rice prot
146	26	83.9	84	3	AAAG57207	Aag57207 Arabidops	219	26	83.9	444	8	ADN27113	Adn27113 Bacterial
147	26	83.9	87	9	ABE38299	Aeb38299 L. pneumo	220	26	83.9	446	7	ABO68439	Abp68439 Pseudomon
148	26	83.9	90	4	AAU31916	Aau31916 Novel hum	221	26	83.9	448	8	ADG25774	Adg25774 Mycobacte
149	26	83.9	91	3	AAAG57206	Aag57206 Arabidops	222	26	83.9	453	7	ABO61786	Abp61786 Klebsiell
150	26	83.9	93	4	AAW92337	Aam92337 Human dig	223	26	83.9	459	8	ADS29238	Ads29238 Bacterial
151	26	83.9	96	3	AAAG57205	Aag57205 Arabidops	224	26	83.9	479	3	AAAG41541	Aag41541 Arabidops
152	26	83.9	96	3	AAAG61259	Aag61259 Arabidops	225	26	83.9	483	8	ADN22834	Adn22834 Bacterial
153	26	83.9	101	8	ADX94447	Adx94447 Plant ful	226	26	83.9	483	8	ADN22833	Adn22833 Bacterial
154	26	83.9	111	4	ABBS0355	Abbs0355 Human sec	227	26	83.9	493	7	ABO80246	Abp80246 Pseudomon
155	26	83.9	111	7	ABO44612	Abp44612 Novel hum	228	26	83.9	504	4	ABE64964	Abp64964 Drosophil
156	26	83.9	111	7	ABO26092	Abp26092 Human pro	229	26	83.9	510	8	ADM67214	Adm67214 Murine ad
157	26	83.9	115	8	ADP84584	Adp84584 Human bre	230	26	83.9	511	6	ABM68291	Abm68291 Photorhab
158	26	83.9	116	6	ABP71848	Abp71848 Human Pur	231	26	83.9	512	3	AAAG41540	Aag41540 Arabidops
159	26	83.9	118	5	ABBO9650	Abbo9650 Amino aci	232	26	83.9	518	5	ABP74027	Abp74027 Candida a
160	26	83.9	118	6	ABG72548	Abg72548 Streptoco	233	26	83.9	526	8	ADN21271	Adn21271 Bacterial
161	26	83.9	118	8	ADU80825	Adu80825 OrfZ, SEQ	234	26	83.9	540	7	ABM86731	Abm86731 Rice abio
162	26	83.9	137	4	AAO05457	Aao05457 Human pol	235	26	83.9	548	6	ABU35322	Abu35322 Protein e
163	26	83.9	138	4	AAO08691	Aao08691 Human pol	236	26	83.9	557	7	ADL04520	Adl04520 M. catarr
164	26	83.9	186	2	AAO33725	Aay33725 Photorhab	237	26	83.9	573	8	ABO65367	Abp65367 Klebsiell
165	26	83.9	187	6	ABM69853	Abm69853 Photorhab	238	26	83.9	581	4	ABB63013	Abb63013 Drosophil
166	26	83.9	188	5	ABBS4792	Abbs4792 Lactococc	239	26	83.9	597	7	ABO73814	Abp73814 Pseudomon
167	26	83.9	191	4	AAAG92339	Aag92339 C. glutam	240	26	83.9	618	4	ABG226117	Abg226117 Novel hum
168	26	83.9	218	5	ABBS5107	Abbs5107 Lactococc	241	26	83.9	641	4	ABG225497	Abg225497 Novel hum
169	26	83.9	220	6	ABP78312	Abp78312 N. gonorr	242	26	83.9	673	6	ABM65701	Abm65701 Propionib
170	26	83.9	223	5	AAE17475	Aae17475 Alpha-S2	243	26	83.9	690	8	ADY05578	Ady05578 Plant ful





XX PI Chalifour R, Gervais F, Gupta A;  
 XX DR WPI; 2001-031852/04.  
 XX PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.  
 XX PS Claim 7; Page 25; 46pp; English.  
 XX CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein  
 XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 31; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KFVFFA 6  
 Db 1 KFVFFA 6  
 RESULT 3  
 AAB82625  
 ID AAB82625 standard; peptide; 6 AA.  
 AC AAB82625;  
 XX DT 02-OCT-2001 (first entry)  
 XX DE All-D peptide used in Alzheimer's disease vaccine.  
 XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 XX KW therapy; antigen.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 1..6 /note= "all D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"  
 XX WO200139796-A2.  
 XX 07-JUN-2001.  
 XX 29-NOV-2000; 2000WO-CA001413.  
 XX 29-NOV-1999; 99US-0168594P.  
 XX 28-NOV-2000; 2000US-00724842.  
 XX (NEUR-) NEUROCHEM INC.  
 XX PI Chalifour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT which elicits production of antibodies to prevent fibrillogenesis and  
 PT associated cellular toxicity.  
 XX Disclosure; Page 11; 31pp; English.  
 XX PS The present sequence is that of an all-D peptide suitable for use for  
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self',  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients  
 XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 31; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KFVFFA 6  
 Db 1 KFVFFA 6  
 RESULT 4  
 AAB82633  
 ID AAB82633 standard; peptide; 6 AA.  
 AC AAB82633;  
 XX DT 02-OCT-2001 (first entry)  
 XX DE All-D peptide used in Alzheimer's disease vaccine.  
 XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 XX KW therapy; antigen.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 1..6 /note= "all D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"  
 XX WO200139796-A2.  
 XX 07-JUN-2001.  
 XX 29-NOV-2000; 2000WO-CA001413.  
 XX 29-NOV-1999; 99US-0168594P.  
 XX 28-NOV-2000; 2000US-00724842.  
 XX (NEUR-) NEUROCHEM INC.  
 XX PI Chalifour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and  
 FT associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in  
 CC preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see A482622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in A482623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6  
 |||||  
 Db 1 KPVFFA 6

RESULT 5  
 AAU96813  
 ID AAU96813 standard; peptide; 6 AA.

AC AAU96813;

DT 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #3.

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6 /note= "Preferably D-form residue"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A t-(A 1 n k) z-A 1 a b (I) where z = 0 - 1;  
 CC A t = an amyloid targeting moiety; A 1 n k = a linker moiety; and A 1 a b  
 CC = a labelling moiety. Also included are imaging amyloid deposition or  
 CC diagnosing an amyloid-related condition in a patient involving  
 CC administering (I) to the patient, and ultrasound imaging (I) in the  
 CC patient to determine the presence of amyloid or amyloid-related condition  
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising  
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and  
 CC instructions for the preparation and use of the radiopharmaceutical in  
 CC the imaging of amyloid or an amyloid-related condition. The agents are  
 CC used for imaging amyloid deposition and for diagnosing an amyloid related  
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible  
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6  
 |||||  
 Db 1 KPVFFA 6

RESULT 6

AAU96821

ID AAU96821 standard; peptide; 6 AA.

AC AAU96821;

DT 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #11.

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6

FT Modified-site 6 /note= "Preferably D-form residue"  
 FT 6 /note= "Ala is amidated"  
 XX WO200207781-A2.  
 PN 31-JAN-2002.  
 PD 25-JUL-2001; 2001WO-CA001071.  
 XX 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.  
 XX (NEUR-) NEUROCHEM INC.  
 PA Gervais P, Kong X, Chalifour R, Migneault D;  
 XX WPI; 2002-371447/40.  
 DR New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 FT plaques and/or for the treatment of amyloidosis disorders.  
 PT Claim 49; Page 21; 57pp; English.  
 PS  
 XX The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A-t-(A-l)n-k-z-A-l-a-b (I) where z = 0 - 1;  
 CC A-t = an amyloid targeting moiety; A-l-n-k = a linker moiety; and A-l-a-b  
 CC = a labelling moiety. Also included are imaging amyloid deposition or  
 CC diagnosing an amyloid-related condition in a patient involving  
 CC administering (I) to the patient, and ultrasound imaging (I) in the  
 CC patient to determine the presence of amyloid or amyloid-related condition  
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising  
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and  
 CC instructions for the preparation and use of the radiopharmaceutical in  
 CC the imaging of amyloid or an amyloid-related condition. The agents are  
 CC used for imaging amyloid deposition and for diagnosing an amyloid related  
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible  
 CC cerebral amyloidoses (transmissible virus dementias), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention  
 XX Sequence 6 AA;  
 SQ  
 Query Match 100.0%; Score 31; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVFA 6  
 DB 1 KVFVFA 6  
 RESULT 7  
 AAU11659  
 ID AAU11659 standard; peptide; 6 AA.  
 XX  
 AC AAU11659;  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Peptide #12, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 6 /note= "C-terminal amide"  
 FT  
 FT  
 XX WO200185093-A2.  
 PN 15-NOV-2001.  
 PD 22-DEC-2000; 2000WO-IB002078.  
 XX 23-DEC-1999; 99US-0171877P.  
 XX (NEUR-) NEUROCHEM INC.  
 PA Green AM, Gervais P;  
 XX WPI; 2002-075222/10.  
 DR Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
 FT disease comprises contacting blood vessel wall cell with amyloid-beta 40  
 PT inhibitor.  
 PT  
 XX Disclosure; Page 10; 68pp; English.  
 PS  
 CC The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting a  
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
 CC The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11659, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 31; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVFA 6  
 DB 1 KVFVFA 6  
 RESULT 8  
 AAU11651  
 ID AAU11651 standard; peptide; 6 AA.  
 XX  
 AC AAU11651;  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Peptide #4, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.  
 XX Synthetic.  
 OS  
 XX WO200185093-A2.  
 PN 15-NOV-2001.  
 PD 22-DEC-2000; 2000WO-IB002078.  
 XX 23-DEC-1999; 99US-0171877P.  
 XX

XX PA (NEUR-) NEUROCHEM INC.  
 XX PI Green AM, Gervais F;  
 XX DR WPI; 2002-075222/10.  
 XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
 XX FT disease comprises contacting blood vessel wall cell with amyloid-beta 40  
 XX PT inhibitor.  
 XX PS Disclosure; Page 10; 68pp; English.  
 XX CC The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting a  
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
 CC The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)  
 XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 31; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6  
 |||||  
 Db 1 KVFVFFA 6

RESULT 9  
 AAE35447  
 ID AAE35447 standard; peptide; 6 AA.  
 AC AAE35447;  
 XX 17-JUN-2003 (first entry)  
 DT  
 XX Abeta peptide #18.  
 DE  
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.  
 XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..6  
 FT Modified-site 6 /note= "D-form residues"  
 FT /note= "C-terminal amide"  
 XX WO200296937-A2.  
 XX 05-DEC-2002.  
 XX 29-MAY-2002; 2002WO-CA000763.  
 XX 29-MAY-2001; 2001US-00867847.  
 XX (NEUR-) NEUROCHEM INC.  
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.  
 XX Prevention and/or treatment of an amyloid-related disease e.g.  
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 XX Claim 1; Page 59; 44pp; English.  
 XX The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention  
 XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 31; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6  
 |||||  
 Db 1 KVFVFFA 6

RESULT 10  
 AAE35440  
 ID AAE35440 standard; peptide; 6 AA.  
 XX AAE35440;  
 AC AAE35440;  
 XX 17-JUN-2003 (first entry)  
 DT  
 XX Abeta peptide #11.  
 DE  
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.  
 XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..6  
 FT /note= "D-form residues"  
 FT /note= "D-form residues"  
 XX WO200296937-A2.  
 XX 05-DEC-2002.  
 XX 29-MAY-2002; 2002WO-CA000763.  
 XX 29-MAY-2001; 2001US-00867847.  
 XX (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;  
 XX WPI; 2003-201269/19.  
 XX  
 XX Prevention and/or treatment of an amyloid-related disease e.g.  
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 XX  
 XX Claim 1; Page 59; 44pp; English.  
 XX  
 CC The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D-  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 100.0%; Score 31; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVFA 6  
 Db 1 KVFVFA 6  
 RESULT 11  
 ADQ37264  
 ID ADQ37264 standard; peptide; 6 AA.  
 XX  
 XX ADQ37264;  
 AC  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Vaccine antigen amyloid-beta related amino acid sequence.  
 XX  
 KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..6  
 FT /note= "D-form residues"  
 XX  
 XX WO2004058239-A1.

XX 15-JUL-2004.  
 XX  
 XX 24-DEC-2003; 2003WO-CA002021.  
 XX  
 XX 24-DEC-2002; 2002US-0436379P.  
 XX 23-JUN-2003; 2003US-0482214P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX  
 XX Gervais F, Bellini F;  
 XX WPI; 2004-543342/52.  
 XX  
 CC Composition for treating e.g. Alzheimer's disease comprises first agent  
 CC that prevents or treats amyloid-beta related disease and second agent  
 CC that is either a peptide or peptidomimetic or an immune system modulator.  
 XX  
 XX Disclosure; Page 67; 143pp; English.  
 XX  
 CC The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as a vaccine antigen in the exemplification of the  
 CC present invention.  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 100.0%; Score 31; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVFA 6  
 Db 1 KVFVFA 6  
 RESULT 12  
 ADQ37316  
 ID ADQ37316 standard; peptide; 6 AA.

XX AC ADQ37316;  
 XX DT 07-OCT-2004 (first entry)  
 XX DE Antifibrillogenic amyloidosis inhibiting peptide.  
 XX KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment; vascular  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychosocial condition;  
 KW vaccine antigen.  
 XX OS Synthetic.  
 XX PN WO2004058239-A1.  
 XX PD 15-JUL-2004.  
 XX PF 24-DEC-2003; 2003WO-CA002021.  
 XX PR 24-DEC-2002; 2002US-0436379P.  
 XX PR 23-JUN-2003; 2003US-0482214P.  
 XX PA (NEUR-) NEUROCHEM INT LTD.  
 XX FI Gervais F, Bellini F;  
 XX DR WPI; 2004-543342/52.  
 XX PT Composition for treating e.g. Alzheimer's disease comprises first agent  
 PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.  
 XX PS Disclosure; Page 69; 143pp; English.  
 XX CC The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 26+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYVFFA 6

DB 1 KFYVFFA 6

RESULT 13

ADQ37324  
 ID ADQ37324 standard; peptide; 6 AA.

XX AC ADQ37324;

XX DT 07-OCT-2004 (first entry)

XX DE Antifibrillogenic amyloidosis inhibiting peptide.

XX KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychosocial condition;  
 KW vaccine antigen.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 XX FT Modified-site 6 /note= "amidated"

XX PN WO2004058239-A1.

XX PD 15-JUL-2004.

XX PF 24-DEC-2003; 2003WO-CA002021.

XX PR 24-DEC-2002; 2002US-0436379P.

XX PR 23-JUN-2003; 2003US-0482214P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX FI Gervais F, Bellini F;

XX DR WPI; 2004-543342/52.

XX PT Composition for treating e.g. Alzheimer's disease comprises first agent  
 PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.

XX PS Disclosure; Page 70; 143pp; English.

XX CC The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

XX CC nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic delirium, hallucination, sexual disorder, weight loss, psychosis, a sleep ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt) in a subject e.g. human having a presenilin gene; having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

XX CC Sequence 6 AA;

Query Match 100.0%; Score 31; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
|||||  
Db 1 KVFVFA 6

RESULT 14  
ADQ37272  
ID ADQ37272 standard; peptide; 6 AA.

XX AC ADQ37272;  
XX DT 07-OCT-2004 (first entry)  
XX DE Vaccine antigen amyloid-beta related amino acid sequence.

XX KW amyloid-beta; amyloid-beta related disease;  
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
KW cardiant; antidepressant; endocrine; hypnotic;  
KW amyloid-beta fibril formation modulator; immune system modulator;  
KW Alzheimer's disease; mild cognitive impairment;  
KW mild-to-moderate cognitive impairment; vascular dementia;  
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

KW senile dementia; Down's syndrome; inclusion body myositis;  
KW age-related macular degeneration; hypothyroidism;  
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
KW behavioural dysfunction; neurological condition; psychological condition; vaccine antigen.

XX OS Synthetic.

Key Location/Qualifiers  
Misc-difference 1..6 /note= "D-form residues"  
Modified-site 6 /note= "amidated"

WO2004058239-A1.  
15-JUL-2004.  
24-DEC-2003; 2003WO-CA002021.  
24-DEC-2002; 2002US-0436379P.  
23-JUN-2003; 2003US-0482214P.  
(NEUR-) NEUROCHEM INT LTD.  
Gervais F, Bellini F;  
WPI; 2004-543342/52.

Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.

Disclosure; Page 67; 143pp; English.

The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

XX CC nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic delirium, hallucination, sexual disorder, weight loss, psychosis, a sleep ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt) in a subject e.g. human having a presenilin gene; having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.



XX SQ Sequence 6 AA;  
Query Match 100.0%; Score 31; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KPVFFA 6  
Db 1 KPVFFA 6  
RESULT 15  
ADY37931  
ID ADY37931 standard; peptide; 6 AA.  
XX AC ADY37931;  
XX DT 19-MAY-2005 (first entry)  
XX DE Amyloid-targeting peptide, SEQ ID NO:11, for use in imaging agent.  
XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
KW transmissible spongiform encephalopathy; scrapie; BSE;  
KW Alzheimers disease; neurological disease; amyloidosis;  
KW non-insulin dependent diabetes; metabolic disorder.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Modified-site 6 /note= "C-terminal amide"  
XX FN US2005048000-A1.  
XX PD 03-MAR-2005.  
XX PF 03-DEC-2003; 2003US-00728028.  
XX PR 25-JUL-2000; 2000US-0220808P.  
XX PR 24-JUL-2001; 2001US-00915092.  
XX PR 29-JAN-2003; 2003US-0443291P.  
XX PA (NEUR-) NEUROCHEM INT LTD.  
XX PI Gervais F, Kong X, Chalifour R, Migneault D;  
XX WPI; 2005-212201/22.  
XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform encephalopathy, primary amyloidosis or Alzheimer's disease.  
XX PS Disclosure; SEQ ID NO 11; 34pp; English.  
XX CC The invention relates to an amyloid-targeting imaging agent. The imaging agent comprises an amyloid targeting moiety (such as a peptide) joined to a labeling moiety via a linking moiety, and is preferably able to cross the blood-brain barrier. The invention also relates to a kit for preparing a radiopharmaceutical preparation from the imaging agent of the invention, a method for imaging amyloid deposition in a patient and a method for diagnosing an amyloid-related condition in a patient. The amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-related conditions such as Creutzfeld-Jakob disease (CJD), Kuru, transmissible cerebral amyloidoses (also known as transmissible virus dementias), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a patient. The agent does not exhibit excessive toxicity or irritation, does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence prevention of the undesirable effects of such disorders. Sequences ADY37921-ADY3947 and ADY37949 represent peptides which may be used as the amyloid-targeting moiety in an imaging agent of the invention.  
XX SQ Sequence 6 AA;  
Query Match 100.0%; Score 31; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KPVFFA 6  
Db 1 KPVFFA 6  
RESULT 16  
ADY37923  
ID ADY37923 standard; peptide; 6 AA.  
XX AC ADY37923;  
XX DT 19-MAY-2005 (first entry)  
XX DE Amyloid-targeting peptide, SEQ ID NO:3, for use in imaging agent.  
XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
KW transmissible spongiform encephalopathy; scrapie; BSE;  
KW Alzheimers disease; neurological disease; amyloidosis;  
KW non-insulin dependent diabetes; metabolic disorder.  
XX OS Synthetic.  
XX FN US2005048000-A1.  
XX PD 03-MAR-2005.  
XX PF 03-DEC-2003; 2003US-00728028.  
XX PR 25-JUL-2000; 2000US-0220808P.  
XX PR 24-JUL-2001; 2001US-00915092.  
XX PR 29-JAN-2003; 2003US-0443291P.  
XX PA (NEUR-) NEUROCHEM INT LTD.  
XX PI Gervais F, Kong X, Chalifour R, Migneault D;  
XX WPI; 2005-212201/22.  
XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform encephalopathy, primary amyloidosis or Alzheimer's disease.  
XX PS Disclosure; SEQ ID NO 3; 34pp; English.  
XX CC The invention relates to an amyloid-targeting imaging agent. The imaging agent comprises an amyloid targeting moiety (such as a peptide) joined to a labeling moiety via a linking moiety, and is preferably able to cross the blood-brain barrier. The invention also relates to a kit for preparing a radiopharmaceutical preparation from the imaging agent of the invention, a method for imaging amyloid deposition in a patient and a method for diagnosing an amyloid-related condition in a patient. The amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-related conditions such as Creutzfeld-Jakob disease (CJD), Kuru, transmissible cerebral amyloidoses (also known as transmissible virus dementias), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a patient. The agent does not exhibit excessive toxicity or irritation, does not induce an allergic response, and permits an earlier diagnosis of



CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.  
 XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
 DB 1 KVFVFA 6  
 |||||

RESULT 17  
 ABM89186  
 ID ABM89186 standard; protein; 336 AA.  
 XX  
 AC ABM89186;  
 XX  
 DT 02-JUN-2005 (first entry)  
 XX  
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:7432.  
 XX  
 KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.  
 XX  
 OS Oryza sativa.  
 XX  
 PN WO2003008540-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 XX 21-JUN-2002; 2002WO-US019668.  
 XX  
 PR 22-JUN-2001; 2001US-0300112P.  
 PR 24-AUG-2001; 2001US-0314662P.  
 PR 26-SEP-2001; 2001US-0325277P.  
 PR 21-NOV-2001; 2001US-0332132P.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;  
 PI Moughamer T, Provart N, Ricke D, Zhu T;  
 XX  
 DR WPI; 2003-248011/24.  
 XX  
 PT New stress-responsive nucleic acid, useful for altering the  
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
 PT stress, salt stress or osmotic stress.  
 XX  
 PS Claim 1; SEQ ID NO 7432; 89pp; English.  
 XX  
 CC The invention relates to novel abiotic stress responsive polynucleotides  
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
 CC cells, and plants containing such polynucleotides. Also disclosed are  
 CC methods for using the polynucleotides and polypeptides to alter the  
 CC responsiveness of a plant to abiotic stress. The invention is useful in  
 CC agriculture. The nucleic acid is useful for determining whether a test  
 CC plant has been exposed to an abiotic stress condition. It is also useful  
 CC for selecting an agent that alters abiotic stress regulated  
 CC polynucleotide expression in a plant cell, and to identify a homolog or  
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
 CC molecule and the polypeptide encoded by it are useful in altering the  
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
 CC stress, osmotic stress or any of their combinations. The present sequence  
 CC is used in the exemplification of the invention  
 XX  
 SQ Sequence 336 AA;

Query Match 100.0%; Score 31; DB 7; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
 DB 80 KVFVFA 85  
 |||||

RESULT 18  
 ADK35620  
 ID ADK35620 standard; protein; 202 AA.  
 XX  
 AC ADK35620;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Novel human polypeptide SeqID7702.  
 XX  
 KW antiarthritic; antiparkinsonian; neuroprotective; nootropic;  
 KW immunosuppressive; cytostatic; antiposoriatic; antiinflammatory;  
 KW antibacterial; antiviral; antifungal; antiparasitic; gene therapy;  
 KW arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer;  
 KW psoriasis; inflammatory bowel disease; infection; bacteria; virus;  
 KW fungus; parasite; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..202  
 FT /label= OTHER  
 FT /note= "OTHER= All Xaa's in this sequence are unknown  
 FT amino acids or the site of a stop codon within the DNA  
 FT sequence"  
 XX  
 PN WO200216439-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 XX 05-MAR-2001; 2001WO-US004941.  
 PF  
 PR 07-MAR-2000; 2000US-00519705.  
 PR 19-MAY-2000; 2000US-00574454.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2002-280918/32.  
 XX  
 PT Isolated polynucleotide encoding bone marrow derived polypeptides useful  
 PT for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's  
 PT disease, and inflammatory bowel disease.  
 XX  
 PS Claim 20; SEQ ID NO 7702; 504pp; English.  
 XX  
 CC This invention relates to a novel isolated polynucleotide comprising a  
 CC nucleotide sequence selected from one of 1680 sequences, a mature protein  
 CC coding portion of them, an active domain of them and their complementary  
 CC sequences. The invention may be useful for the production of compounds  
 CC with an antiarthritic, antiparkinsonian, neuroprotective, nootropic,  
 CC immunosuppressive, cytostatic, antiposoriatic, antiinflammatory, In  
 CC antibacterial, antiviral, antifungal or antiparasitic activity. In  
 CC addition, the disclosed sequences may be useful for gene therapy. The  
 CC polypeptides or their antibodies are useful for treating many diseases  
 CC such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer,  
 CC psoriasis, inflammatory bowel disease and infections caused by bacteria,  
 CC viruses, fungi or parasites. The present sequence is that of a human  
 CC polypeptide of the invention.  
 XX  
 SQ Sequence 202 AA;

Query Match 96.8%; Score 30; DB 5; Length 202;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPVFFA 6  
Db 35 KFIFFA 40

RESULT 19  
ABBI7989  
ID ABB17989 standard; protein; 75 AA.  
XX ABB17989;  
XX  
DT 23-JAN-2002 (first entry)  
XX  
DE Human nervous system related polypeptide SEQ ID NO 6646.  
XX  
XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW antiparkinsonian; antischlicking; antianemic; antiarthritic; cancer;  
KW antineumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
XX WO200159063-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US001334.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239335P.  
PR 13-OCT-2000; 2000US-0239337P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 01-DEC-2000; 2000US-0251160P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-541565/60.  
DR N-PSDB; ABA14315.  
XX  
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating nervous system cancers  
PT and metastases.  
XX  
XX Claim 11; SEQ ID NO 6646; 1701pp + Sequence Listing; English.  
XX  
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins  
CC (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)  
XX  
XX Sequence 75 AA;  
SQ  
Query Match 90.3%; Score 28; DB 4; Length 75;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVFVFFA 6  
||:||||  
Db 5 KLFVFA 10  
RESULT 20  
ADN23626  
ID ADN23626 standard; protein; 452 AA.  
XX  
AC ADN23626;  
XX  
DT 02-DEC-2004 (first entry)  
XX

DE Bacterial polypeptide #6279.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
XX US2003233675-A1.  
XX 18-DEC-2003.  
XX 20-FEB-2003; 2003US-00369493.  
XX 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
XX (SLAT/) SLATER S C.  
XX (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
XX  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 6279; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
XX Sequence 452 AA;  
SQ  
Query Match 90.3%; Score 28; DB 8; Length 452;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVFVFFA 6  
:|||||  
Db 291 RVVFFA 296  
RESULT 21

```

ADN46740
ID  ADN46740 standard; protein; 485 AA.
XX
AC  ADN46740;
XX
DT  01-JUL-2004 (first entry)
XX
XX  Thermococcus kodakaraensis KOD1 protein sequence SeqID618.
DE
XX
XX  gene disruption; gene targeting; marker gene; transformation;
KW  homologous recombination; hyperthermostable archaeobacterium; KOD1;
KW  gene structure; gene function; enzyme activity; medicine;
KW  forensic science; food; drug inspection; molecular biology; immunology.
XX
XX  Thermococcus kodakaraensis.
OS
XX
XX  WO2004022736-A1.
XX
XX  18-MAR-2004.
PD
XX
XX  29-AUG-2003; 2003WO-IB003597.
XX
XX  30-AUG-2002; 2002JP-00319011.
XX
XX  (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA
XX
XX  Imanaka T, Atomi H;
PI
XX
XX  WPI; 2004-257583/24.
DR
XX
XX  Method for disrupting targeted gene in genome of organism particularly
PT  thermostable bacterium and with genome chips for analysis, applicable in
PT  studying gene structure and functions.
XX
XX  Claim 9; SEQ ID NO 618; 598pp; Japanese.
XX
XX  This invention relates to a novel method for targeting disruption of an
CC  arbitrary gene in a genome of an organism which comprises providing the
CC  whole sequential data of the genome of such organism, selecting at least
CC  1 arbitrary region in the sequence, providing a vector that contains a
CC  sequence homologous with the selected region and a marker gene,
CC  transformation, and homologous recombination. The genome is preferably
CC  the genome of a hyperthermostable archaeobacterium, particularly
CC  Thermococcus kodakaraensis KOD1. The method is for targeting the
CC  disruption of a gene in the genome of an organism, which is applicable in
CC  studying gene structure and functions as well as enzyme activities of
CC  encoded proteins and useful in medicine, forensic science, food or drug
CC  inspection, molecular biology and immunology. With this method, the
CC  disruption of a gene at an arbitrary position in a genome can be achieved
CC  efficiently and reliably. The present sequence is that of a protein
CC  encoded by the genome of Thermococcus kodakaraensis which was derived
CC  using the method of the invention. Note: The sequence data for this
CC  patent did not form part of the printed specification, but was obtained
CC  in electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 485 AA;
SQ
    Query Match          90.3%; Score 28; DB 8; Length 485;
    Best Local Similarity 83.3%; Pred. No. 9.9e+02;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy  1 KFVFPA 6
    :|||||
Db  339 RFVFPA 344

RESULT 22
AAY19993
ID  AAY19993 standard; protein; 490 AA.
XX
XX  AAY19993;
AC
XX

```

---

```

DT  19-JUL-1999 (first entry)
XX
XX  B. burgdorferi antigenic protein, t752.aa.
DE
XX
XX  Antigenic protein; vaccine; Lyme disease; infection; detection.
KW
XX
XX  Borrelia burgdorferi.
OS
XX
XX  WO9859071-A1.
XX
XX  30-DEC-1998.
PD
XX
XX  18-JUN-1998; 98WO-US012718.
XX
XX  20-JUN-1997; 97US-0050359P.
XX  22-JUL-1997; 97US-0053344P.
XX  22-JUL-1997; 97US-0053377P.
XX  03-SEP-1997; 97US-0057483P.
XX
XX  (HUMA-) HUMAN GENOME SCI INC.
PA  (MEDI-) MEDIMMUNE INC.
XX
XX  Choi GH, Erwin AL, Hanson MS, Lathigra R;
PI
XX
XX  WPI; 1999-189980/16.
DR  N-PSDB; ARX61690.
XX
XX  New isolated Borrelia burgdorferi nucleic acids - used to develop
PT  products for the diagnosis, prevention and treatment of diseases caused
PT  by Borrelia, particularly Lyme disease.
XX
XX  Claim 12; Page 153; 275pp; English.
XX
XX  This sequence represents a Borrelia burgdorferi (Bb) protein of the
CC  invention, which is suitable for use in a vaccine. The Bb polypeptides
CC  can be used in vaccines for eliciting protective antibodies to members of
CC  the Borrelia genus, particularly for the use against Lyme disease in
CC  humans and animals. They can be used for preventing or attenuating an
CC  infection caused by a member of the Borrelia genus. The products can also
CC  be used for detection of members of the Borrelia genus
XX
XX  Sequence 490 AA;
SQ
    Query Match          90.3%; Score 28; DB 2; Length 490;
    Best Local Similarity 83.3%; Pred. No. 1e+03;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy  1 KFVFPA 6
    :|||||
Db  23 RFVFPA 28

RESULT 23
AAR95594
ID  AAR95594 standard; protein; 506 AA.
XX
XX  AAR95594;
AC
XX
XX  16-OCT-2003 (revised)
DT
XX  14-OCT-1996 (first entry)
XX
XX  Arabidopsis fatty acid elongation FAEL enzyme.
DE
XX
XX  Fatty acid elongation gene; FAEL; transgenic plant; seed oil;
KW  vegetable oil; Brassica napus; canola; oilseed rape; eicosenoic acid;
KW  erucic acid.
XX
XX  Arabidopsis thaliana; ecotype WS.
OS
XX
XX  WO9613582-A1.
XX
XX  09-MAY-1996.
PD
XX

```

PP	23-OCT-1995;	95WO-US013918.
XX		
XX	26-OCT-1994;	94US-00329603.
PP	(DNAP ) DNA PLANT TECHNOLOGY CORP.	
XX		
XX	James DW, Lim B, Keller J, Dooner HK,	
PI	WPI; 1996-239495/24.	
XX	N-PSDB; AAT27036.	
DR		
DR	New DNA constructs contg. FAE1 gene sequences - used to produce	
PT	transgenic plants with modified fatty acid content in plant organs or	
FT	parts, esp. seeds.	
XX		
PS	Example 1; Page 36; 48pp; English.	
XX		
CC	Arabidopsis fatty acid elongation enzyme FAE1 (AAR95594) catalyses the	
CC	conversion of oleic acid (18:1) to eicosenoic acid (20:1) and of	
CC	eicosenoic acid to erucic acid (22:1). Its amino acid sequence was	
CC	deduced from that of a clone (AAT27036) isolated from a cDNA library	
CC	prep'd. from Arabidopsis green siliques. Expression of the FAE1 enzyme in	
CC	transgenic plants, e.g. Brassica napus, can be used to modulate the fatty	
CC	acid content of the plant, partic. the seed oil. Use of antisense DNA	
CC	constructs suppresses the native FAE1 gene, allowing prodn. of edible	
CC	oils with reduced content of very long chain fatty acids (VLCFA). Use of	
CC	sense DNA constructs allows prodn. of oils with raised VLCFA content for	
CC	industrial use. (Updated on 16-OCT-2003 to standardise OS field)	
XX		
SQ	Sequence 506 AA;	
	Query Match	90.3%; Score 28; DB 2; Length 506;
	Best Local Similarity	83.3%; Pred. No. 1e+03;
	Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy	1 KVFVEFA 6	
Dd		
	356 KFLPFPA 361	
RESULT 24		
AAE17850	ID	AAE17850 standard; protein; 506 AA.
XX	AC	AAE17850;
XX	DT	29-AUG-2003 (revised)
XX	DT	22-APR-2002 (first entry)
DE	XX	Alternative version of At399 protein.
KW	XX	Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW	XX	very long chain fatty acid; VLCFA; FAE1 protein; chlmeric.
OS	XX	Arabidopsis thaliana.
OS	XX	Brassica napus.
OS	XX	Chimeric.
Key	XX	Location/Qualifiers
Region	XX	1..399
FT	FT	/note= "Arabidopsis thaliana elongase KCS protein"
FT	FT	400..506
FT	FT	/note= "Brassica napus elongase KCS protein"
FT	FT	Misc-difference 502
FT	FT	/note= "Encoded by CMA"
XX	XX	WO200194565-A2.
PN	XX	
XX	XX	13-DEC-2001.
PD	XX	
XX	XX	08-JUN-2001; 2001WO-US018737.
XX	XX	08-JUN-2000; 2000US-0210326P.
PR	XX	

PI Jaworski JG, Blacklock BJ;  
 XX WPI; 2002-154572/20.  
 DR N-PSDB; AAD28514.  
 XX  
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic  
 PT acids encoding the polypeptide, useful for producing very long chain  
 PT fatty acids.  
 XX  
 PS Example 1; Fig 1-5; 139pp; English.  
 XX  
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase  
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic  
 CC activity and nucleic acid molecules encoding such polypeptides.  
 CC Polypeptides of the invention are useful for catalysing the condensation  
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of  
 CC C20 fatty acyl CoA. They are especially useful for producing very long  
 CC chain fatty acids (VLCFA) and may be used in the development of reagents  
 CC for various purposes, e.g., immunological reagents to monitor expression  
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor  
 CC inheritance of an elongase KCS gene in plant breeding programs. The  
 CC present sequence is Arabidopsis thaliana FAE1-Brassica napus elongase  
 CC KCS chimeric protein designated as At399. (Updated on 29-AUG-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 506 AA;

Query Match 90.3%; Score 28; DB 5; Length 506;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
 ||:||||  
 Db 356 KFLFFA 361

RESULT 26  
 AAEL17625  
 ID AAEL17625 standard; protein; 506 AA.  
 XX  
 AC AAEL17625;  
 XX  
 DT 22-APR-2002 (first entry)  
 XX  
 DE Arabidopsis thaliana FAE1 protein mutant, At K92R.  
 XX  
 KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;  
 KW very long chain fatty acid; VLCFA; FAE1 gene; mutant; mutein.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 92  
 FT /note= "Wild-type Lys substituted with Arg"  
 XX  
 XX WO200194565-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 08-JUN-2001; 2001WO-US018737.  
 XX  
 PR 08-JUN-2000; 2000US-0210326P.  
 XX  
 PA (UTMI-) UNIV MIAMI.  
 XX  
 PI Jaworski JG, Blacklock BJ;  
 XX WPI; 2002-154572/20.  
 DR N-PSDB; AAD28517.  
 XX  
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic  
 PT acids encoding the polypeptide, useful for producing very long chain  
 PT fatty acids.

XX Claim 7; Fig 1-6; 139pp; English.  
 XX  
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase  
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic  
 CC activity and nucleic acid molecules encoding such polypeptides.  
 CC Polypeptides of the invention are useful for catalysing the condensation  
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of  
 CC C20 fatty acyl CoA. They are especially useful for producing very long  
 CC chain fatty acids (VLCFA) and may be used in the development of reagents  
 CC for various purposes, e.g., immunological reagents to monitor expression  
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor  
 CC inheritance of an elongase KCS gene in plant breeding programs. The  
 CC present sequence is a mutant of Arabidopsis thaliana elongase KCS  
 CC protein/FAE1 protein designated as At K92R  
 XX  
 SQ Sequence 506 AA;

Query Match 90.3%; Score 28; DB 5; Length 506;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
 ||:||||  
 Db 356 KFLFFA 361

RESULT 27  
 AAEL17621  
 ID AAEL17621 standard; protein; 506 AA.  
 XX  
 AC AAEL17621;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 22-APR-2002 (first entry)  
 XX  
 DE Brassica napus elongase KCS-A. thaliana FAE1 chimeric protein, Bnl76.  
 XX  
 KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;  
 KW very long chain fatty acid; VLCFA; FAE1 gene; chimeric.  
 XX  
 OS Brassica napus.  
 OS Arabidopsis thaliana.  
 OS Chimeric.  
 XX  
 XX Key Location/Qualifiers  
 FH Region 1. .176  
 FT /note= "Brassica napus elongase KCS protein"  
 FT Region 177. .506  
 FT /note= "Arabidopsis thaliana FAE1 protein"  
 XX  
 XX WO200194565-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 08-JUN-2001; 2001WO-US018737.  
 XX  
 PR 08-JUN-2000; 2000US-0210326P.  
 XX  
 PA (UTMI-) UNIV MIAMI.  
 XX  
 PI Jaworski JG, Blacklock BJ;  
 XX WPI; 2002-154572/20.  
 DR N-PSDB; AAD28513.  
 XX  
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic  
 PT acids encoding the polypeptide, useful for producing very long chain  
 PT fatty acids.  
 XX  
 PS Example 1; Fig 1-5; 139pp; English.  
 XX  
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase

CC (KCS) polypeptides with altered substrate specificity and/or catalytic  
 CC activity and nucleic acid molecules encoding such polypeptides.  
 CC Polypeptides of the invention are useful for catalyzing the condensation  
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of  
 CC C20 fatty acyl CoA. They are especially useful for producing very long  
 CC chain fatty acids (VLCFA) and may be used in the development of reagents  
 CC for various purposes, e.g., immunological reagents to monitor expression  
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor  
 CC inheritance of an elongase KCS gene in plant breeding programs. The  
 CC present sequence is *Brassica napus* elongase KCS- Arabidopsis thaliana  
 CC FAE1 chimeric protein designated as Bn176. (Updated on 29-AUG-2003 to  
 CC standardise OS field)  
 CC XX

XX SQ Sequence 506 AA;

Query Match 90.3%; Score 28; DB 5; Length 506;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFPA 6  
 ||:||||  
 Db 356 KFLFFPA 361

RESULT 28

AAE17608  
 ID AAE17608 standard; protein; 506 AA.

XX AC AAE17608;

XX DT 22-APR-2002 (first entry)

XX DE Arabidopsis thaliana elongase KCS protein.

XX KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;  
 XX very long chain fatty acid; VLCFA; FAE1 protein.

XX OS Arabidopsis thaliana.

XX PN W0200194565-A2.

XX PD 13-DEC-2001.

XX PF 08-JUN-2001; 2001WO-US018737.

XX PR 08-JUN-2000; 2000US-0210326P.

XX PA (UYMI-) UNIV MIAMI.

XX PI Jaworski JG, Blacklock BJ;

XX WPI; 2002-154572/20.

XX DR N-PSDB; AAD28500.

XX PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic  
 PT acids encoding the polypeptide, useful for producing very long chain  
 PT fatty acids.

XX PS Example 3; Fig 1-1; 139pp; English.

XX CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase  
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic  
 CC activity and nucleic acid molecules encoding such polypeptides.

XX CC Polypeptides of the invention are useful for catalyzing the condensation  
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of  
 CC C20 fatty acyl CoA. They are especially useful for producing very long  
 CC chain fatty acids (VLCFA) and may be used in the development of reagents  
 CC for various purposes, e.g., immunological reagents to monitor expression  
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor  
 CC inheritance of an elongase KCS gene in plant breeding programs. The  
 CC present sequence is Arabidopsis thaliana elongase KCS protein encoded by  
 CC FAE1 gene  
 CC XX

SQ Sequence 506 AA;

Query Match 90.3%; Score 28; DB 5; Length 506;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFPA 6  
 ||:||||  
 Db 356 KFLFFPA 361

RESULT 29

AEA37517  
 ID AEA37517 standard; protein; 506 AA.

XX AC AEA37517;

XX DT 11-AUG-2005 (first entry)

XX DE Arabidopsis sp. fatty acid elongase 1 (FAE1) protein.

XX KW vector; transformation; plant; fatty acid elongase 1;

XX 3-ketoacyl-CoA synthase; promoter; gene expression; seed; oil; enzyme.

XX OS Arabidopsis sp.

XX PN W02005052162-A1.

XX PD 09-JUN-2005.

XX PF 24-NOV-2004; 2004WO-CA002021.

XX PR 25-NOV-2003; 2003US-0524645P.

XX PA (CANA ) NAT RES COUNCIL CANADA.

XX PI Mietkiewska E, Taylor DC, Katavic V;

XX DR WPI; 2005-418004/42.

XX N-PSDB; AEA37518.

XX PT New expression vector for transforming a cell comprising a gene coding  
 PT for a plant fatty acid elongase, useful for altering erucic acid content  
 PT or the very long chain fatty acid content (C20 or greater) in a plant.

XX PS Disclosure; SEQ ID NO 26; 72pp; English.

XX CC The invention relates to an expression vector for transforming a cell.  
 CC The expression vector comprises a gene coding for a plant fatty acid  
 CC elongase (FAE, also designated 3-ketoacyl-CoA synthase (KCS)) in reading  
 CC frame alignment with a promoter capable of increasing the expression of  
 CC the gene, when the transformed cell is in a seed, sufficient to increase  
 CC the proportion of very long chain monounsaturated fatty acid when  
 CC compared with a control cell. Also described are: (1) a cell comprising a  
 CC heterologous gene coding for a heterologous plant fatty acid elongase or  
 CC its allelic variant, the cell being capable of producing an increase in  
 CC proportion of a very long chain monounsaturated fatty acid when compared  
 CC a control cell lacking the heterologous gene; (2) a seed comprising the  
 CC plant cells above; (3) a plant comprising the plant cells; and (4) a  
 CC method of altering erucic acid content of a plant-derived oil. The gene  
 CC coding for a plant fatty acid elongase is a Nasturtium, Crambe, or  
 CC Arabidopsis fatty acid elongase gene. The cell is a fungal cell,  
 CC preferably yeast cell, or a plant cell, specifically a plant seed cell.  
 CC The plant cell additionally comprises a further heterologous gene coding  
 CC for an additional heterologous plant fatty acid elongase or its allelic  
 CC variant or a heterologous plant desaturase gene or its allelic variant.  
 CC It is capable of producing oil with an increased content of erucic acid  
 CC or other very long chain fatty acid (C20 or greater). The heterologous  
 CC gene codes for a 3-ketoacyl-CoA synthase. The very long chain  
 CC monounsaturated fatty acid comprises erucic acid. The heterologous plant  
 CC fatty acid elongase gene is useful for altering erucic acid content in a  
 CC plant or the very long chain fatty acid content (C20 or greater) in a  
 CC plant. The vector is useful for altering erucic acid content in a plant.

CC This sequence represents a *Arabidopsis* sp. FAE1.

XX Sequence 506 AA;

Query Match 90.3%; Score 28; DB 9; Length 506;

Best Local Similarity 83.3%; Pred. No. 1e+03; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6

Db 356 KFLFFA 361

RESULT 30

AAV1992 ID AAV1992 standard; protein; 508 AA.

XX AC AAV1992;

DT 19-JUL-1999 (first entry)

DE B. burgdorferi antigenic protein, f752.aa.

KW Antigenic protein; vaccine; Lyme disease; infection; detection.

XX OS Borrelia burgdorferi.

XX PN W09859071-A1.

XX PD 30-DEC-1998.

XX PF 18-JUN-1998; 98WO-US012718.

XX PR 20-JUN-1997; 97US-0050359P.

XX PR 22-JUL-1997; 97US-0053344P.

XX PR 22-JUL-1997; 97US-0053377P.

XX PR 03-SEP-1997; 97US-0057483P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (MEDI-) MEDIMMUNE INC.

XX PI Choi GH, Erwin AL, Hanson MS, Lathigra R;

XX WPI; 1999-189980/16.

XX DR N-PSDB; AAX61689.

XX PT New isolated *Borrelia burgdorferi* nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by *Borrelia*, particularly Lyme disease.

XX PS Claim 12; Page 153; 275pp; English.

XX CC This sequence represents a *Borrelia burgdorferi* (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the *Borrelia* genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the *Borrelia* genus. The products can also be used for detection of members of the *Borrelia* genus

XX SQ Sequence 508 AA;

Query Match 90.3%; Score 28; DB 2; Length 508;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6

Db 41 RVPFFA 46

RESULT 31

ABU19128

ID ABU19128 standard; protein; 508 AA.

XX AC ABU19128;

DT 19-JUN-2003 (first entry)

DE Protein encoded by *Prokaryotic essential gene #4655*.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX KW *Borrelia burgdorferi*.

XX OS WO200277183-A2.

XX PN 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA22998.

XX New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 47052; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 508 AA;

Query Match

90.3%; Score 28; DB 6; Length 508;



Best Local Similarity 83.3%; Pred. No. 1e+03; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
:|||||  
Db 41 RFVFFA 46

RESULT 32  
ABU24005  
ID ABU24005 standard; protein; 571 AA.  
XX  
AC ABU24005;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #9532.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Clostridium acetobutylicum.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
WPI; 2003-029926/02.  
DR N-PSDB; ACA27875.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 51929; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 571 AA;  
Query Match 90.3%; Score 28; DB 6; Length 571;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVFVFA 6  
:|||||  
Db 314 KFMFFA 319

RESULT 33  
ADN19501  
ID ADN19501 standard; protein; 1089 AA.  
XX  
AC ADN19501;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #2154.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 2154; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 1089 AA;

Query Match 90.3%; Score 28; DB 8; Length 1089;

Best Local Similarity 83.3%; Pred. No. 2.2e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6

Db 13 KPVFFS 18

#### RESULT 34

AAG61668

ID AAG61668 standard; protein; 52 AA.

XX

AC AAG61668;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 80017.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; Genetic mapping; gene expression control; promoter;  
 KW termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-00301439.

XX

PR 25-FEB-1999; 99US-0121825P.

PR

PR 05-MAR-1999; 99US-0123180P.

PR

PR 09-MAR-1999; 99US-0123548P.

PR

PR 23-MAR-1999; 99US-0125788P.

PR

PR 25-MAR-1999; 99US-0126264P.

PR

PR 29-MAR-1999; 99US-0126785P.

PR

PR 01-APR-1999; 99US-0127462P.

PR

PR 06-APR-1999; 99US-0128234P.

PR

PR 08-APR-1999; 99US-0128714P.

PR

PR 16-APR-1999; 99US-0129845P.

PR

PR 19-APR-1999; 99US-0130077P.

PR

PR 21-APR-1999; 99US-0130449P.

PR

PR 23-APR-1999; 99US-0130510P.

PR

PR 23-APR-1999; 99US-0130891P.

PR

PR 28-APR-1999; 99US-0131449P.

PR 14-MAY-1999; 99US-0134370P.  
 PR 18-MAY-1999; 99US-0134768P.  
 PR 19-MAY-1999; 99US-0134941P.  
 PR 20-MAY-1999; 99US-0135124P.  
 PR 21-MAY-1999; 99US-0135353P.  
 PR 24-MAY-1999; 99US-0135629P.  
 PR 25-MAY-1999; 99US-0136021P.  
 PR 27-MAY-1999; 99US-0136392P.  
 PR 28-MAY-1999; 99US-0136782P.  
 PR 01-JUN-1999; 99US-0137222P.  
 PR 03-JUN-1999; 99US-0137528P.  
 PR 04-JUN-1999; 99US-0137502P.  
 PR 07-JUN-1999; 99US-0137724P.  
 PR 08-JUN-1999; 99US-0138094P.  
 PR 10-JUN-1999; 99US-0138540P.  
 PR 10-JUN-1999; 99US-0138847P.  
 PR 14-JUN-1999; 99US-0139119P.  
 PR 16-JUN-1999; 99US-0139452P.  
 PR 16-JUN-1999; 99US-0139453P.  
 PR 17-JUN-1999; 99US-0139492P.  
 PR 18-JUN-1999; 99US-0139454P.  
 PR 18-JUN-1999; 99US-0139455P.  
 PR 18-JUN-1999; 99US-0139456P.  
 PR 18-JUN-1999; 99US-0139457P.  
 PR 18-JUN-1999; 99US-0139458P.  
 PR 18-JUN-1999; 99US-0139459P.  
 PR 18-JUN-1999; 99US-0139460P.  
 PR 18-JUN-1999; 99US-0139461P.  
 PR 18-JUN-1999; 99US-0139462P.  
 PR 18-JUN-1999; 99US-0139463P.  
 PR 18-JUN-1999; 99US-0139750P.  
 PR 18-JUN-1999; 99US-0139763P.  
 PR 21-JUN-1999; 99US-0139817P.  
 PR 22-JUN-1999; 99US-0139899P.  
 PR 23-JUN-1999; 99US-0140353P.  
 PR 24-JUN-1999; 99US-0140354P.  
 PR 28-JUN-1999; 99US-0140895P.  
 PR 29-JUN-1999; 99US-0140991P.  
 PR 30-JUN-1999; 99US-0141287P.  
 PR 01-JUL-1999; 99US-0141842P.  
 PR 02-JUL-1999; 99US-0142154P.  
 PR 06-JUL-1999; 99US-0142390P.  
 PR 08-JUL-1999; 99US-0142803P.  
 PR 09-JUL-1999; 99US-0142920P.  
 PR 12-JUL-1999; 99US-0142977P.  
 PR 13-JUL-1999; 99US-0143542P.  
 PR 14-JUL-1999; 99US-0143624P.  
 PR 15-JUL-1999; 99US-0144005P.  
 PR 16-JUL-1999; 99US-0144085P.  
 PR 16-JUL-1999; 99US-0144086P.  
 PR 19-JUL-1999; 99US-0144325P.  
 PR 19-JUL-1999; 99US-0144331P.  
 PR 19-JUL-1999; 99US-0144332P.  
 PR 19-JUL-1999; 99US-0144333P.  
 PR 19-JUL-1999; 99US-0144334P.  
 PR 19-JUL-1999; 99US-0144335P.  
 PR 20-JUL-1999; 99US-0144352P.  
 PR 20-JUL-1999; 99US-0144632P.  
 PR 20-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0144814P.  
 PR 21-JUL-1999; 99US-0145086P.  
 PR 21-JUL-1999; 99US-0145088P.  
 PR 22-JUL-1999; 99US-0145085P.  
 PR 22-JUL-1999; 99US-0145087P.  
 PR 22-JUL-1999; 99US-0145089P.  
 PR 23-JUL-1999; 99US-0145192P.  
 PR 23-JUL-1999; 99US-0145145P.  
 PR 23-JUL-1999; 99US-0145218P.  
 PR 23-JUL-1999; 99US-0145219P.  
 PR 26-JUL-1999; 99US-0145276P.  
 PR 27-JUL-1999; 99US-0145913P.

```
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151330P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.

PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      87.1%; Score 27; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFF 5
      |||||
Db      31 KFVFF 35

RESULT 35
ADX67964
ID ADX67964 standard; protein; 57 AA.
XX
AC ADX67964;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 38807.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
DR New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 38807; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
```

CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This is the amino acid sequence of a plant full length insert  
CC polypeptide that can be used in the recombinant DNA construct of the  
CC invention.

XX SQ Sequence 57 AA;

Query Match 87.1%; Score 27; DB 8; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5

DB 29 KPVFF 33

#### RESULT 36

ABB03189  
ID ABB03189 standard; protein; 62 AA.

XX AC ABB03189;

XX DT 08-JAN-2002 (first entry)

XX DE Human musculoskeletal system related polypeptide SEQ ID NO 1136.

XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
XX KW anti-allergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
XX KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
XX KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
XX KW neurological disease; infection; human; secreted protein;  
XX KW musculoskeletal system.

XX OS Homo sapiens.

XX FN WO200155367-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US0011338.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190078P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-0216647P.

XX PR 07-JUL-2000; 2000US-0216880P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 11-JUL-2000; 2000US-0217496P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 26-JUL-2000; 2000US-0220964P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225213P.

XX PR 14-AUG-2000; 2000US-0225214P.

XX PR 14-AUG-2000; 2000US-0225266P.

XX PR 14-AUG-2000; 2000US-0225267P.

XX PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI  
 XX WPI; 2001-451937/48.  
 DR N-PSDB; AAL34771.  
 XX  
 PT Isolated polypeptide for treating, preventing and/ or prognosing  
 disorders related to the musculoskeletal system including musculoskeletal  
 cancers and also for testing and detection e.g. diagnosis.  
 PT  
 XX Claim 11; SEQ ID NO 1136; 781pp + Sequence Listing; English.  
 XX  
 CC The invention relates to novel genes (AAL34669-AAL37666) and proteins  
 CC (AB03087-AB04109) associated with the musculoskeletal system useful for  
 CC preventing, treating or ameliorating medical conditions e.g. by protein  
 CC or gene therapy. The genes are isolated from a range of human tissues  
 CC disclosed in the specification. The nucleic acids, proteins, antibodies  
 CC and (ant)agonists are useful in the diagnosis, treatment and prevention  
 CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the  
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,  
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as  
 CC myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.  
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,  
 CC bacterial, fungal and parasitic infections. Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 62 AA;

Query Match 87.1%; Score 27; DB 4; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVF 5  
 Db 31 KVFVF 35  
 RESULT 37  
 ABU12483  
 ID ABU12483 standard; protein; 62 AA.  
 XX  
 AC ABU12483;  
 XX  
 DT 26-FEB-2003 (first entry)  
 XX  
 DE Novel human musculoskeletal system antigen #103.  
 XX  
 KW Musculoskeletal system antigen; cancer; metastasis; re-vascularisation;  
 KW thrombosis; arteriosclerosis; mineral content; cardiovascular condition;  
 KW wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair;  
 KW limb regeneration; neuronal growth; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; AIDS-related complex;  
 KW chondrocyte growth; bone regeneration; periodontal regeneration;  
 KW tissue transport; bone graft; skin aging; keratinocyte growth; hair loss;  
 KW melanocyte growth; cell proliferation; cell growth; organ transplant;  
 KW cell differentiation; body height; weight; hair colour; eye colour; skin;  
 KW percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism;  
 KW biorhythm; cardiac rhythm; depression; tendency for violence; pain;  
 KW reproductive capability; hormone level; endocrine level; appetite;  
 KW libido; memory; stress; storage capability; fat content; lipid content;  
 KW protein content; carbohydrate content; vitamin content; cofactor content;  
 KW nutritional component.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX US2002147140-A1.  
 XX  
 XX 10-OCT-2002.  
 XX  
 XX 17-JAN-2001; 2001US-00764877.  
 XX  
 XX 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 22-AUG-2000; 2000US-0226688P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.

PR 27-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 13-OCT-2000; 2000US-0237040P.  
 PR 20-OCT-2000; 2000US-0239935P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.

(ROSE/) ROSEN C A.  
 (RUBE/) RUBEN S M.  
 (BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;

WPI; 2003-128199/12.  
 N-PSDB; ABX57759.

Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.

Claim 11; SEQ ID NO 1136; 321pp; English.

The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes mammal's metal state or physical state by influencing biorhythms, cardiac rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This is the amino acid sequence of a novel human musculoskeletal system antigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at ftp.secdatal.uspto.gov/sequence.html?docID=20020147140

Sequence 62 AA;

Query Match

87.1%; Score 27; DB 6; Length 62;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;  
 QY 1 KFVFF 5  
 Db 31 KFVFF 35  
 RESULT 38  
 ADJ28509  
 ID ADJ28509 standard; protein; 62 AA.  
 AC ADJ28509;  
 XX 20-MAY-2004 (first entry)  
 DT Human musculoskeletal system-associated protein - SEQ ID 1136.  
 DE musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;  
 KW gene therapy; vaccine; human.  
 XX Homo sapiens.  
 OS US2004009488-A1.  
 PN 15-JAN-2004.  
 PD 13-SEP-2002; 2002US-00242515.  
 PF 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 14-AUG-2000; 2000US-0225759P.  
 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-0226688P.  
 PR 23-AUG-2000; 2000US-0227182P.  
 PR 30-AUG-2000; 2000US-0227009P.  
 PR 01-SEP-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.

```
PR 08-SEP-2000; 2000US-0231342P.
PR 08-SEP-2000; 2000US-02311243P.
PR 08-SEP-2000; 2000US-02311244P.
PR 08-SEP-2000; 2000US-02311245P.
PR 08-SEP-2000; 2000US-02311413P.
PR 08-SEP-2000; 2000US-02311414P.
PR 08-SEP-2000; 2000US-02320801P.
PR 08-SEP-2000; 2000US-02320802P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249247P.
PR 17-NOV-2000; 2000US-0249248P.
PR 17-NOV-2000; 2000US-0249249P.
PR 17-NOV-2000; 2000US-0249250P.
PR 17-NOV-2000; 2000US-0249251P.
PR 17-NOV-2000; 2000US-0249252P.
PR 17-NOV-2000; 2000US-0249253P.
PR 17-NOV-2000; 2000US-0249254P.
PR 17-NOV-2000; 2000US-0249255P.
PR 17-NOV-2000; 2000US-0249256P.
PR 17-NOV-2000; 2000US-0249257P.
PR 17-NOV-2000; 2000US-0249258P.
PR 17-NOV-2000; 2000US-0249259P.
PR 17-NOV-2000; 2000US-0249260P.
PR 17-NOV-2000; 2000US-0249261P.
PR 17-NOV-2000; 2000US-0249262P.
PR 17-NOV-2000; 2000US-0249263P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249266P.
PR 17-NOV-2000; 2000US-0249267P.
PR 17-NOV-2000; 2000US-0249268P.
PR 17-NOV-2000; 2000US-0249269P.
PR 17-NOV-2000; 2000US-0249270P.
PR 17-NOV-2000; 2000US-0249271P.
PR 17-NOV-2000; 2000US-0249272P.
PR 17-NOV-2000; 2000US-0249273P.
PR 17-NOV-2000; 2000US-0249274P.
PR 17-NOV-2000; 2000US-0249275P.
PR 17-NOV-2000; 2000US-0249276P.
PR 17-NOV-2000; 2000US-0249277P.
PR 17-NOV-2000; 2000US-0249278P.
PR 17-NOV-2000; 2000US-0249279P.
PR 17-NOV-2000; 2000US-0249280P.
PR 17-NOV-2000; 2000US-0249281P.
PR 17-NOV-2000; 2000US-0249282P.
PR 17-NOV-2000; 2000US-0249283P.
PR 17-NOV-2000; 2000US-0249284P.
PR 17-NOV-2000; 2000US-0249285P.
PR 17-NOV-2000; 2000US-0249286P.
PR 17-NOV-2000; 2000US-0249287P.
PR 17-NOV-2000; 2000US-0249288P.
PR 17-NOV-2000; 2000US-0249289P.
PR 17-NOV-2000; 2000US-0249290P.
PR 17-NOV-2000; 2000US-0249291P.
PR 17-NOV-2000; 2000US-0249292P.
PR 17-NOV-2000; 2000US-0249293P.
PR 17-NOV-2000; 2000US-0249294P.
PR 17-NOV-2000; 2000US-0249295P.
PR 17-NOV-2000; 2000US-0249296P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249298P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250161P.
PR 05-DEC-2000; 2000US-0250303P.
PR 05-DEC-2000; 2000US-0250304P.
PR 05-DEC-2000; 2000US-0250305P.
PR 05-DEC-2000; 2000US-0250306P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251857P.
PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251859P.
PR 08-DEC-2000; 2000US-0251860P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI N-PSDB; ADJ27486.
XX
XX WPI; 2004-090458/09.
XX
XX N-PSDB; ADJ27486.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX
XX Claim 11; SEQ ID NO 1136; 289pp; English.
XX
XX The invention relates to a novel isolated musculoskeletal system-
CC associated nucleic acid molecule. The nucleic acid of the invention
CC demonstrates cytostatic and osteopathic activities and may be useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
CC possibly via gene therapy or vaccine production. The current sequence is
CC that of the human musculoskeletal system-associated polypeptide of the
CC invention. The current sequence is not shown within the specification per
CC se but is available on the USPTO web-site
CC http:seqdata.uspto.gov/sequence.html?DocID=20040009488.
XX
XX Sequence 62 AA;
SQ
Query Match 87.1%; Score 27; DB 8; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRVFF 5
Db 31 KRVFF 35
RESULT 39
AAG00778
ID AAG00778 standard; protein; 82 AA.
XX
XX AAG00778;
AC AAG00778;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein, SEQ ID NO: 4859.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
```

PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-00200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 XX WPI; 2000-500381/45.  
 DR N-PSDB; AAC00784.  
 DR  
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 XX  
 XX Claim 13; SEQ ID NO 4859; 71pp + Sequence Listing; English.  
 PS  
 XX The present sequence is a polypeptide encoded by one of a large number of  
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
 CC sequences derived from the 5' ends of mRNAs and even in those cases where  
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
 CC are also used in diagnostic, forensic, gene therapy and chromosome  
 CC mapping procedures. They are used to obtain upstream regulatory sequences  
 CC and to design expression and secretion vectors  
 XX  
 SQ Sequence 82 AA;  
 Query Match 87.1%; Score 27; DB 3; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KPVFF 5  
 Db 32 KVFVP 36  
 |||||  
 |||||  
 RESULT 40  
 ABG13797  
 ID ABG13797 standard; protein; 82 AA.  
 XX  
 AC ABG13797;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #13798.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200175067-A2.  
 PN  
 XX 11-OCT-2001.  
 PD  
 XX 30-MAR-2001; 2001WO-US008631.  
 PF  
 XX 31-MAR-2000; 2000US-00540217.  
 PR  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Drmanac RT, Liu C, Tang YT;  
 PI  
 XX WPI; 2001-639362/73.  
 DR

DR N-PSDB; AAS77984.  
 XX  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 XX Claim 20; SEQ ID NO 44156; 103pp; English.  
 PS  
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have application in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 82 AA;  
 Query Match 87.1%; Score 27; DB 4; Length 82;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVFA 6  
 Db 11 EFVFFA 16  
 :|||  
 |||||  
 RESULT 41  
 AAO12276  
 ID AAO12276 standard; protein; 91 AA.  
 XX  
 AC AAO12276;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 26168.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200164835-A2.  
 PN  
 XX 07-SEP-2001.  
 PD  
 XX 26-FEB-2001; 2001WO-US004927.  
 PF  
 XX 28-FEB-2000; 2000US-00515126.  
 PR  
 PR 18-MAY-2000; 2000US-00577409.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Tang YT, Liu C, Drmanac RT;  
 PI  
 XX WPI; 2001-514838/56.  
 DR



DR N-PSDB; AAI922207.  
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.  
 XX  
 PS Claim 20; SEQ ID NO 26168; 1399pp + Sequence Listing; English.  
 XX  
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC actin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 91 AA;

Query Match 87.1%; Score 27; DB 4; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVF 5  
 DB 17 KVFVF 21  
 |||||

RESULT 42  
 AAO10108  
 ID AAO10108 standard; protein; 99 AA.  
 XX  
 AC AAO10108;  
 XX  
 XX 06-NOV-2001 (first entry)  
 XX Human polypeptide SEQ ID NO 24000.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200164835-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 26-FEB-2001; 2001WO-US004927.  
 XX  
 PR 28-FEB-2000; 2000US-00515126.  
 PR 18-MAY-2000; 2000US-00577409.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Liu C, Drmanac RT;  
 XX WPI; 2001-514838/56.  
 DR N-PSDB; AAI90039.  
 XX  
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.  
 XX  
 PS Claim 20; SEQ ID NO 24000; 1399pp + Sequence Listing; English.  
 XX  
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC actin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 99 AA;

Query Match 87.1%; Score 27; DB 4; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVF 5  
 DB 39 KVFVF 43  
 |||||

RESULT 43  
 AAE12897  
 ID AAE12897 standard; protein; 104 AA.  
 XX  
 AC AAE12897;  
 XX  
 DT 15-JAN-2002 (first entry)  
 XX  
 DE Human recombinant beta-amyloid precursor protein (betaAPP) C-83.  
 XX  
 KW Human; Alzheimer's disease; gamma-secretase; integral-membrane protein;  
 KW beta-amyloid precursor protein; betaAPP.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175435-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US010453.  
 XX  
 PR 03-APR-2000; 2000US-0194495P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Roberts SB, Hendrick JP, Vinitzky A, Lewis M, Smith DW, Pak R;  
 XX WPI; 2001-648575/74.  
 DR N-PSDB; AAD20982.  
 XX  
 PT Novel gamma secretase protein, useful in the production of amyloids, is  
 PT capable of cleaving beta-amyloid precursor protein to produce beta  
 PT amyloid peptide.  
 XX  
 PS Claim 83; Fig 3; 127pp; English.  
 XX  
 CC The invention relates to the field of plaque amyloid deposits that are  
 CC the hallmarks of Alzheimer's disease. In particular, the invention  
 CC relates to an isolated, functionally-active protein that has gamma-  
 CC secretase activity. Gamma-secretase activity is necessary for amyloid  
 CC production. The present invention also relates to methods for isolating  
 CC integral-membrane proteins and protein complexes, including the gamma-  
 CC secretase protein of the invention. The method is useful for monitoring  
 CC the cleavage of beta-amyloid precursor protein (betaAPP) by gamma-  
 CC secretase. The present sequence is human recombinant betaAPP protein (C-  
 CC 83)  
 XX  
 SQ Sequence 104 AA;

Query Match 87.1%; Score 27; DB 4; Length 104;  
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6  
:|||||  
Db 21 EFVFFA 26

RESULT 44  
AAB93728  
ID AAB93728 standard; protein; 114 AA.  
AC AAB93728;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human protein sequence SEQ ID NO:13358.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PP 28-JUL-2000; 2000EP-00116126.  
XX  
PR 29-JUL-1999; 99JP-00248036.  
PR 27-AUG-1999; 99JP-00300253.  
PR 11-JAN-2000; 2000JP-00118776.  
PR 02-MAY-2000; 2000JP-00183767.  
PR 09-JUN-2000; 2000JP-00241899.  
XX  
(HELI-) HELIX RES INST.  
XX  
PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;  
FI Ishii S, Sugiyama T, Wakamatsu A, Negai K, Otsuki T;  
XX  
WPI; 2001-318749/34.  
XX  
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.  
XX  
Claim 8; SEQ ID NO 13358; 2537pp + Sequence Listing; English.  
XX  
The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH03166 to AAH05893 represent human amino acid sequences; and AAH13629 to AAH13632 represent polynucleotides, all of which are used in the exemplification of the present invention  
XX  
Sequence 114 AA;

Query Match 87.1%; Score 27; DB 4; Length 114;

Best Local Similarity 66.7%; Pred. No. 4e+02; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6  
:|||||  
Db 24 KPIFFS 29

RESULT 45  
ABP33134  
ID ABP33134 standard; protein; 115 AA.  
XX  
AC ABP33134;  
XX  
DT 09-JUL-2002 (first entry)  
XX  
DE Human isomerase-like ORP2107 protein, SEQ ID NO:4214.  
XX  
KW Human; ORP; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnery; vasotropic; antipsoriatic; antidiabetic; cytostatic; neurotropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiact; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.  
XX  
OS Homo sapiens.  
XX  
WO200190366-A2.  
XX  
PN  
PD 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US017076.  
XX  
XX 24-MAY-2000; 2000US-0206690P.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Leach MD, Shinkets RA;  
XX  
WPI; 2002-106200/14.  
XX  
N-PSDB; ABN77160.  
XX  
Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.  
XX  
Claim 10; Page 1311; 2508pp; English.  
XX  
Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (Open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides or polypeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopoiesis regulation, tissue growth, angiogenesis, activin or inhibin activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity, and antiinfective activity, and may also be involved in the determination

CC of bodily characteristics, fertility and behaviour. ORFX proteins,  
 CC nucleic acids and antibodies may be used in the treatment of cancers,  
 CC other proliferative disorders such as psoriasis and benign tumours,  
 CC neurological disorders such as epilepsy and Alzheimer's disease,  
 CC cardiovascular diseases, immune system disorders, disorders related to  
 CC organ transplantation, disorders of tissue growth and regeneration,  
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester  
 CC storage disease, and infectious diseases caused by viral, bacterial,  
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a  
 CC source of primers and probes, in the detection of ORFX genomic sequences  
 CC or transcripts, in the identification and cloning of homologous  
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX  
 CC nucleic acids may additionally be used to produce transgenic animals  
 CC which may be useful for studying the function and/or activity of ORFX  
 CC protein, and in drug screening. The ORFX proteins may also be used as  
 CC immunogens to generate specific antibodies, which are useful in the  
 CC diagnosis, treatment and monitoring of ORFX-associated diseases  
 CC  
 CC  
 CC Sequence 115 AA;

Query Match 87.1%; Score 27; DB 5; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5  
 DB 67 KPVFF 71

RESULT 46  
 AAO02898  
 ID AAO02898 standard; protein; 126 AA.

AC AAO02898;  
 DT 06-NOV-2001 (first entry)  
 DE Human polypeptide SEQ ID NO 16790.  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

PN WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US004927.

PR 28-FEB-2000; 2000US-00515126.

PT 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-514838/56.

DR N-PSDB; AAI82829.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 16790; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 126 AA;

Query Match 87.1%; Score 27; DB 4; Length 126;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5

DB 90 KPVFF 94

RESULT 47  
 AAO00490  
 ID AAO00490 standard; protein; 132 AA.

AC AAO00490;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 14382.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

PN WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US004927.

PR 28-FEB-2000; 2000US-00515126.

PT 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-514838/56.

DR N-PSDB; AAI80421.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 14382; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 132 AA;

Query Match 87.1%; Score 27; DB 4; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5  
 |||||  
 Db 22 KPVFF 26

RESULT 48  
 ABG26562  
 ID ABG26562 standard; protein; 144 AA.

XX AC ABG26562;  
 XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #26553.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS90749.

XX PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 56921; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 144 AA;

Query Match 87.1%; Score 27; DB 4; Length 144;  
 Best Local Similarity 66.7%; Pred. No. 5e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KPVFFA 6  
 :|||  
 Db 111 RRIFFA 116

RESULT 49  
 AAO07503  
 ID AAO07503 standard; protein; 146 AA.

XX AC AAO07503;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 21395.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US004927.

XX PR 28-FEB-2000; 2000US-00515126.

XX PR 18-MAY-2000; 2000US-00577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-514838/56.

XX DR N-PSDB; AAI87434.

XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX PS Claim 20; SEQ ID NO 21395; 1399pp + Sequence Listing; English.

XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to  
 CC cytokine cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and/or  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 146 AA;

Query Match 87.1%; Score 27; DB 4; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5  
 |||||  
 Db 24 KPVFF 28

RESULT 50  
 ADQ65558  
 ID ADQ65558 standard; protein; 148 AA.

XX ADQ66558;  
AC  
XX 07-OCT-2004 (first entry)  
XX  
DE Novel human protein sequence #1531.  
XX  
XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
KW Gene therapy; diagnostic marker; morbid state; osteoporosis;  
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;  
KW cancer.  
XX  
XX Homo sapiens.  
OS  
XX EP1440981-A2.  
PN  
XX 28-JUL-2004.  
PD  
XX 21-JAN-2004; 2004EP-00001196.  
PF  
XX 21-JAN-2003; 2003JP-00102206.  
PR  
XX 09-MAY-2003; 2003JP-00131392.  
PR  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
PA  
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Nagai K, Irie R;  
PI  
XX WPI; 2004-535376/52.  
DR  
XX N-PSDB; ADQ64370.  
DR  
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,  
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
PT  
XX Claim 1; SEQ ID NO 3719; 2449pp; English.  
PS  
XX The invention relates to 2495 novel polynucleotides (I) and their encoded  
CC polypeptides, sequences hybridizing to these nucleotides, sequences  
CC encoding partial polypeptides and sequences having 70% or 90% identity to  
CC the nucleotide and protein sequences. The nucleotides and polypeptides  
CC are useful as diagnostic markers or therapeutic target for the diseases  
CC or morbid states. They are also useful for treating osteoporosis,  
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,  
CC dementia and various cancers. This sequence corresponds to a protein  
CC sequence of the invention.  
XX  
XX Sequence 148 AA;  
SQ  
Query Match 87.1%; Score 27; DB 8; Length 148;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVFVF 5  
Db 17 KVFVF 21  
RESULT 51  
AAU27710  
ID AAU27710 standard; protein; 173 AA.  
XX  
XX AAU27710;  
XX  
XX 18-DEC-2001 (first entry)  
DT  
XX Human full-length polypeptide sequence #35.  
DE  
XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;  
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;  
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;  
KW nervous system disorder; inflammatory disorder; cell differentiation;  
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;  
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;

KW Cytostatic; antirheumatic; antiarthritic; vulnery; antiinflammatory;  
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;  
KW neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;  
KW immunostimulant; analgesic; gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX WO200164834-A2.  
PN  
XX 07-SEP-2001.  
PD  
XX 26-FEB-2001; 2001WO-US004926.  
PF  
XX 28-FEB-2000; 2000US-00515126.  
PR  
XX 18-MAY-2000; 2000US-00577409.  
PR  
XX 17-JUN-2000; 2000US-00597707.  
PR  
XX 14-JUL-2000; 2000US-00616807.  
PR  
XX 19-SEP-2000; 2000US-00664641.  
PR  
XX (HYSE-) HYSEQ INC.  
PA  
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QH, Ren F;  
PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;  
PI Drmanac R;  
XX  
XX WPI; 2001-589862/66.  
DR  
XX N-PSDB; AAS44610.  
DR  
XX Novel polypeptides and nucleic acids obtained from cDNA libraries  
PT prepared from various human tissues, for diagnosis, treatment of cancer,  
PT neurological, inflammatory disorders and for use in arrays for detection.  
PT  
XX Claim 10; SEQ ID NO 207; 153pp; English.  
XX  
XX Sequences AAU27676-AAU28019 represent full-length polypeptides and contig  
CC polypeptides of the invention. The proteins and their associated DNA  
CC sequences are useful for the treatment, diagnosis and prevention of  
CC various types of disorder in a mammalian subject such as a human, dog,  
CC monkey, mouse, hamster or rat. The disorders include cancers such as  
CC leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as  
CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,  
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system  
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's  
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and  
CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's  
CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory  
CC bowel disease. The sequences exhibit activity relating to angiogenesis,  
CC cell proliferation, cell differentiation, stem cell growth factor,  
CC activin or inhibin. Therefore, they can be used to manipulate stem cells  
CC in culture to give rise to neuroepithelial cells that can be used to  
CC augment or replace cells damaged by illness, accidental damage or genetic  
CC disorders. The sequences may also be used for regeneration of bone,  
CC cartilage, tendons and ligaments and in tissue repair and burn healing.  
CC Note: Some sequences for this patent did not form part of the printed  
CC specification, but were obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 173 AA;  
SQ  
Query Match 87.1%; Score 27; DB 4; Length 173;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVFVF 5  
Db 46 KVFVF 50  
RESULT 52  
AAU77842  
ID AAU77842 standard; protein; 173 AA.  
XX  
XX AAU77842;  
AC

```

XX DT 05-JUN-2002 (first entry)
XX DE Oestrogen receptor associated protein 19.03.
XX KW Oestrogen receptor associated protein 19.03; cytostatic; antiinfertility;
XX KW reproductive system; tumour; sex growth impediment.
XX OS Unidentified.
XX PN WO200212317-A1.
XX PD 14-FEB-2002.
XX PF 11-JUN-2001; 2001WO-CN000930.
XX PR 12-JUN-2000; 2000CN-00116442.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX PS WPI; 2002-172145/22.
XX DR N-PSDB; ABK12230.
XX PT Estrogen receptor associated protein 19.03 and encoded polynucleotide,
XX PT used in diagnosis and treatment of reproductive system tumors.
XX PS Claim 1; Page 30; 38pp; Chinese.
XX CC This invention relates to the cDNA and protein sequences of a novel
XX CC isolated protein estrogen receptor associated protein 19.03 and a method
XX CC for producing the protein by recombinant means. The protein of the
XX CC invention may have cytostatic and antiinfertility activities. The DNA and
XX CC protein sequences of the invention may be used in the diagnosis and
XX CC treatment of reproductive system tumors and sex growth impediment in the
XX CC adolescence. The present sequence represents the Estrogen receptor
XX CC associated protein 19.03 of the invention
XX SQ Sequence 173 AA;
Query Match 87.1%; Score 27; DB 5; Length 173;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVF 5
Db 46 KVFVF 50
RESULT 53
ADJ69976
ID ADJ69976 standard; protein; 173 AA.
AC ADJ69976;
XX 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SeqID1782.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
XX KW Huntington's disease; osteoarthritis;
XX KW Leber's hereditary optic neuropathy; LHON;
XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
XX KW osteopathic; ophthalmological; cytostatic.
XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX PD 23-OCT-2003.

```

```

XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
XX PI Warnock DE;
XX DR WPI; 2003-845369/78.
XX PT Identifying a mitochondrial target for drug screening assays and for
XX PT treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.
XX PS Claim 1; SEQ ID NO 1782; 180pp; English.
XX CC This invention relates to novel mitochondrial targets that can be used
XX CC for therapeutic intervention in treating a disease associated with
XX CC altered mitochondrial function. Specifically, it refers to a method for
XX CC identifying proteins of the human heart mitochondrial proteome that are
XX CC useful for drug screening assays, as well as therapeutic targets. The
XX CC present invention describes a method for identifying such proteins that
XX CC can be used in the treatment of various diseases associated with altered
XX CC mitochondrial function including diabetes mellitus, Huntington's disease,
XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX CC compositions have neuroprotective, nootropic, antidiabetic,
XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX CC cytostatic activities. This polypeptide sequence is a human heart
XX CC mitochondrial protein of the invention.
XX SQ Sequence 173 AA;
Query Match 87.1%; Score 27; DB 7; Length 173;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVF 5
Db 46 KVFVF 50
RESULT 54
AAG47987
ID AAG47987 standard; protein; 184 AA.
AC AAG47987;
XX 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 60548.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.

```

PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-01334256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 02-JUL-1999; 99US-0142154P.  
PR 06-JUL-1999; 99US-0142055P.  
PR 08-JUL-1999; 99US-0142390P.  
PR 09-JUL-1999; 99US-0142803P.  
PR 12-JUL-1999; 99US-0142920P.  
PR 13-JUL-1999; 99US-0142977P.  
PR 14-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-015656P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.

PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
 PR 08-OCT-1999; 99US-0158232P.  
 PR 12-OCT-1999; 99US-0158369P.  
 PR 13-OCT-1999; 99US-0159293P.  
 PR 13-OCT-1999; 99US-0159294P.  
 PR 13-OCT-1999; 99US-0159295P.  
 PR 14-OCT-1999; 99US-0159329P.  
 PR 14-OCT-1999; 99US-0159330P.  
 PR 14-OCT-1999; 99US-0159331P.  
 PR 14-OCT-1999; 99US-0159637P.  
 PR 14-OCT-1999; 99US-0159638P.  
 PR 18-OCT-1999; 99US-0159584P.  
 PR 21-OCT-1999; 99US-0160741P.  
 PR 21-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
 PR 21-OCT-1999; 99US-0160770P.  
 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160980P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160989P.  
 PR 25-OCT-1999; 99US-0161404P.  
 PR 25-OCT-1999; 99US-0161405P.  
 PR 25-OCT-1999; 99US-0161406P.  
 PR 26-OCT-1999; 99US-0161359P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161922P.  
 PR 28-OCT-1999; 99US-0161993P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 184;

Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
 ||:|:  
 Db 29 RFIFFS 34

# RESULT 55

ID AEB38594 standard; protein; 186 AA.

AC AEB38594;

DT 08-SEP-2005 (first entry)

DE L. pneumophila protein SEQ ID NO 2926.

KW detection; infection; Antibacterial; Vaccine.

XX Legionella pneumophila.

OS WO2005049642-A2.

PD 02-JUN-2005.

PF 23-SEP-2004; 2004WO-IB003578.

PR 21-NOV-2003; 2003FR-00013687.

PA (INSP ) INST PASTEUR.

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (UVDY-) UNIV LYON 1 BERNARD CLAUDE.

PA (CNRS ) CNRS CENT NAT RECH SCI.

PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;

PI Rueniok C, Bouchier C, Zidane N, Magnier A, Kunst P, Vandenesch P;

PI Jarraud S;

XX

DR WPI; 2005-388305/40.  
 XX New genome of Legionella pneumophila Paris strain and derived  
 PT polypeptides, useful for detection or identification of the strain and  
 for treatment and prevention of infections.  
 XX  
 PS Claim 3; SEQ ID NO 2926; 660pp; English.  
 XX  
 CC The invention relates to an isolated or purified nucleotide sequences (I)  
 from Legionella pneumophila Paris strain. (I), and their related  
 CC sequences or fragments, are useful as primers and probes for detection  
 CC and amplification, including differentiation between the Paris and  
 CC Philadelphia strains of Legionella pneumophila and to prepare recombinant  
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of  
 CC specific antibodies (Ab), also used for detection/identification of  
 CC Legionella, and some (I), specifically those involved in synthesis of  
 CC surface proteins, are targets for identification of inhibitors. (II), or  
 CC vectors that contain (I), are useful as vaccines and immunogenic  
 CC compositions, for treatment and prevention of infections by L.  
 CC pneumophila. The present sequence represents the amino acid sequence of a  
 CC L. pneumophila protein.  
 XX  
 SQ Sequence 186 AA;

Query Match 87.1%; Score 27; DB 9; Length 186;

Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
 ||:|:  
 Db 7 RFIFFA 12

# RESULT 56

AAU79255  
 ID AAU79255 standard; protein; 189 AA.

AC AAU79255;

DT 13-AUG-2002 (first entry)

DE Human membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

XX Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; human;

KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;

KW cytostatic; antiallergic; nootropic; neuroprotective.

XX Homo sapiens.

XX WO200241000-A1.

XX 23-MAY-2002.

XX 20-NOV-2001; 2001WO-JP010136.

XX 20-NOV-2000; 2000JP-00352491.

XX (DAII-) DAIICHI FINE CHEM CO LTD.

XX Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

XX WPI; 2002-435988/46.

XX Immunoassay method for membrane-bound matrix metalloprotease with

PT quantitation using its antibody, applicable in diagnosis of cancer and

PT cancer metastasis, and in drug development.

XX Disclosure; Fig 9; 93pp; Japanese.

XX The invention relates to a method for quantitative immunoassay of a

CC membrane-bound matrix metalloprotease (MT-MMP), involving using an

CC antibody against MT-MMP selected from groups containing MT-MMPs. The

CC method involves releasing and/or solubilising MT-MMP from a cell membrane



CC among a group of MT-MMPs by using a surfactant and reductant. Such a  
 CC method is for detecting a membrane-bound matrix metalloprotease with  
 CC quantitation, which is applicable in diagnosis of cancer and cancer  
 CC metastasis as well as in drug development, and is also used to monitor  
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence  
 CC represents a human MT1-MMP related protein  
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;

Best Local Similarity 100.0%; Pred. No. 6.5e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

QY 1 KKVFF 5  
 DB 60 KKVFF 64  
 |||||

RESULT 57

AAU79257  
 ID AAU79257 standard; protein; 189 AA.

AC AAU79257;

DT 13-AUG-2002 (first entry)

DE Rat membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; rat;  
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;  
 KW cytostatic; antiallergic; neutrotropic; neuroprotective.

OS Rattus sp.

PN WO200241000-A1.

PD 23-MAY-2002.

PF 20-NOV-2001; 2001WO-JP010136.

PR 20-NOV-2000; 2000JP-00352491.

PA (DAIIT-) DAIICHI FINE CHEM CO LTD.

PI Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

DR WPI; 2002-435988/46.

PT Immunoassay method for membrane-bound matrix metalloprotease with  
 PT quantitation using its antibody, applicable in diagnosis of cancer and  
 PT cancer metastasis, and in drug development.

PS Disclosure; Fig 9; 93pp; Japanese.

CC The invention relates to a method for quantitative immunoassay of a  
 CC membrane-bound matrix metalloprotease (MT-MMP), involving using an  
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The  
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane  
 CC among a group of MT-MMPs by using a surfactant and reductant. Such a  
 CC method is for detecting a membrane-bound matrix metalloprotease with  
 CC quantitation, which is applicable in diagnosis of cancer and cancer  
 CC metastasis as well as in drug development, and is also used to monitor  
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence  
 CC represents a rat MT1-MMP related protein  
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;

Best Local Similarity 100.0%; Pred. No. 6.5e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

QY 1 KKVFF 5  
 |||||

Db 60 KKVFF 64

RESULT 58

AAU79258  
 ID AAU79258 standard; protein; 189 AA.

AC AAU79258;

DT 13-AUG-2002 (first entry)

DE Rabbit membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; rabbit;  
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;  
 KW cytostatic; antiallergic; neutrotropic; neuroprotective.

OS Oryctolagus cuniculus.

PN WO200241000-A1.

PD 23-MAY-2002.

PF 20-NOV-2001; 2001WO-JP010136.

PR 20-NOV-2000; 2000JP-00352491.

PA (DAIIT-) DAIICHI FINE CHEM CO LTD.

PI Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

DR WPI; 2002-435988/46.

PT Immunoassay method for membrane-bound matrix metalloprotease with  
 PT quantitation using its antibody, applicable in diagnosis of cancer and  
 PT cancer metastasis, and in drug development.

PS Disclosure; Fig 9; 93pp; Japanese.

CC The invention relates to a method for quantitative immunoassay of a  
 CC membrane-bound matrix metalloprotease (MT-MMP), involving using an  
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The  
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane  
 CC among a group of MT-MMPs by using a surfactant and reductant. Such a  
 CC method is for detecting a membrane-bound matrix metalloprotease with  
 CC quantitation, which is applicable in diagnosis of cancer and cancer  
 CC metastasis as well as in drug development, and is also used to monitor  
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence  
 CC represents a rabbit MT1-MMP related protein  
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;

Best Local Similarity 100.0%; Pred. No. 6.5e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

QY 1 KKVFF 5  
 DB 60 KKVFF 64  
 |||||

RESULT 59

AAU79256  
 ID AAU79256 standard; protein; 189 AA.

AC AAU79256;

DT 13-AUG-2002 (first entry)

DE Murine membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; mouse;  
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;

KW cytostatic; antiallergic; nootropic; neuroprotective.  
 XX MHS SP.  
 OS WO200241000-A1.  
 PN 23-MAY-2002.  
 XX 20-NOV-2001; 2001WO-JP010136.  
 XX 20-NOV-2000; 2000JP-00352491.  
 XX (DAII-) DALICHI FINE CHEM CO LTD.  
 PA Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;  
 XX WPI; 2002-435988/46.  
 XX Immunassay method for membrane-bound matrix metalloprotease with  
 PT quantitation using its antibody, applicable in diagnosis of cancer and  
 PT cancer metastasis, and in drug development.  
 XX Disclosure; Fig 9; 93pp; Japanese.  
 XX The invention relates to a method for quantitative immunoassay of a  
 CC membrane-bound matrix metalloprotease (MT-MMP), involving using an  
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The  
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane  
 CC among a group of MT-MMPs by using a surfactant and reductant. Such a  
 CC method is for detecting a membrane-bound matrix metalloprotease with  
 CC quantitation, which is applicable in diagnosis of cancer and cancer  
 CC metastasis as well as in drug development, and is also used to monitor  
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence  
 CC represents a mouse MT1-MMP related protein  
 XX Sequence 189 AA;  
 SQ

Query Match 87.1%; Score 27; DB 5; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFP 5  
 Db 60 KFVFP 64

RESULT 60  
 ABM73888  
 ID ABM73888 standard; protein; 197 AA.  
 XX ABM73888;  
 AC 17-OCT-2003 (first entry)  
 XX DNA clone originating in barley containing SNP sequence #299.  
 XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.  
 XX Hordeum vulgare.  
 XX WO2003057877-A1.  
 XX 17-JUL-2003.  
 XX 16-DEC-2002; 2002WO-1B005403.  
 XX 20-DEC-2001; 2001JP-00387059.  
 XX 20-DEC-2001; 2001JP-00387131.  
 XX 20-DEC-2001; 2001JP-00403299.  
 XX 20-DEC-2001; 2001JP-00403300.  
 XX 27-SEP-2002; 2002JP-00327515.  
 XX (UTNI-) UNIV JAPAN OKAYAMA.

XX Sato K, Takeda K, Kohara Y;  
 XX WPI; 2003-587127/55.  
 XX Single nucleotide polymorphism sites in barley varieties and DNA  
 PT sequences containing them for analysis and identification of barley  
 PT varieties and production of barley transformants with desired  
 PT characteristics.  
 XX Disclosure; SEQ ID XX; 284pp; Japanese.  
 XX The present invention relates to oligonucleotide clones originating in  
 CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms  
 CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley  
 CC varieties, identification of particular varieties and genotype-phenotype  
 CC analysis, isolation of specific genes and creation of new varieties by  
 CC transformation of barley varieties with them and production of new barley  
 CC varieties with desired properties. The present sequence represents an  
 CC oligonucleotide clone sequence featured in the specification. The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published-pct-sequences  
 XX Sequence 197 AA;  
 SQ

Query Match 87.1%; Score 27; DB 7; Length 197;  
 Best Local Similarity 66.7%; Pred. No. 6.8e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFP 6  
 Db 140 KPIFYA 145

RESULT 61  
 ABB52559  
 ID ABB52559 standard; protein; 206 AA.  
 XX ABB52559;  
 AC 11-FEB-2002 (first entry)  
 XX Escherichia coli polypeptide SEQ ID NO 489.  
 XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;  
 XX immunosuppressive; extra-intestinal infection; phylogeny; meningitis;  
 XX systemic infection; non-diarrhoeal infection; septicaemia;  
 XX pyelonephritis; antibiotic resistance.  
 XX Escherichia coli.  
 XX WO200166572-A2.  
 XX 13-SEP-2001.  
 XX 12-MAR-2001; 2001WO-EP003445.  
 XX 10-MAR-2000; 2000FR-00003145.  
 XX 02-FEB-2001; 2001FR-00001449.  
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;  
 XX WPI; 2001-550253/61.  
 XX A library of DNA fragments of Escherichia coli strains for the phylogenetic  
 PT determination of a given strain comprises polynucleotides of nature B2/D+  
 PT A-.  
 XX Example 6; Fig 6; 646pp; English.  
 XX

CC The invention relates to a library of DNA fragments of Escherichia coli  
 CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and  
 CC encoded proteins (AB852459-AB852919 and AB852954-AB853094) of nature  
 CC B2/D-A-. The polynucleotides have potential antiinflammatory.  
 CC antibacterial and immunosuppressive activity as part of pharmaceutical  
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli  
 CC infections. The polypeptides are useful for determining the phylogenetic  
 CC group of a given E. coli strain. These polypeptides can detect and treat  
 CC an undesired development of E. coli, particularly an extra-intestinal  
 CC infection that include systemic and non-diarrhoeal infections such as  
 CC septicemia, pyelonephritis and meningitis this is particularly  
 CC advantageous as bacterial resistance is increasing with the more frequent  
 CC use of broad spectrum antibiotics  
 XX  
 SQ Sequence 206 AA;

Query Match 87.1%; Score 27; DB 4; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5  
 |||||  
 Db 25 KVFVF 29

RESULT 62  
 ABG22983  
 ID ABG22983 standard; protein; 221 AA.

XX AC ABG22983;  
 XX DT 18-FEB-2002 (first entry)  
 XX DE Novel human diagnostic protein #22974.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS87170.

XX PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 53342; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 221 AA;

Query Match 87.1%; Score 27; DB 4; Length 221;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5  
 |||||  
 Db 36 KVFVF 40

RESULT 63  
 ABG06994  
 ID ABG06994 standard; protein; 221 AA.

XX AC ABG06994;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #6985.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS71181.

XX PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 37353; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC [ftp.wipo.int/pub/published\\_pct\\_sequences](http://www.wipo.int/pub/published_pct_sequences)  
 XX

XX SQ Sequence 221 AA;

Query Match 87.1%; Score 27; DB 4; Length 221;  
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFPVFFA 6

Db 11 EFPVFFA 16

RESULT 64

ADH45453  
 ID ADH45453 standard; protein; 227 AA.

XX AC ADH45453;

XX DT 25-MAR-2004 (first entry)

XX DE Human molecule useful for disease detection and treatment, SEQ ID NO 47.

XX KW human; molecule; disease detection; treatment; MDDT; cytostatic;  
 KW antiarteriosclerotic; anti-HIV; anti-allergic; cerebroprotective;  
 KW antiparkinsonian; anticonvulsant; nootropic; neuroprotective;  
 KW antiinflammatory; ophthalmological; antithyroid; antiarthritic;  
 KW antibacterial; virucide; protozoacide; antiparasitic; fungicide;  
 KW anorectic; cardiac; hypotensive; antiinfertility; hepatotropic;  
 KW gene therapy.

XX OS Homo sapiens.

XX PN WO2003093427-A2.

XX PD 13-NOV-2003.

XX PF 30-APR-2003; 2003WO-US013629.

XX PR 30-APR-2002; 2002US-0376988P.

XX PR 14-JUN-2002; 2002US-0389095P.

XX PR 22-AUG-2002; 2002US-0405860P.

XX PR 27-AUG-2002; 2002US-0406512P.

XX PA (INCY-) INCYTE CORP.

XX PI Swarnakar A, Tran UK, Khare R, Marquis JP, Hafalia AJA;

XX PI Elliott VS, Becha SD, Ramkumar J, Kable AE, Wilson AD, Yue H;

XX PI Forsythe IJ, Griffin JA, Bulloch SA, Jin P, Jiang X, Jackson AA;

XX PI Mason PM, Chawla NK, Chang H, Richardson TW, Tang YT, Lee SY;

XX PI Gietzen KJ, Fu GK;

XX DR WPI; 2004-022653/02.

XX DR N-PSDB; ADH45507.

XX PT New human molecules for disease detection and treatment (MDDT) and  
 PT encoding polynucleotides, useful for diagnosing, preventing or treating  
 PT diseases associated with aberrant MDDT expression, e.g. cancer, stroke,  
 PT obesity or AIDS.

XX PS Claim 1; SEQ ID NO 47; 267pp; English.

XX CC The invention relates to human molecules useful for disease detection and  
 CC treatment (MDDT) and also the polynucleotides which encode and identify  
 CC and encode MDDT. The MDDT polypeptides and encoding polynucleotides have

CC the following activities: cytostatic, antiarteriosclerotic, anti-HIV,  
 CC antiallergic, cerebroprotective, antiparkinsonian, anticonvulsant,  
 CC nootropic, neuroprotective, antiinflammatory, ophthalmological,  
 CC antithyroid, antiarthritic, antibacterial, virucide, protozoacide,  
 CC antiparasitic, fungicide, anorectic, cardiac, hypotensive,  
 CC antiinfertility, and hepatotropic. The MDDT polynucleotide may be used in  
 CC gene therapy to treat disorders. The polypeptides and polynucleotides are  
 CC useful in diagnosing, preventing or treating diseases or conditions  
 CC associated with the decreased expression or overexpression of MDDT, such  
 CC as autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis,  
 CC arthritis or thyroiditis), infections (e.g. bacterial, viral, parasitic,  
 CC protozoal or fungal), metabolic disorders (e.g. obesity), reproductive  
 CC disorders (e.g. infertility), neurological disorders (Parkinson's  
 CC disease, Alzheimer's disease, stroke, epilepsy), cardiovascular disorders  
 CC (e.g. myocardial infarction or hypertension), eye disorders, or cell  
 CC proliferative diseases (e.g. cancer, atherosclerosis, hepatitis). These  
 CC are also useful in assessing the effects of exogenous compounds on the  
 CC expression of nucleic acid and amino acid sequences of MDDT. The MDDT or  
 CC its fragments are useful in screening compounds for effectiveness as  
 CC agonist or antagonist of the polypeptides, or in altering the expression  
 CC of the target polynucleotide and compounds that specifically bind to or  
 CC modulate the activity of the polypeptide. The microarray of the invention  
 CC is useful in monitoring or measuring protein-protein interactions, drug-  
 CC target interactions, and gene expression profiles. This sequence  
 CC represents an MDDT polypeptide of the invention.

XX SQ Sequence 227 AA;

Query Match 87.1%; Score 27; DB 8; Length 227;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFPVFF 5

Db 32 KFPVFF 36

RESULT 65

ABM91660  
 ID ABM91660 standard; protein; 238 AA.

XX AC ABM91660;

XX DT 02-JUN-2005 (first entry)

XX DE M. xanthus protein sequence, seq id 10859.

XX KW Transgenic plant; DNA replication; gene regulation; gene expression.

XX OS Myxococcus xanthus.

XX PN US6833447-B1.

XX PD 21-DEC-2004.

XX PF 10-JUL-2001; 2001US-00902540.

XX PR 10-JUL-2000; 2000US-0217883P.

XX PA (MONS ) MONSANTO TECHNOLOGY LLC.

XX PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

XX PI WPI; 2005-028716/03.

XX PT New substantially purified Myxococcus xanthus nucleic acid molecule  
 PT encoding a nitrite reductase, useful for determining gene expression,  
 PT identifying mutations in a gene of interest, and for constructing  
 PT mutations in a gene of interest.

XX PS Example 2; SEQ ID NO 10859; 25pp; English.

XX CC The invention relates to a substantially purified nucleic acid molecule

CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a  
 CC recombinant DNA construct for expression of a nitrite reductase gene in a  
 CC plant cell, and a plant cell comprising the recombinant DNA construct.  
 CC The nucleic acid is useful for determining gene expression, identifying  
 CC mutations in a gene of interest, and for constructing mutations in a gene  
 CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent  
 CC a group of 7134 *Mycococcus xanthus* proteins and peptides. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from USPTO  
 XX  
 SQ Sequence 238 AA;

Query Match 87.1%; Score 27; DB 9; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQVFF 5  
 Db 132 KQVFF 136

RESULT 66  
 ABP40600  
 ID ABP40600 standard; protein; 240 AA.  
 AC ABP40600;  
 XX  
 XX 24-JUL-2002 (first entry)  
 DT  
 XX  
 XX Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5445.

DE  
 XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
 KW antibacterial; gene therapy.  
 XX  
 XX Staphylococcus epidermidis.  
 OS  
 XX US6380370-B1.

FN  
 XX 30-APR-2002.  
 PD  
 XX 13-AUG-1998; 98US-00134001.  
 PF  
 XX 14-AUG-1997; 97US-0055779P.  
 PR  
 XX 08-NOV-1997; 97US-0064964P.  
 XX  
 XX (GENO-) GENOME THERAPEUTICS CORP.

XX Doucette-Stamm LA, Bush D;  
 PI  
 XX WPI; 2002-381255/41.  
 DR  
 XX N-PSDB; ABN93145.  
 XX  
 XX Novel isolated nucleic acid encoding a Staphylococcus epidermis  
 PT polypeptide, useful for diagnosing and treating bacterial infections.  
 PT  
 XX Disclosure; SEQ ID NO 5445; 267pp; English.

XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have  
 CC antibacterial activity and can be used in gene therapy. The sequences can  
 CC also be used in the diagnosis and treatment of bacterial infections,  
 CC particularly S. epidermidis infections. The sequences can be used to  
 CC screen for compounds able to interfere with the S. epidermidis life cycle  
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from the USPTO web site  
 XX

Sequence 240 AA;  
 Query Match 87.1%; Score 27; DB 5; Length 240;  
 Best Local Similarity 83.3%; Pred. No. 8.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
 Db 168 QFVFFA 173  
 RESULT 67  
 ADS07805  
 ID ADS07805 standard; protein; 240 AA.  
 XX  
 AC ADS07805;  
 XX  
 XX 04-NOV-2004 (first entry)  
 DT  
 XX Staphylococcus epidermis polypeptide seqid 7100.

DE  
 XX antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;  
 KW recombinant expression vector; infection; computer readable medium;  
 KW computer based system.  
 XX  
 XX Staphylococcus epidermidis.  
 OS  
 XX US2004147734-A1.  
 PN  
 XX 29-JUL-2004.  
 PD  
 XX 01-DEC-2003; 2003US-00724972.

PF  
 XX 08-NOV-1997; 97US-0064964P.  
 PR  
 XX 13-AUG-1998; 98US-00134001.  
 PR  
 XX 29-NOV-1999; 99US-00450969.  
 XX  
 XX (DOUC/) DOUCETTE-STAMM L.  
 PA (BUSH/) BUSH D.

XX Doucette-Stamm L, Bush D;  
 PI  
 XX WPI; 2004-580138/56.  
 DR  
 XX N-PSDB; ADS04033.

XX New isolated polypeptide and encoding nucleic acid derived from  
 PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or  
 PT treating an S. epidermidis bacterial infection.  
 XX  
 XX Claim 17; SEQ ID NO 7100; 741pp; English.

XX The invention describes an isolated nucleic acid comprising a nucleotide  
 CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:  
 CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any  
 CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as  
 CC given in the specification. Also described are: a recombinant expression  
 CC vector; a cell comprising a recombinant expression vector of (1);  
 CC producing an S. epidermidis polypeptide; an isolated nucleic acid  
 CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
 CC vaccine composition for prevention or treatment of an S. epidermidis  
 CC infection, comprising a nucleic acid cited above and a carrier; treating  
 CC a subject for S. epidermidis infection; a recombinant or substantially  
 CC pure preparation of an S. epidermidis polypeptide or its fragment; a  
 CC vaccine composition for prevention or treatment of an S. epidermidis  
 CC infection; detecting the presence of a Staphylococcus nucleic acid in a  
 CC sample; a computer readable medium having recorded in it the nucleotide  
 CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
 CC system for identifying fragments of the Staphylococcus genome of  
 CC commercial importance; a computer based system for identifying fragments  
 CC of the Staphylococcus plasmids of commercial importance; identifying  
 CC commercially important nucleic acid fragments of the Staphylococcus  
 CC genome and/or plasmids; and identifying an expression modulating fragment  
 CC of the Staphylococcus genome and/or plasmids. The methods and  
 CC compositions of the present invention are useful for the diagnosis,  
 CC prevention and/or treatment of an Staphylococcus epidermidis bacterial  
 CC infection. This is the amino acid sequence of a S. epidermidis protein of  
 CC the invention.

XX

```
SQ Sequence 240 AA;
Query Match      87.1%; Score 27; DB 8; Length 240;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 168 QVFVFA 173

RESULT 68
AAG10914
ID AAG10914 standard; protein; 248 AA.
XX AC AAG10914;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 9429.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydriidation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EPI033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
XX PR 25-MAR-1999; 99US-0126264P.
XX PR 29-MAR-1999; 99US-0126785P.
XX PR 01-APR-1999; 99US-0127462P.
XX PR 06-APR-1999; 99US-0128234P.
XX PR 08-APR-1999; 99US-0128714P.
XX PR 16-APR-1999; 99US-0129845P.
XX PR 19-APR-1999; 99US-0130077P.
XX PR 21-APR-1999; 99US-0130449P.
XX PR 23-APR-1999; 99US-0130510P.
XX PR 28-APR-1999; 99US-0130891P.
XX PR 30-APR-1999; 99US-0131449P.
XX PR 30-APR-1999; 99US-0132048P.
XX PR 04-MAY-1999; 99US-0132407P.
XX PR 05-MAY-1999; 99US-0132484P.
XX PR 06-MAY-1999; 99US-0132485P.
XX PR 06-MAY-1999; 99US-0132486P.
XX PR 07-MAY-1999; 99US-0132487P.
XX PR 11-MAY-1999; 99US-0132863P.
XX PR 14-MAY-1999; 99US-0134256P.
XX PR 14-MAY-1999; 99US-0134218P.
XX PR 14-MAY-1999; 99US-0134219P.
XX PR 14-MAY-1999; 99US-0134221P.
XX PR 18-MAY-1999; 99US-0134370P.
XX PR 19-MAY-1999; 99US-0134768P.
XX PR 20-MAY-1999; 99US-0134941P.
XX PR 21-MAY-1999; 99US-0135124P.
XX PR 25-MAY-1999; 99US-0135353P.
XX PR 27-MAY-1999; 99US-0135629P.
XX PR 28-MAY-1999; 99US-0136021P.
XX PR 28-MAY-1999; 99US-0136392P.
XX PR 01-JUN-1999; 99US-0136782P.
XX PR 03-JUN-1999; 99US-0137222P.
XX PR 04-JUN-1999; 99US-0137528P.
XX PR 07-JUN-1999; 99US-0137503P.
XX PR 08-JUN-1999; 99US-0137724P.
XX PR 08-JUN-1999; 99US-0138094P.
XX PR 10-JUN-1999; 99US-0138540P.
XX PR 10-JUN-1999; 99US-0138847P.
XX PR 14-JUN-1999; 99US-0139119P.
XX PR 16-JUN-1999; 99US-0139452P.
XX PR 17-JUN-1999; 99US-0139453P.
XX PR 17-JUN-1999; 99US-0139492P.
XX PR 18-JUN-1999; 99US-0139454P.
XX PR 18-JUN-1999; 99US-0139455P.
XX PR 18-JUN-1999; 99US-0139456P.
XX PR 18-JUN-1999; 99US-0139457P.
XX PR 18-JUN-1999; 99US-0139458P.
XX PR 18-JUN-1999; 99US-0139459P.
XX PR 18-JUN-1999; 99US-0139460P.
XX PR 18-JUN-1999; 99US-0139461P.
XX PR 18-JUN-1999; 99US-0139462P.
XX PR 18-JUN-1999; 99US-0139463P.
XX PR 18-JUN-1999; 99US-0139750P.
XX PR 18-JUN-1999; 99US-0139763P.
XX PR 21-JUN-1999; 99US-0139817P.
XX PR 22-JUN-1999; 99US-0139899P.
XX PR 23-JUN-1999; 99US-0140353P.
XX PR 24-JUN-1999; 99US-0140354P.
XX PR 28-JUN-1999; 99US-0140695P.
XX PR 28-JUN-1999; 99US-0140823P.
XX PR 29-JUN-1999; 99US-0140991P.
XX PR 30-JUN-1999; 99US-0141287P.
XX PR 01-JUL-1999; 99US-0141842P.
XX PR 01-JUL-1999; 99US-0142154P.
XX PR 02-JUL-1999; 99US-0142055P.
XX PR 06-JUL-1999; 99US-0142390P.
XX PR 08-JUL-1999; 99US-0142803P.
XX PR 09-JUL-1999; 99US-0142920P.
XX PR 12-JUL-1999; 99US-0142977P.
XX PR 13-JUL-1999; 99US-0143542P.
XX PR 14-JUL-1999; 99US-0143624P.
XX PR 15-JUL-1999; 99US-0144005P.
XX PR 16-JUL-1999; 99US-0144085P.
XX PR 16-JUL-1999; 99US-0144086P.
XX PR 19-JUL-1999; 99US-0144325P.
XX PR 19-JUL-1999; 99US-0144331P.
XX PR 19-JUL-1999; 99US-0144332P.
XX PR 19-JUL-1999; 99US-0144333P.
XX PR 19-JUL-1999; 99US-0144334P.
XX PR 19-JUL-1999; 99US-0144335P.
XX PR 19-JUL-1999; 99US-0144352P.
XX PR 20-JUL-1999; 99US-0144632P.
XX PR 20-JUL-1999; 99US-0144884P.
XX PR 21-JUL-1999; 99US-0144814P.
XX PR 21-JUL-1999; 99US-0145086P.
XX PR 21-JUL-1999; 99US-0145088P.
XX PR 22-JUL-1999; 99US-0145085P.
XX PR 22-JUL-1999; 99US-0145087P.
XX PR 22-JUL-1999; 99US-0145089P.
XX PR 22-JUL-1999; 99US-0145192P.
XX PR 23-JUL-1999; 99US-0145145P.
XX PR 23-JUL-1999; 99US-0145218P.
XX PR 23-JUL-1999; 99US-0145224P.
XX PR 26-JUL-1999; 99US-0145276P.
XX PR 27-JUL-1999; 99US-0145913P.
XX PR 27-JUL-1999; 99US-0145918P.
XX PR 28-JUL-1999; 99US-0145919P.
XX PR 28-JUL-1999; 99US-0145951P.
XX PR 02-AUG-1999; 99US-0146386P.
XX PR 02-AUG-1999; 99US-0146388P.
XX PR 02-AUG-1999; 99US-0146389P.
XX PR 03-AUG-1999; 99US-0147038P.
XX PR 04-AUG-1999; 99US-0147204P.
XX PR 04-AUG-1999; 99US-0147302P.
XX PR 05-AUG-1999; 99US-0147192P.
XX PR 05-AUG-1999; 99US-0147260P.
XX PR 06-AUG-1999; 99US-0147303P.
XX PR 06-AUG-1999; 99US-0147416P.
XX PR 09-AUG-1999; 99US-0147493P.
```

PR 09-AUG-1999;	99US-0147935P.	Db	: :
PR 10-AUG-1999;	99US-0148171P.		206 KFIFYA 211
PR 11-AUG-1999;	99US-0148319P.		
PR 12-AUG-1999;	99US-0148341P.		
PR 13-AUG-1999;	99US-0148565P.		
PR 13-AUG-1999;	99US-0148584P.		
PR 16-AUG-1999;	99US-0149368P.		
PR 17-AUG-1999;	99US-0149175P.		
PR 18-AUG-1999;	99US-0149426P.		
PR 20-AUG-1999;	99US-0149722P.		
PR 20-AUG-1999;	99US-0149723P.		
PR 20-AUG-1999;	99US-0149829P.		
PR 23-AUG-1999;	99US-0149902P.		
PR 23-AUG-1999;	99US-0149930P.		
PR 25-AUG-1999;	99US-0150566P.		
PR 26-AUG-1999;	99US-0150884P.		
PR 27-AUG-1999;	99US-0151065P.		
PR 27-AUG-1999;	99US-0151066P.		
PR 27-AUG-1999;	99US-0151080P.		
PR 30-AUG-1999;	99US-0151303P.		
PR 31-AUG-1999;	99US-0151438P.		
PR 01-SEP-1999;	99US-0151930P.		
PR 07-SEP-1999;	99US-0152363P.		
PR 10-SEP-1999;	99US-0153070P.		
PR 13-SEP-1999;	99US-0153758P.		
PR 15-SEP-1999;	99US-0154018P.		
PR 16-SEP-1999;	99US-0154039P.		
PR 20-SEP-1999;	99US-0154779P.		
PR 22-SEP-1999;	99US-0155139P.		
PR 23-SEP-1999;	99US-0155486P.		
PR 24-SEP-1999;	99US-0155659P.		
PR 28-SEP-1999;	99US-0156458P.		
PR 29-SEP-1999;	99US-0156596P.		
PR 04-OCT-1999;	99US-0157117P.		
PR 05-OCT-1999;	99US-0157533P.		
PR 06-OCT-1999;	99US-0157865P.		
PR 07-OCT-1999;	99US-0158029P.		
PR 08-OCT-1999;	99US-0158232P.		
PR 12-OCT-1999;	99US-0158369P.		
PR 13-OCT-1999;	99US-0159293P.		
PR 13-OCT-1999;	99US-0159294P.		
PR 14-OCT-1999;	99US-0159295P.		
PR 14-OCT-1999;	99US-0159329P.		
PR 14-OCT-1999;	99US-0159330P.		
PR 14-OCT-1999;	99US-0159331P.		
PR 14-OCT-1999;	99US-0159637P.		
PR 18-OCT-1999;	99US-0159638P.		
PR 21-OCT-1999;	99US-0160741P.		
PR 21-OCT-1999;	99US-0160767P.		
PR 21-OCT-1999;	99US-0160768P.		
PR 21-OCT-1999;	99US-0160770P.		
PR 21-OCT-1999;	99US-0160814P.		
PR 21-OCT-1999;	99US-0160815P.		
PR 22-OCT-1999;	99US-0160980P.		
PR 22-OCT-1999;	99US-0160981P.		
PR 22-OCT-1999;	99US-0160989P.		
PR 25-OCT-1999;	99US-0161404P.		
PR 25-OCT-1999;	99US-0161405P.		
PR 25-OCT-1999;	99US-0161406P.		
PR 26-OCT-1999;	99US-0161359P.		
PR 26-OCT-1999;	99US-0161360P.		
PR 26-OCT-1999;	99US-0161361P.		
PR 28-OCT-1999;	99US-0161920P.		
PR 28-OCT-1999;	99US-0161922P.		
PR 28-OCT-1999;	99US-0161933P.		
PR 29-OCT-1999;	99US-0162142P.		
<p>Query Match 87.1%; Score 27; DB 3; Length 248;            Best Local Similarity 66.7%; Pred. No. 8.5e+02;            Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;</p>			
QY	1 KVFVFA 6		

AGI0913	RESULT 69		
ID AAG10913 standard; protein; 252 AA.			
XX AAG10913;			
XX 17-OCT-2000 (first entry)			
XX Arabidopsis thaliana protein fragment SEQ ID NO: 9428.			
DE Arabidopsis thaliana			
XX Protein identification; signal transduction pathway; metabolic pathway;			
KW hybridisation assay; genetic mapping; gene expression control; promoter;			
KW termination sequence.			
XX Arabidopsis thaliana			
XX EP1033405-A2.			
PD 06-SEP-2000.			
XX 25-FEB-2000; 2000EP-00301439.			
XX 25-FEB-1999; 99US-0121825P.			
PR 05-MAR-1999; 99US-0123180P.			
PR 09-MAR-1999; 99US-0123548P.			
PR 23-MAR-1999; 99US-0125788P.			
PR 25-MAR-1999; 99US-0126264P.			
PR 29-MAR-1999; 99US-0126785P.			
PR 01-APR-1999; 99US-0127462P.			
PR 06-APR-1999; 99US-0128234P.			
PR 08-APR-1999; 99US-0128714P.			
PR 16-APR-1999; 99US-0129845P.			
PR 19-APR-1999; 99US-0130077P.			
PR 21-APR-1999; 99US-0130449P.			
PR 23-APR-1999; 99US-0130510P.			
PR 23-APR-1999; 99US-0130891P.			
PR 28-APR-1999; 99US-0131445P.			
PR 30-APR-1999; 99US-0132048P.			
PR 30-APR-1999; 99US-0132407P.			
PR 04-MAY-1999; 99US-0132484P.			
PR 05-MAY-1999; 99US-0132485P.			
PR 06-MAY-1999; 99US-0132486P.			
PR 06-MAY-1999; 99US-0132487P.			
PR 07-MAY-1999; 99US-0132863P.			
PR 11-MAY-1999; 99US-0134256P.			
PR 14-MAY-1999; 99US-0134218P.			
PR 14-MAY-1999; 99US-0134219P.			
PR 14-MAY-1999; 99US-0134221P.			
PR 14-MAY-1999; 99US-0134370P.			
PR 18-MAY-1999; 99US-0134768P.			
PR 19-MAY-1999; 99US-0134941P.			
PR 20-MAY-1999; 99US-0135124P.			
PR 21-MAY-1999; 99US-0135353P.			
PR 24-MAY-1999; 99US-0135629P.			
PR 25-MAY-1999; 99US-0136021P.			
PR 27-MAY-1999; 99US-0136392P.			
PR 28-MAY-1999; 99US-0136782P.			
PR 01-JUN-1999; 99US-0137222P.			
PR 03-JUN-1999; 99US-0137528P.			
PR 04-JUN-1999; 99US-0137503P.			
PR 07-JUN-1999; 99US-0137724P.			
PR 08-JUN-1999; 99US-0138094P.			
PR 10-JUN-1999; 99US-0138540P.			
PR 10-JUN-1999; 99US-0138847P.			
PR 14-JUN-1999; 99US-0139119P.			
PR 16-JUN-1999; 99US-0139453P.			
PR 16-JUN-1999; 99US-0139453P.			
PR 17-JUN-1999; 99US-0139492P.			
PR 18-JUN-1999; 99US-0139454P.			

PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140981P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149369P.

PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 23-AUG-1999; 99US-0150566P.  
PR 25-AUG-1999; 99US-0150884P.  
PR 26-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 11-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 252;  
Best Local Similarity 66.7%; Pred. No. 8.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy : 1 KFIFFA 6  
Db : 210 KFIFFA 215

RESULT 70  
AAG10912  
ID AAG10912 standard; protein; 270 AA.





PR 25-AUG-1999; 99US-0150566P.  
 PR 26-AUG-1999; 99US-0150884P.  
 PR 27-AUG-1999; 99US-0151065P.  
 PR 27-AUG-1999; 99US-0151066P.  
 PR 27-AUG-1999; 99US-0151080P.  
 PR 30-AUG-1999; 99US-0151303P.  
 PR 31-AUG-1999; 99US-0151438P.  
 PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0153070P.  
 PR 13-SEP-1999; 99US-0153758P.  
 PR 15-SEP-1999; 99US-0154018P.  
 PR 16-SEP-1999; 99US-0154039P.  
 PR 20-SEP-1999; 99US-0154779P.  
 PR 22-SEP-1999; 99US-0155139P.  
 PR 23-SEP-1999; 99US-0155486P.  
 PR 24-SEP-1999; 99US-0156599P.  
 PR 28-SEP-1999; 99US-0156458P.  
 PR 29-SEP-1999; 99US-0156596P.  
 PR 04-OCT-1999; 99US-0157117P.  
 PR 05-OCT-1999; 99US-0157753P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
 PR 08-OCT-1999; 99US-0158232P.  
 PR 12-OCT-1999; 99US-0158369P.  
 PR 13-OCT-1999; 99US-0159293P.  
 PR 13-OCT-1999; 99US-0159294P.  
 PR 13-OCT-1999; 99US-0159295P.  
 PR 14-OCT-1999; 99US-0159329P.  
 PR 14-OCT-1999; 99US-0159330P.  
 PR 14-OCT-1999; 99US-0159331P.  
 PR 14-OCT-1999; 99US-0159637P.  
 PR 14-OCT-1999; 99US-0159638P.  
 PR 18-OCT-1999; 99US-0159584P.  
 PR 21-OCT-1999; 99US-0160741P.  
 PR 21-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
 PR 21-OCT-1999; 99US-0160770P.  
 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160980P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160989P.  
 PR 25-OCT-1999; 99US-0161405P.  
 PR 25-OCT-1999; 99US-0161406P.  
 PR 25-OCT-1999; 99US-0161406P.  
 PR 26-OCT-1999; 99US-0161359P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161992P.  
 PR 28-OCT-1999; 99US-0161993P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 270;  
 Best Local Similarity 66.7%; Pred. NO. 9.2e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6  
 |||:|  
 Db 228 KPIFYA 233

RESULT 71  
 AAU80872  
 ID AAU80872 standard; protein; 297 AA.  
 XX AC  
 XX AAU80872;  
 DT 26-MAR-2002 (first entry)  
 XX Human CLAN NACHT.  
 DE  
 XX

KW Caspase recruitment domain; CARD; NB-ARC; ANGIO-R; LRR; SAM;  
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
 KW leukemia; allergy; arthritis; lupus; Schrogen's syndrome;  
 KW Crohn's disease; graft-versus-host disease; stroke;  
 KW myocardial infarction; heart failure; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; HIV;  
 KW human immunodeficiency virus infection.  
 XX Homo sapiens.  
 XX WO200190156-A2.  
 XX 29-NOV-2001.  
 XX 24-MAY-2001; 2001WO-US017158.  
 XX 24-MAY-2000; 2000US-00579240.  
 PR 10-OCT-2000; 2000US-00686347.  
 PR 14-MAR-2001; 2001US-0275980P.  
 PR 23-MAY-2001; 2001US-00864921.  
 XX (BURN-) BURNHAM INST.  
 XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
 PI Oliveira VAM, Hayashi H, Pawlowski K;  
 XX WPI; 2002-083086/11.  
 DR N-PSDB; ABK22766.  
 XX New caspase recruitment domain (CARD)-containing polypeptides and  
 PT encoding nucleic acids, useful for treating abnormal cell proliferation  
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
 PT arthritis or stroke.  
 XX Claim 9; Page 201-202; 216pp; English.  
 XX The invention relates to an isolated caspase recruitment domain (CARD) -  
 CC containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
 CC from it, and the polynucleotides encoding them. Also included are a  
 CC recombinant vector comprising the polynucleotide, recombinant cells  
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian and  
 CC insect cells) and an anti-CARD antibody. The CARD-containing polypeptide  
 CC and CARD-encoding nucleic acid are useful for treating a pathology  
 CC characterised by abnormal cell proliferation (e.g. cancer), abnormal cell  
 CC death (apoptosis), autoimmune diseases or inflammation. In particular,  
 CC the polypeptide and nucleic acid are useful for treating keratinocyte  
 CC hyperplasia, inflammatory hyperplasia, fibrosis, smooth muscle cell  
 CC proliferation in arteries following balloon angioplasty (restenosis),  
 CC gliomas, carcinomas, sarcomas, melanomas, leukemias, allergies,  
 CC arthritis, lupus, Schrogen's syndrome, Crohn's disease, graft-versus-host  
 CC diseases, stroke, myocardial infarction, heart failure, neurodegenerative  
 CC diseases (e.g. Parkinson's disease or Alzheimer's disease) or  
 CC immunodeficiency associated disease (e.g. human immunodeficiency virus  
 CC (HIV) infection). The nucleic acids are useful in a variety of diagnostic  
 CC applications. The present sequence is a CARD domain containing protein  
 XX Sequence 297 AA;

Query Match 87.1%; Score 27; DB 5; Length 297;  
 Best Local Similarity 100.0%; Pred. NO. 1e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5  
 |||||  
 Db 38 KPVFF 42

RESULT 72  
 ABU81731  
 ID ABU81731 standard; protein; 297 AA.

XX ABU81731;  
 XX  
 XX 26-JUN-2003 (first entry)  
 XX  
 XX Human caspase recruitment domain-containing polypeptide #15.  
 XX  
 XX Human; caspase recruitment domain-containing polypeptide; CARD; NB-ARC;  
 KW ANGIO-R; leucine rich repeat; LRR; S-adenosyl methionine domain;  
 KW apoptosis; NF-kappaB induction; cytokine processing; SAM; transcription;  
 KW cJun N-terminal kinase induction; caspase-mediated proteolysis; cancer;  
 KW inflammation; cell adhesion; cell proliferation; abnormal cell death;  
 KW keratinocyte hyperplasia; neoplasia; benign prostatic hypertrophy; lupus;  
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
 KW angioplasty; artery; keloid; restenosis; autoimmune disease; allergy;  
 KW arthritis; Sjogren's syndrome; Crohn's disease; ulcerative colitis;  
 KW allograft rejection; graft versus host disease; myocardial infarction;  
 KW heart failure; neurodegenerative disease; stroke; HIV.  
 XX  
 XX Homo sapiens.  
 XX  
 XX US2002176853-A1.  
 XX  
 XX 28-NOV-2002.  
 XX  
 XX 23-MAY-2001; 2001US-00864921.  
 XX  
 XX 24-MAY-2000; 2000US-0325756P.  
 PR 10-OCT-2000; 2000US-0367337P.  
 PR 14-MAR-2001; 2001US-0275980P.  
 XX  
 XX (REED/) REED J C.  
 PA (PIOF/) PIO F F.  
 PA (GODZ/) GODZIK A.  
 PA (STEH/) STEHLIK C.  
 PA (DAMI/) DAMIANO J S.  
 PA (LEES/) LEE S H.  
 PA (OLIV/) OLIVEIRA V A.  
 PA (HAYA/) HAYASHI H.  
 PA (PAWL/) PAWLOWSKI K.  
 XX  
 XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
 PI Oliveira VA, Hayashi H, Pawlowski K;  
 PI  
 XX WPI; 2002-083086/11.  
 DR N-PSDB; ACA68180.  
 XX  
 XX New caspase recruitment domain (CARD)-containing polypeptides and  
 PT encoding nucleic acids, useful for treating abnormal cell proliferation  
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
 PT arthritis or stroke.  
 XX  
 XX Claim 1; Page 85-86; 106pp; English.  
 PS  
 XX The invention relates to an isolated caspase recruitment domain (CARD)-  
 CC containing polypeptide, or its CARD, NB-ARC, ANGIO-R, leucine rich repeat  
 CC (LRR) or S-adenosyl methionine (SAM) domain, and its associated  
 CC polynucleotide. The DNA is useful for altering the level of a biochemical  
 CC process (including apoptosis, NF-kappaB induction, cytokine processing,  
 CC cJun N-terminal kinase induction, caspase-mediated proteolysis,  
 CC transcription, inflammation and cell adhesion) modulated by the DNA. The  
 CC sequences are useful for treating a pathology characterised by abnormal  
 CC cell proliferation, abnormal cell death or inflammation. The treatable  
 CC diseases include cancer, keratinocyte hyperplasia, neoplasia, keloids,  
 CC benign prostatic hypertrophy, inflammatory hyperplasia, fibrosis, smooth  
 CC muscle cell proliferation in arteries following angioplasty, restenosis,  
 CC autoimmune diseases including allergies, inflammatory diseases including  
 CC arthritis, lupus, Sjogren's syndrome, Crohn's disease, ulcerative  
 CC colitis, allograft rejection such as graft versus host disease, stroke,  
 CC myocardial infarction, heart failure, neurodegenerative diseases such as  
 CC Parkinson's disease and Alzheimer's disease and immunodeficiency  
 CC associated diseases such as human immunodeficiency virus (HIV) infection.  
 CC Sequences ABU81714-ABU81735 represent human CARD-containing polypeptides

CC of the invention  
 XX  
 XX Sequence 297 AA;  
 SQ  
 Query Match 87.1%; Score 27; DB 5; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 1.e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KRVFF 5  
 |||||  
 Db 38 KRVFF 42  
 RESULT 73  
 ADP47907  
 ID ADP47907 standard; protein; 312 AA.  
 XX  
 XX ADP47907;  
 XX  
 XX 12-AUG-2004 (first entry)  
 XX  
 XX Human CATERPILLER Ipad nucleotide binding domain (NBD) protein.  
 XX  
 XX Monarch-1; CATERPILLER 11.2; caspase recruitment domain;  
 KW CARD, transcription enhancer, R-binding, pyrin, lots of leucine repeat;  
 KW CATERPILLER 11.3; CATERPILLER 16.1; CATERPILLER 16.2; CIAS1;  
 KW cold-induced autoinflammatory syndrome 1; antiinflammatory; cytostatic;  
 KW inflammatory disease; cancer; gene therapy; human; purine;  
 KW nucleotide binding domain; NBD; Ipaf.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2004034093-A2.  
 PN  
 XX 22-APR-2004.  
 PD  
 XX 30-APR-2003; 2003WO-US013562.  
 PF  
 XX 30-APR-2002; 2002US-0376626P.  
 PR  
 XX (UYNC-) UNIV NORTH CAROLINA.  
 PA  
 XX Ting JY, Linhoff MW, Harton JA, Williams KL, Lich J, O'Connor W;  
 PI Moore CB, Davis B, Brickey J, Conti B, Zhang J, Zhu X;  
 PI  
 XX WPI; 2004-348215/32.  
 DR  
 XX  
 XX New nucleic acid encoding Monarch-1, CATERPILLER 11.2, CATERPILLER 11.3,  
 PT CATERPILLAR 16.1, CATERPILLER 16.2 or CIAS1 polypeptide, useful in  
 PT preparing a composition for treating inflammatory disease or cancer.  
 PT  
 XX Example 1; Fig 3; 205pp; English.  
 PS  
 XX The invention relates to a novel isolated nucleic acid encoding a Monarch  
 CC -1, CATERPILLER (CARD [caspase recruitment domain], transcription  
 CC enhancer, R(purine)-binding, pyrin, lots of leucine repeats) 11.2,  
 CC CATERPILLER 11.3, CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 (cold-  
 CC induced autoinflammatory syndrome 1) polypeptide comprising the amino  
 CC acids encoded by exon 6 and lacking the amino acids encoded by exon 4 or  
 CC its fragment. The nucleic acid of the invention demonstrates  
 CC antiinflammatory and cytostatic activities and may be useful in preparing  
 CC a composition for treating an inflammatory disease or cancer, possibly  
 CC via gene therapy. The current sequence is that of a human CATERPILLER  
 CC nucleotide binding domain (NBD) protein of the invention.  
 CC  
 XX Sequence 312 AA;  
 SQ  
 Query Match 87.1%; Score 27; DB 8; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KRVFF 5  
 |||||

Db 51 KVFVF 55

RESULT 74  
AAG33404  
ID AAG33404 standard; protein; 313 AA.  
XX AAG33404;  
AC AAG33404;  
XX 18-OCT-2000 (first entry)  
XX Zea mays protein fragment SEQ ID NO: 40468.  
DE Zea mays protein fragment SEQ ID NO: 40468.  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence; corn.  
XX Zea mays subsp. mays.  
XX EP1033405-A2.  
XX 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-00301439.  
XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130501P.  
PR 28-APR-1999; 99US-0130891P.  
PR 30-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 04-MAY-1999; 99US-0132407P.  
PR 05-MAY-1999; 99US-0132484P.  
PR 06-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 07-MAY-1999; 99US-0132487P.  
PR 11-MAY-1999; 99US-0132863P.  
PR 14-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 18-MAY-1999; 99US-0134370P.  
PR 19-MAY-1999; 99US-0134768P.  
PR 20-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137503P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 21-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 22-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 23-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 03-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.

PR	18-AUG-1999;	99US-0149426P.	AC	ADT58396;
PR	20-AUG-1999;	99US-0149722P.	XX	
PR	20-AUG-1999;	99US-0149723P.	DT	13-JAN-2005 (first entry)
PR	20-AUG-1999;	99US-0149929P.	XX	
PR	23-AUG-1999;	99US-0149902P.	DE	Plant polypeptide, SEQ ID 8473.
PR	23-AUG-1999;	99US-0149930P.	XX	
PR	25-AUG-1999;	99US-0150366P.	KW	Plant; transgenic; cold tolerance; growth rate; drought tolerance;
PR	26-AUG-1999;	99US-0150884P.	KW	disease resistance; galactomannan production; plant growth regulator;
PR	27-AUG-1999;	99US-0151065P.	KW	heat tolerance; herbicide tolerance; lignin production;
PR	27-AUG-1999;	99US-0151066P.	KW	extreme osmotic condition tolerance; pathogens resistance;
PR	27-AUG-1999;	99US-0151080P.	KW	pest resistance; yield improvement; seed oil yield; seed protein yield.
PR	30-AUG-1999;	99US-0151303P.	XX	
PR	31-AUG-1999;	99US-0151438P.	OS	Viridiplantae.
PR	01-SEP-1999;	99US-0151930P.	XX	
PR	07-SEP-1999;	99US-0152363P.	PN	US2004216190-A1.
PR	10-SEP-1999;	99US-0153070P.	XX	28-OCT-2004.
PR	13-SEP-1999;	99US-0153758P.	PD	
PR	15-SEP-1999;	99US-0154018P.	XX	
PR	16-SEP-1999;	99US-0154039P.	PF	18-DEC-2003; 2003US-00739930.
PR	20-SEP-1999;	99US-0154779P.	XX	
PR	22-SEP-1999;	99US-0155139P.	PR	28-APR-2003; 2003US-00424599.
PR	23-SEP-1999;	99US-0155486P.	XX	28-APR-2003; 2003US-00425115.
PR	24-SEP-1999;	99US-0155659P.	XX	(KOVA/) KOVALIC D K.
PR	28-SEP-1999;	99US-0156458P.	PA	
PR	29-SEP-1999;	99US-0156596P.	XX	
PR	04-OCT-1999;	99US-0157117P.	PI	Kovalic DK;
PR	05-OCT-1999;	99US-0157753P.	XX	
PR	06-OCT-1999;	99US-0157865P.	DR	WPI; 2004-757369/74.
PR	07-OCT-1999;	99US-0158029P.	XX	
PR	08-OCT-1999;	99US-0158232P.	PT	New recombinant DNA constructs useful in the field of biochemistry and
PR	12-OCT-1999;	99US-0158369P.	PT	genetics, and in particular for producing transgenic plants with improved
PR	13-OCT-1999;	99US-0159293P.	XX	biological characteristics.
PR	13-OCT-1999;	99US-0159294P.	XX	Claim 2; SEQ ID NO 8473; 14pp; English.
PR	13-OCT-1999;	99US-0159295P.	PS	
PR	14-OCT-1999;	99US-0159329P.	XX	
PR	14-OCT-1999;	99US-0159330P.	XX	
PR	14-OCT-1999;	99US-0159331P.	CC	The invention relates a recombinant DNA construct comprising a
PR	14-OCT-1999;	99US-0159637P.	CC	polynucleotide having any of 5544 nucleotide sequences (CDNAS SEQ ID NO:
PR	14-OCT-1999;	99US-0159638P.	CC	1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
PR	18-OCT-1999;	99US-0159584P.	CC	(SEQ ID NO: 5545-11088). The CDNAS and proteins are from corn, soybean,
PR	21-OCT-1999;	99US-0160741P.	CC	Arabidopsis, wheat and rape but the specification does not indicate which
PR	21-OCT-1999;	99US-0160767P.	CC	sequences is derived from which organism. Also included is a method of
PR	21-OCT-1999;	99US-0160768P.	CC	producing a plant having an improved property, comprising transforming a
PR	21-OCT-1999;	99US-0160770P.	CC	plant with a recombinant DNA construct comprising a promoter region
PR	21-OCT-1999;	99US-0160814P.	CC	functional in a plant cell operably joined to a polynucleotide encoding a
PR	21-OCT-1999;	99US-0160815P.	CC	polypeptide associated with the property, and growing the transformed
PR	22-OCT-1999;	99US-0160980P.	CC	plant. The property is selected from improving plant cold tolerance, for
PR	22-OCT-1999;	99US-0160981P.	CC	manipulating growth rate in plant cells by modification of the cell cycle
PR	22-OCT-1999;	99US-0160989P.	CC	pathway, for improving plant drought tolerance, for providing increased
PR	22-OCT-1999;	99US-0161404P.	CC	resistance to plant disease, for galactomannan production, for production
PR	25-OCT-1999;	99US-0161405P.	CC	of plant growth regulators, for improving plant heat tolerance, for
PR	25-OCT-1999;	99US-0161406P.	CC	improving plant tolerance to herbicides, for increasing the rate of
PR	25-OCT-1999;	99US-0161359P.	CC	homologous recombination in plants, for lignin production, for improving
PR	26-OCT-1999;	99US-0161360P.	CC	plant tolerance to extreme osmotic conditions, for improving plant
PR	26-OCT-1999;	99US-0161361P.	CC	tolerance to pathogens or pests, for yield improvement by modification of
PR	26-OCT-1999;	99US-0161920P.	CC	photosynthesis, for modifying seed oil yield and/or content, for
PR	28-OCT-1999;	99US-0161922P.	CC	modifying seed protein yield and/or content, for yield improvement by
PR	28-OCT-1999;	99US-0161993P.	CC	modification of carbohydrate, nitrogen or phosphorus use and/or uptake
PR	29-OCT-1999;	99US-0162142P.	CC	and for yield improvement by providing improved plant growth and
PR	29-OCT-1999;		CC	development under at least one stress condition. The polynucleotide may
PR			CC	also encode a plant transcription factor. The methods and compositions of
PR			CC	the present invention are useful in the field of biochemistry and
PR			CC	genetics, in particular for producing transgenic plants with improved
PR			CC	biological characteristics such as increased yield, improved nitrogen
PR			CC	flow, increasing plant tolerance to cold or heat, improving plant
PR			CC	tolerance to extreme osmotic and drought conditions, and improving plant
PR			CC	tolerance to plant pests or pathogens. They can also be used in physical
PR			CC	arrays of molecules, plant breeding markers, computer-based storage and
PR			CC	analysis systems. The present sequence is one of the 5544 plant protein
PR			CC	sequences of the invention. Note: The sequence data for this patent did
PR			CC	not form part of the printed specification, but was obtained in
PR			CC	electronic format directly from USPTO at
PR			CC	seqdata.uspto.gov/sequence.html?docID=20040216190.
PR			CC	
PR			XX	

Query Match 87.1%; Score 27; DB 3; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5  
 Db 86 KVFVF 90

RESULT 75  
 ADT58396  
 ID ADT58396 standard; protein; 335 AA.  
 XX

SQ Sequence 335 AA;

Query Match 87.1%; Score 27; DB 8; Length 335;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVPPA 6  
|||  
Db 80 KPAPPA 85

Search completed: December 29, 2005, 17:33:26  
Job time : 93.7742 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 77.3387 Seconds  
(without alignments)  
37.818 Million cell updates/sec

Title: US-10-009-122-2

Perfect score: 34

Sequence: 1 KKLFFFA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications AA\_Main:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	7	3	US-09-867-847-12
2	34	100.0	7	3	US-09-915-092-2
3	34	100.0	7	3	US-09-747-408-2
4	34	100.0	7	5	US-10-728-028-2
5	34	100.0	7	5	US-10-825-958-10
6	34	100.0	9	4	US-10-235-483-64
7	31	91.2	1640	4	US-10-437-963-109646
8	30	88.2	7	3	US-09-972-475-7
9	30	88.2	7	4	US-10-463-729-7
10	30	88.2	7	5	US-10-810-881A-128
11	30	88.2	8	3	US-09-972-475-5
12	30	88.2	8	4	US-10-463-729-5
13	30	88.2	9	3	US-09-867-847-9
14	30	88.2	9	3	US-09-747-408-20
15	30	88.2	9	4	US-10-235-483-54
16	30	88.2	9	4	US-10-619-454-28
17	30	88.2	10	3	US-09-867-847-29
18	30	88.2	10	3	US-09-915-092-19
19	30	88.2	10	5	US-10-889-999-20
20	30	88.2	10	5	US-10-889-999-21
21	30	88.2	10	5	US-10-889-999-22
22	30	88.2	10	5	US-10-889-999-23
23	30	88.2	10	5	US-10-890-070-20
24	30	88.2	10	5	US-10-890-070-21
25	30	88.2	10	5	US-10-890-070-22
26	30	88.2	10	5	US-10-890-070-23
27	30	88.2	10	5	US-10-890-000-20

28	30	88.2	10	5	US-10-890-000-21	Sequence 21, Appl
29	30	88.2	10	5	US-10-890-000-22	Sequence 22, Appl
30	30	88.2	10	5	US-10-890-000-23	Sequence 23, Appl
31	30	88.2	10	5	US-10-823-463-20	Sequence 20, Appl
32	30	88.2	10	5	US-10-823-463-21	Sequence 21, Appl
33	30	88.2	10	5	US-10-823-463-22	Sequence 22, Appl
34	30	88.2	10	5	US-10-823-463-23	Sequence 23, Appl
35	30	88.2	10	5	US-10-728-028-19	Sequence 19, Appl
36	30	88.2	10	5	US-10-822-968-20	Sequence 20, Appl
37	30	88.2	10	5	US-10-822-968-21	Sequence 21, Appl
38	30	88.2	10	5	US-10-822-968-22	Sequence 22, Appl
39	30	88.2	10	5	US-10-822-968-23	Sequence 23, Appl
40	30	88.2	10	5	US-10-777-792-20	Sequence 20, Appl
41	30	88.2	10	5	US-10-777-792-21	Sequence 21, Appl
42	30	88.2	10	5	US-10-777-792-22	Sequence 22, Appl
43	30	88.2	10	5	US-10-777-792-23	Sequence 23, Appl
44	30	88.2	10	5	US-10-825-958-27	Sequence 27, Appl
45	30	88.2	10	5	US-10-890-071-20	Sequence 20, Appl
46	30	88.2	10	5	US-10-890-071-21	Sequence 21, Appl
47	30	88.2	10	5	US-10-890-071-22	Sequence 22, Appl
48	30	88.2	10	5	US-10-890-071-23	Sequence 23, Appl
49	30	88.2	10	5	US-10-890-024-20	Sequence 20, Appl
50	30	88.2	10	5	US-10-890-024-21	Sequence 21, Appl
51	30	88.2	10	5	US-10-890-024-22	Sequence 22, Appl
52	30	88.2	10	5	US-10-890-024-23	Sequence 23, Appl
53	30	88.2	10	5	US-10-828-926-20	Sequence 20, Appl
54	30	88.2	10	5	US-10-828-926-21	Sequence 21, Appl
55	30	88.2	10	5	US-10-828-926-22	Sequence 22, Appl
56	30	88.2	10	6	US-10-828-926-23	Sequence 23, Appl
57	30	88.2	10	6	US-11-058-757-20	Sequence 20, Appl
58	30	88.2	10	6	US-11-058-757-21	Sequence 21, Appl
59	30	88.2	10	6	US-11-058-757-22	Sequence 22, Appl
60	30	88.2	10	6	US-11-058-757-23	Sequence 23, Appl
61	30	88.2	11	3	US-09-988-842-9	Sequence 9, Appl
62	30	88.2	11	3	US-09-988-842-25	Sequence 25, Appl
63	30	88.2	11	4	US-10-235-483-14	Sequence 14, Appl
64	30	88.2	11	4	US-10-050-200-33	Sequence 33, Appl
65	30	88.2	11	5	US-10-464-117-13	Sequence 13, Appl
66	30	88.2	11	5	US-10-772-230-9	Sequence 9, Appl
67	30	88.2	11	5	US-10-772-230-25	Sequence 25, Appl
68	30	88.2	12	5	US-09-867-847-8	Sequence 8, Appl
69	30	88.2	12	5	US-10-810-881A-115	Sequence 115, Appl
70	30	88.2	12	5	US-10-508-586-2	Sequence 2, Appl
71	30	88.2	12	5	US-10-508-586-3	Sequence 3, Appl
72	30	88.2	12	5	US-10-625-854-139	Sequence 139, Appl
73	30	88.2	12	6	US-11-012-797A-33	Sequence 33, Appl
74	30	88.2	13	4	US-10-281-458-1	Sequence 1, Appl
75	30	88.2	13	5	US-10-625-854-127	Sequence 127, Appl
76	30	88.2	13	5	US-10-625-854-140	Sequence 140, Appl
77	30	88.2	14	3	US-09-992-800-5	Sequence 5, Appl
78	30	88.2	14	3	US-09-992-994-5	Sequence 5, Appl
79	30	88.2	14	4	US-10-385-065-5	Sequence 5, Appl
80	30	88.2	14	5	US-10-810-881A-114	Sequence 114, Appl
81	30	88.2	14	5	US-10-505-313-2	Sequence 2, Appl
82	30	88.2	14	5	US-10-625-854-115	Sequence 115, Appl
83	30	88.2	14	5	US-10-625-854-128	Sequence 128, Appl
84	30	88.2	14	5	US-10-625-854-141	Sequence 141, Appl
85	30	88.2	14	6	US-11-063-350-5	Sequence 5, Appl
86	30	88.2	15	4	US-10-235-483-56	Sequence 56, Appl
87	30	88.2	15	4	US-10-235-483-57	Sequence 57, Appl
88	30	88.2	15	4	US-10-235-483-60	Sequence 60, Appl
89	30	88.2	15	4	US-10-235-483-61	Sequence 61, Appl
90	30	88.2	15	4	US-10-235-483-63	Sequence 63, Appl
91	30	88.2	15	4	US-10-235-483-65	Sequence 65, Appl
92	30	88.2	15	5	US-10-625-854-103	Sequence 103, Appl
93	30	88.2	15	5	US-10-625-854-116	Sequence 116, Appl
94	30	88.2	15	5	US-10-625-854-129	Sequence 129, Appl
95	30	88.2	16	5	US-10-625-854-142	Sequence 142, Appl
96	30	88.2	16	5	US-10-625-854-91	Sequence 91, Appl
97	30	88.2	16	5	US-10-625-854-104	Sequence 104, Appl
98	30	88.2	16	5	US-10-625-854-117	Sequence 117, Appl
99	30	88.2	16	5	US-10-625-854-130	Sequence 130, Appl
100	30	88.2	16	5	US-10-625-854-143	Sequence 143, Appl



101	30	88.2	17	3	US-09-992-800-3	Sequence 3, Appli	174	30	88.2	30	4	US-10-666-423-1	Sequence 1, Appli
102	30	88.2	17	3	US-09-992-994-3	Sequence 3, Appli	175	30	88.2	30	4	US-10-617-876-9	Sequence 9, Appli
103	30	88.2	17	3	US-09-998-491-8	Sequence 8, Appli	176	30	88.2	30	4	US-10-619-454-24	Sequence 24, Appli
104	30	88.2	17	3	US-10-385-065-3	Sequence 3, Appli	177	30	88.2	30	4	US-10-301-448-1	Sequence 1, Appli
105	30	88.2	17	4	US-10-451-367-26	Sequence 26, Appli	178	30	88.2	30	5	US-10-775-562-5	Sequence 5, Appli
106	30	88.2	17	4	US-10-475-281-8	Sequence 8, Appli	179	30	88.2	32	4	US-10-732-862A-99	Sequence 99, Appli
107	30	88.2	17	4	US-10-810-919-3	Sequence 3, Appli	180	30	88.2	33	3	US-09-930-915A-295	Sequence 295, App
108	30	88.2	17	5	US-10-684-346-24	Sequence 24, Appli	181	30	88.2	33	4	US-10-082-014-84	Sequence 84, Appli
109	30	88.2	17	5	US-10-997-078-46	Sequence 46, Appli	182	30	88.2	33	4	US-10-372-076-85	Sequence 85, Appli
110	30	88.2	17	5	US-10-997-700-19	Sequence 19, Appli	183	30	88.2	33	4	US-10-732-862A-98	Sequence 98, Appli
111	30	88.2	17	6	US-11-063-350-3	Sequence 3, Appli	184	30	88.2	33	4	US-10-806-006-235	Sequence 295, App
112	30	88.2	17	6	US-11-066-697-950	Sequence 950, App	185	30	88.2	33	4	US-10-677-074-85	Sequence 85, Appli
113	30	88.2	17	6	US-11-066-697-983	Sequence 983, App	186	30	88.2	33	4	US-10-805-913-295	Sequence 295, App
114	30	88.2	17	3	US-09-825-242-5	Sequence 5, Appli	187	30	88.2	35	3	US-09-867-847-3	Sequence 3, Appli
115	30	88.2	19	4	US-10-429-216-5	Sequence 5, Appli	188	30	88.2	35	3	US-09-972-475-16	Sequence 16, Appli
116	30	88.2	19	4	US-10-816-022-5	Sequence 5, Appli	189	30	88.2	35	4	US-10-463-729-16	Sequence 16, Appli
117	30	88.2	19	4	US-10-816-523-5	Sequence 5, Appli	190	30	88.2	35	5	US-10-825-958-3	Sequence 3, Appli
118	30	88.2	19	4	US-10-815-353-5	Sequence 5, Appli	191	30	88.2	35	6	US-11-066-697-979	Sequence 979, App
119	30	88.2	19	4	US-10-815-391-5	Sequence 5, Appli	192	30	88.2	35	6	US-11-066-697-1006	Sequence 1006, Ap
120	30	88.2	19	5	US-10-828-548-5	Sequence 5, Appli	193	30	88.2	36	3	US-09-861-847-6	Sequence 6, Appli
121	30	88.2	19	5	US-10-816-380-5	Sequence 5, Appli	194	30	88.2	36	3	US-09-861-847-11	Sequence 11, Appli
122	30	88.2	19	5	US-10-889-999-75	Sequence 75, Appli	195	30	88.2	36	4	US-10-301-488A-5	Sequence 6, Appli
123	30	88.2	19	5	US-10-890-070-75	Sequence 75, Appli	196	30	88.2	36	4	US-10-301-488A-11	Sequence 11, Appli
124	30	88.2	19	5	US-10-890-000-75	Sequence 75, Appli	197	30	88.2	36	4	US-10-666-423-6	Sequence 6, Appli
125	30	88.2	19	5	US-10-788-666-5	Sequence 5, Appli	198	30	88.2	36	4	US-10-666-423-11	Sequence 11, Appli
126	30	88.2	19	5	US-10-923-471-5	Sequence 5, Appli	199	30	88.2	36	4	US-10-301-448-6	Sequence 6, Appli
127	30	88.2	19	5	US-10-923-463-5	Sequence 5, Appli	200	30	88.2	36	4	US-10-301-448-11	Sequence 11, Appli
128	30	88.2	19	5	US-10-923-469-5	Sequence 5, Appli	201	30	88.2	36	4	US-10-732-862A-436	Sequence 436, App
129	30	88.2	19	5	US-10-933-559-5	Sequence 5, Appli	202	30	88.2	38	4	US-10-425-115-290955	Sequence 290955, S
130	30	88.2	19	5	US-10-934-404-5	Sequence 5, Appli	203	30	88.2	38	6	US-11-066-697-975	Sequence 975, App
131	30	88.2	19	5	US-10-934-609-5	Sequence 5, Appli	204	30	88.2	38	6	US-11-066-697-1002	Sequence 1002, Ap
132	30	88.2	19	5	US-10-923-474-5	Sequence 5, Appli	205	30	88.2	39	4	US-10-051-496-5	Sequence 5, Appli
133	30	88.2	19	5	US-10-884-892-5	Sequence 5, Appli	206	30	88.2	39	4	US-10-190-548A-5	Sequence 5, Appli
134	30	88.2	19	5	US-10-822-968-75	Sequence 75, Appli	207	30	88.2	40	3	US-09-861-847-7	Sequence 7, Appli
135	30	88.2	19	5	US-10-777-792-75	Sequence 75, Appli	208	30	88.2	40	3	US-09-861-847-8	Sequence 8, Appli
136	30	88.2	19	5	US-10-890-071-75	Sequence 75, Appli	209	30	88.2	40	3	US-09-867-847-2	Sequence 2, Appli
137	30	88.2	19	5	US-10-890-024-75	Sequence 75, Appli	210	30	88.2	40	3	US-09-988-842-3	Sequence 3, Appli
138	30	88.2	19	5	US-10-934-819-5	Sequence 5, Appli	211	30	88.2	40	3	US-09-851-071-3	Sequence 3, Appli
139	30	88.2	19	5	US-10-923-267-5	Sequence 5, Appli	212	30	88.2	40	3	US-09-962-955C-36	Sequence 36, Appli
140	30	88.2	19	5	US-10-928-926-75	Sequence 75, Appli	213	30	88.2	40	3	US-09-792-079-12	Sequence 12, Appli
141	30	88.2	19	6	US-11-058-757-75	Sequence 75, Appli	214	30	88.2	40	4	US-10-007-779A-1	Sequence 1, Appli
142	30	88.2	19	6	US-11-108-102-5	Sequence 5, Appli	215	30	88.2	40	4	US-10-051-496-4	Sequence 4, Appli
143	30	88.2	20	3	US-09-908-943A-25	Sequence 25, Appli	216	30	88.2	40	4	US-10-217-584-3	Sequence 3, Appli
144	30	88.2	20	5	US-10-801-487-25	Sequence 25, Appli	217	30	88.2	40	4	US-10-169-580-1	Sequence 1, Appli
145	30	88.2	20	5	US-10-801-938-25	Sequence 25, Appli	218	30	88.2	40	4	US-10-143-534-3	Sequence 3, Appli
146	30	88.2	20	5	US-10-801-509-25	Sequence 25, Appli	219	30	88.2	40	4	US-10-190-548A-4	Sequence 4, Appli
147	30	88.2	20	5	US-10-801-486-25	Sequence 25, Appli	220	30	88.2	40	4	US-10-051-663-3	Sequence 3, Appli
148	30	88.2	20	5	US-10-801-493-25	Sequence 25, Appli	221	30	88.2	40	4	US-10-151-614-1	Sequence 1, Appli
149	30	88.2	24	5	US-10-728-246-6	Sequence 5, Appli	222	30	88.2	40	4	US-10-159-279-12	Sequence 12, Appli
150	30	88.2	24	5	US-10-728-246-6	Sequence 6, Appli	223	30	88.2	40	4	US-10-301-488A-7	Sequence 7, Appli
151	30	88.2	26	4	US-09-792-079-11	Sequence 11, Appli	224	30	88.2	40	4	US-10-455-218-1	Sequence 8, Appli
152	30	88.2	26	4	US-10-159-279-11	Sequence 11, Appli	225	30	88.2	40	4	US-10-301-448-7	Sequence 7, Appli
153	30	88.2	28	3	US-09-867-847-4	Sequence 4, Appli	226	30	88.2	40	4	US-10-366-125-27	Sequence 27, Appli
154	30	88.2	28	3	US-09-865-294-66	Sequence 66, Appli	227	30	88.2	40	4	US-10-337-261-1	Sequence 1, Appli
155	30	88.2	28	3	US-09-792-079-5	Sequence 5, Appli	228	30	88.2	40	4	US-10-666-423-7	Sequence 7, Appli
156	30	88.2	28	4	US-10-159-279-5	Sequence 5, Appli	229	30	88.2	40	4	US-10-666-423-8	Sequence 8, Appli
157	30	88.2	28	4	US-10-363-082-2	Sequence 2, Appli	230	30	88.2	40	4	US-10-301-448-7	Sequence 7, Appli
158	30	88.2	28	4	US-10-433-385-7	Sequence 7, Appli	231	30	88.2	40	4	US-10-301-448-8	Sequence 8, Appli
159	30	88.2	28	4	US-10-390-472-4	Sequence 4, Appli	232	30	88.2	40	4	US-10-683-815-1	Sequence 1, Appli
160	30	88.2	28	4	US-10-741-205-36	Sequence 36, Appli	233	30	88.2	40	4	US-10-683-815-14	Sequence 14, Appli
161	30	88.2	28	4	US-10-416-262B-7	Sequence 7, Appli	234	30	88.2	40	4	US-10-683-815-15	Sequence 15, Appli
162	30	88.2	28	4	US-10-478-308-4	Sequence 4, Appli	235	30	88.2	40	4	US-10-683-815-16	Sequence 16, Appli
163	30	88.2	28	4	US-10-478-307-4	Sequence 4, Appli	236	30	88.2	40	4	US-10-683-815-17	Sequence 17, Appli
164	30	88.2	28	5	US-10-861-614-66	Sequence 66, Appli	237	30	88.2	40	4	US-10-683-815-18	Sequence 18, Appli
165	30	88.2	28	5	US-10-825-958-4	Sequence 4, Appli	238	30	88.2	40	4	US-10-810-919-1	Sequence 1, Appli
166	30	88.2	28	6	US-11-091-309-3	Sequence 3, Appli	239	30	88.2	40	5	US-10-864-107-1	Sequence 1, Appli
167	30	88.2	28	6	US-11-066-697-959	Sequence 959, App	240	30	88.2	40	5	US-10-485-310-18	Sequence 18, Appli
168	30	88.2	28	6	US-11-066-697-965	Sequence 965, App	241	30	88.2	40	5	US-10-481-387-1	Sequence 1, Appli
169	30	88.2	28	6	US-11-066-697-976	Sequence 976, App	242	30	88.2	40	5	US-10-481-954-5	Sequence 5, Appli
170	30	88.2	28	6	US-11-066-697-992	Sequence 992, App	243	30	88.2	40	5	US-10-698-259A-1	Sequence 1, Appli
171	30	88.2	28	6	US-11-066-697-1003	Sequence 1003, App	244	30	88.2	40	5	US-10-884-729-1	Sequence 1, Appli
172	30	88.2	30	3	US-09-861-847-1	Sequence 1, Appli	245	30	88.2	40	5	US-10-728-246-4	Sequence 4, Appli
173	30	88.2	30	4	US-10-301-488A-1	Sequence 1, Appli	246	30	88.2	40	5	US-10-772-230-3	Sequence 3, Appli

247 30 88.2 40 5 US-10-933-206-36 Sequence 36, Appl  
248 30 88.2 40 5 US-10-825-358-2 Sequence 2, Appl1  
249 30 88.2 40 5 US-10-775-562-2 Sequence 2, Appl1  
250 30 88.2 40 5 US-10-296-168-1 Sequence 1, Appl1  
251 30 88.2 40 6 US-11-004-053-36 Sequence 36, Appl  
252 30 88.2 40 6 US-11-007-643-36 Sequence 36, Appl  
253 30 88.2 40 6 US-11-007-644-36 Sequence 36, Appl  
254 30 88.2 40 6 US-11-007-669-36 Sequence 36, Appl  
255 30 88.2 40 6 US-11-066-697-956 Sequence 956, App  
256 30 88.2 40 6 US-11-066-697-962 Sequence 962, App  
257 30 88.2 40 6 US-11-066-697-968 Sequence 968, App  
258 30 88.2 40 6 US-11-066-697-978 Sequence 978, App  
259 30 88.2 40 6 US-11-066-697-989 Sequence 989, App  
260 30 88.2 40 6 US-11-066-697-995 Sequence 995, App  
261 30 88.2 40 6 US-11-066-697-1005 Sequence 1005, App  
262 30 88.2 41 4 US-10-051-496-3 Sequence 3, Appl1  
263 30 88.2 41 4 US-10-190-548A-3 Sequence 3, Appl1  
264 30 88.2 41 4 US-10-683-815-13 Sequence 13, Appl  
265 30 88.2 42 2 US-08-922-930-2 Sequence 2, Appl1  
266 30 88.2 42 2 US-08-923-055-2 Sequence 2, Appl1  
267 30 88.2 42 3 US-09-867-847-1 Sequence 1, Appl1  
268 30 88.2 42 3 US-09-956-625-26 Sequence 26, Appl  
269 30 88.2 42 3 US-09-731-460-1 Sequence 1, Appl1  
270 30 88.2 42 3 US-09-899-815-1 Sequence 1, Appl1  
271 30 88.2 42 3 US-09-962-555C-37 Sequence 37, Appl  
272 30 88.2 42 3 US-09-848-616-174 Sequence 174, App  
273 30 88.2 42 3 US-09-865-294-65 Sequence 65, Appl  
274 30 88.2 42 3 US-09-792-079-13 Sequence 13, Appl  
275 30 88.2 42 3 US-09-825-242-1 Sequence 1, Appl1  
276 30 88.2 42 3 US-09-930-915A-293 Sequence 233, App  
277 30 88.2 42 4 US-10-051-496-2 Sequence 2, Appl1  
278 30 88.2 42 4 US-10-082-804-7 Sequence 7, Appl1  
279 30 88.2 42 4 US-10-217-584-2 Sequence 2, Appl1  
280 30 88.2 42 4 US-10-217-584-8 Sequence 8, Appl1  
281 30 88.2 42 4 US-10-217-584-9 Sequence 9, Appl1  
282 30 88.2 42 4 US-10-217-584-10 Sequence 10, Appl  
283 30 88.2 42 4 US-10-217-584-11 Sequence 11, Appl  
284 30 88.2 42 4 US-10-169-580-2 Sequence 2, Appl1  
285 30 88.2 42 4 US-10-278-181-1 Sequence 1, Appl1  
286 30 88.2 42 4 US-10-143-534-2 Sequence 2, Appl1  
287 30 88.2 42 4 US-10-190-548A-1 Sequence 1, Appl1  
288 30 88.2 42 4 US-10-051-663-2 Sequence 2, Appl1  
289 30 88.2 42 4 US-10-159-279-13 Sequence 13, Appl  
290 30 88.2 42 4 US-10-318-302-4 Sequence 4, Appl1  
291 30 88.2 42 4 US-10-050-902-220 Sequence 220, App  
292 30 88.2 42 4 US-10-050-898-220 Sequence 81, Appl  
293 30 88.2 42 4 US-10-082-014-81 Sequence 81, Appl  
294 30 88.2 42 4 US-10-372-076-82 Sequence 2, Appl1  
295 30 88.2 42 4 US-10-455-218-2 Sequence 2, Appl1  
296 30 88.2 42 4 US-10-231-298B-15 Sequence 15, Appl  
297 30 88.2 42 4 US-10-231-470C-15 Sequence 15, Appl  
298 30 88.2 42 4 US-10-231-063C-15 Sequence 15, Appl  
299 30 88.2 42 4 US-10-366-125-28 Sequence 28, Appl  
300 30 88.2 42 4 US-10-411-544-2 Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-09-867-847-12  
; Sequence 12, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-09-867-847-12

Query Match 100.0%; Score 34; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
Db 1 KKLVPFA 7

## RESULT 2

US-09-915-092-2  
; Sequence 2, Application US/09915092  
; Publication No. US20020115717A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: NBI-139  
; CURRENT APPLICATION NUMBER: US/09/915,092  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220,808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-092-2

Query Match 100.0%; Score 34; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
Db 1 KKLVPFA 7

## RESULT 3

US-09-747-408-2  
; Sequence 2, Application US/09747408  
; Publication No. US20030003141A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-408-2

Query Match 100.0%; Score 34; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
|||  
Db 1 KKLVEFA 7

## RESULT 4

US-10-728-028-2  
; Sequence 2, Application US/10728028  
; Publication No. US20050048000A1  
; GENERAL INFORMATION:  
; APPLICANT: GERVAIS, Francine  
; APPLICANT: KONG, Xiangi  
; APPLICANT: CHALIFOUR, Robert  
; APPLICANT: MIGNEAULT, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; FILE REFERENCE: NBI-139CP  
; CURRENT APPLICATION NUMBER: US/10/728,028  
; PRIOR FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: 60/443291  
; PRIOR FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: 09/915092  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-728-028-2

Query Match 100.0%; Score 34; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
|||  
Db 1 KKLVEFA 7

## RESULT 5

US-10-825-958-10  
; Sequence 10, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-10-825-958-10

Query Match 100.0%; Score 34; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
|||  
Db 1 KKLVEFA 7

## RESULT 6

US-10-235-483-64  
; Sequence 64, Application US/10235483  
; Publication No. US20030087407A1  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIK  
; DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/235,483  
; FILING DATE: 06-Sep-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:  
US-10-235-483-64

Query Match 100.0%; Score 34; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;

QY 1 KKLVPFA 7  
|||  
Db 1 KKLVPFA 7

RESULT 7  
US-10-437-963-109646  
; Sequence 109646, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 109646  
; LENGTH: 1640  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_13784C.1.pep  
US-10-437-963-109646

Query Match 91.2%; Score 31; DB 4; Length 1640;  
Best Local Similarity 85.7%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 0;

QY 1 KKLVPFA 7  
|||  
Db 1595 KKVFFA 1601

RESULT 8  
US-09-972-475-7  
; Sequence 7, Application US/09972475  
; Patent No. US20020098173A1  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/972,475  
; FILING DATE: 04-Oct-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/617,267  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: USSN 08/548,998

FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-972-475-7

Query Match 88.2%; Score 30; DB 3; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 0;

QY 1 KKLVPFA 7  
:|  
Db 1 QKLVPFA 7

RESULT 9  
US-10-463-729-7  
; Sequence 7, Application US/10463729  
; Publication No. US20040005307A1  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/463,729  
; FILING DATE: 17-JUNE-2003  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/617,267C  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

```
/ MOLECULE TYPE: peptide
US-10-463-729-7

Query Match      88.2%; Score 30; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
Db 1 QKLVFFA 7

RESULT 10
US-10-810-881A-128
; Sequence 128, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Mercken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLROID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS021 NP
; CURRENT APPLICATION NUMBER: US/10/810,881A
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PEPTIDE
US-10-810-881A-128

Query Match      88.2%; Score 30; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
Db 1 QKLVFFA 7

RESULT 11
US-09-972-475-5
; Sequence 5, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
```

; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-10-463-729-5

Query Match 88.2%; Score 30; DB 4; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
Db 2 QKLVPFA 8

## RESULT 13

US-09-867-847-9  
; Sequence 9, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Artificial Sequence  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
US-09-867-847-9

Query Match 88.2%; Score 30; DB 3; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
Db 3 QKLVPFA 9

## RESULT 14

US-09-747-408-20  
; Sequence 20, Application US/09747408  
; Publication No. US20030003141A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 9

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-408-20

Query Match 88.2%; Score 30; DB 3; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
Db 3 QKLVPFA 9

## RESULT 15

US-10-235-483-54  
; Sequence 54, Application US/10235483  
; Publication No. US20030087407A1  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASE  
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LI  
; DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/10/235,483  
; FILING DATE: 06-Sep-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:  
US-10-235-483-54

Query Match 88.2%; Score 30; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6  
Db 1 KKLVPF 6

RESULT 16  
US-10-619-454-28  
; Sequence 28, Application US/10619454  
; Publication No. US20040091945A1  
; GENERAL INFORMATION:  
; APPLICANT: Mindset  
; APPLICANT: Pitzer Attas, Cheryl  
; APPLICANT: Chain, Daniel  
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A  
; FILE REFERENCE: P-5202-US  
; CURRENT APPLICATION NUMBER: US/10/619,454  
; PRIOR FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: US 60/396,245  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 187  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: algorithm generated  
US-10-619-454-28

Query Match 88.2%; Score 30; DB 4; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPFA 7  
Db 3 QKLVPFA 9

RESULT 17  
US-09-867-847-29  
; Sequence 29, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangli  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-09-867-847-29

Query Match 88.2%; Score 30; DB 3; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPFA 7  
Db 3 QKLVPFA 9

RESULT 18  
US-09-915-092-19  
; Sequence 19, Application US/09915092  
; Publication No. US20020115717A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xiangli  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; FILE REFERENCE: NBI-139  
; CURRENT APPLICATION NUMBER: US/09/915,092  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220,808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-092-19

Query Match 88.2%; Score 30; DB 3; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPFA 7  
Db 3 QKLVPFA 9

RESULT 19  
US-10-889-999-20  
; Sequence 20, Application US/10889999  
; Publication No. US20040247590A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/889,999  
; CURRENT FILING DATE: 2004-07-13  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: 10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-889-999-20

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVPFA 7  
Db 4 QKLVPFA 10

RESULT 20  
US-10-889-999-21

; Sequence 21, Application US/10889999  
; Publication No. US20040247590A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/889,999  
; CURRENT FILING DATE: 2004-07-13  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-889-999-21

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQLVFFA 7  
:|||||  
Db 3 QKLVFFA 9

## RESULT 21

US-10-889-999-22  
; Sequence 22, Application US/10889999  
; Publication No. US20040247590A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/889,999  
; CURRENT FILING DATE: 2004-07-13  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-889-999-22

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQLVFFA 7  
:|||||  
Db 2 QKLVFFA 8

## RESULT 22

US-10-889-999-23  
; Sequence 23, Application US/10889999  
; Publication No. US20040247590A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/889,999  
; CURRENT FILING DATE: 2004-07-13  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-889-999-23

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQLVFFA 7  
:|||||  
Db 1 QKLVFFA 7

## RESULT 23

US-10-890-070-20  
; Sequence 20, Application US/108900070  
; Publication No. US20040247591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,070  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-070-20

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQLVFFA 7  
:|||||  
Db 4 QKLVFFA 10



RESULT 24  
US-10-890-070-21  
; Sequence 21, Application US/108900070  
; Publication No. US20040247591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,070  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-070-21

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 3 QKLVPFA 9

RESULT 25  
US-10-890-070-22  
; Sequence 22, Application US/108900070  
; Publication No. US20040247591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,070  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-070-22

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 2 QKLVPFA 8

RESULT 26  
US-10-890-070-23  
; Sequence 23, Application US/108900070  
; Publication No. US20040247591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,070  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-070-23

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 1 QKLVPFA 7

RESULT 27  
US-10-890-000-20  
; Sequence 20, Application US/108900000  
; Publication No. US20040265301A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,000  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-000-20

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 4 QKLVPFA 10

RESULT 28  
US-10-890-000-21  
; Sequence 21, Application US/10890000  
; Publication No. US20040265301A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,000  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-000-21

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7  
:|||||  
Db 3 QKLVFPA 9

RESULT 29  
US-10-890-000-22  
; Sequence 22, Application US/10890000  
; Publication No. US20040265301A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,000  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-000-22

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7  
:|||||

Db 2 QKLVFPA 8  
RESULT 30  
US-10-890-000-23  
; Sequence 23, Application US/10890000  
; Publication No. US20040265301A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,000  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-000-23

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7  
:|||||  
Db 1 QKLVFPA 7

RESULT 31  
US-10-823-463-20  
; Sequence 20, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-20

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
:|||||  
Db 4 QKLVEFA 10

## RESULT 32

US-10-823-463-21  
; Sequence 21, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-21

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
:|||||  
Db 3 QKLVEFA 9

## RESULT 33

US-10-823-463-22  
; Sequence 22, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015

; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-22

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
:|||||  
Db 2 QKLVEFA 8

## RESULT 34

US-10-823-463-23  
; Sequence 23, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-23

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFA 7  
Db 1 QKLVEFA 7

## RESULT 35

US-10-728-028-19

; Sequence 19, Application US/10728028  
; Publication No. US20050048000A1  
; GENERAL INFORMATION:  
; APPLICANT: GERVAIS, Francine  
; APPLICANT: KONG, Xianqi  
; APPLICANT: CHALIFOUR, Robert  
; APPLICANT: MIGNEAULT, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; FILE REFERENCE: NBI-139CP  
; CURRENT APPLICATION NUMBER: US/10728,028  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: 60/443291  
; PRIOR FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: 09/915092  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-728-028-19

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFA 7  
Db 3 QKLVEFA 9

## RESULT 36

US-10-822-968-20

; Sequence 20, Application US/10822968  
; Publication No. US20050059591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/822,968  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-822-968-20

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFA 7  
Db 4 QKLVEFA 10

## RESULT 37

US-10-822-968-21

; Sequence 21, Application US/10822968  
; Publication No. US20050059591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/822,968  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-822-968-21

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFA 7  
Db 3 QKLVEFA 9

## RESULT 38

US-10-822-968-22

; Sequence 22, Application US/10822968  
; Publication No. US20050059591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
US-10-822-968-22

```
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-22

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
        :|||||
Db      2 QKLVPFA 8

RESULT 39
US-10-822-968-23
; Sequence 23, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-23
```

```
Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
        :|||||
Db      1 QKLVPFA 7

RESULT 40
US-10-777-792-20
; Sequence 20, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-777-792-20

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
        :|||||
Db      4 QKLVPFA 10

RESULT 41
US-10-777-792-21
; Sequence 21, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-777-792-21
```

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 3 QKLVPFA 9

## RESULT 42

US-10-777-792-22  
; Sequence 22, Application US/10777792  
; Publication No. US20050059802A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/777,792  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-777-792-22

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 2 QKLVPFA 8

## RESULT 43

US-10-777-792-23  
; Sequence 23, Application US/10777792  
; Publication No. US20050059802A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/777,792  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)

## US-10-777-792-23

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 1 QKLVPFA 7

## RESULT 44

US-10-825-958-27  
; Sequence 27, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-10-825-958-27

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 3 QKLVPFA 9

## RESULT 45

US-10-890-071-20  
; Sequence 20, Application US/10890071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-20

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
Db 4 QKLVEFA 10

## RESULT 46

US-10-890-071-21  
; Sequence 21, Application US/10890071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-21

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
Db 3 QKLVEFA 9

## RESULT 47

US-10-890-071-22  
; Sequence 22, Application US/10890071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-22

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
Db 2 QKLVEFA 8

## RESULT 48

US-10-890-071-23  
; Sequence 23, Application US/10890071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-23

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
Db 1 QKLVEFA 7

## RESULT 49

US-10-890-024-20  
; Sequence 20, Application US/10890024  
; Publication No. US20050158304A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,024  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-024-20

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 4 QKLVPFA 10

## RESULT 50

US-10-890-024-21  
; Sequence 21, Application US/10890024  
; Publication No. US20050158304A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,024  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-024-21

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 3 QKLVPFA 9

## RESULT 51

US-10-890-024-22  
; Sequence 22, Application US/10890024  
; Publication No. US20050158304A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,024  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-024-22

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 2 QKLVPFA 8

## RESULT 52

US-10-890-024-23  
; Sequence 23, Application US/10890024  
; Publication No. US20050158304A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,024  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-024-23

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 1 QKLVPFA 7

## RESULT 53

US-10-928-926-20  
; Sequence 20, Application US/10928926  
; Publication No. US20050196399A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/928,926  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US/09/724,961  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430



; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-928-926-20

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
DB 4 QKLVEFA 10

RESULT 54

US-10-928-926-21  
; Sequence 21, Application US/10928926

; Publication No. US20050196399A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vasquez, Nicki

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004750UC

; CURRENT APPLICATION NUMBER: US/10/928,926

; CURRENT FILING DATE: 2004-08-27

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/580,015

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07

; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 21

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)  
US-10-928-926-21

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
DB 4 QKLVEFA 10

Db 3 QKLVEFA 9

RESULT 55

US-10-928-926-22

; Sequence 22, Application US/10928926

; Publication No. US20050196399A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vasquez, Nicki

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004750UC

; CURRENT APPLICATION NUMBER: US/10/928,926

; CURRENT FILING DATE: 2004-08-27

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/580,015

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07

; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 22

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)  
US-10-928-926-22

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
DB 2 QKLVEFA 8

RESULT 56

US-10-928-926-23

; Sequence 23, Application US/10928926

; Publication No. US20050196399A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vasquez, Nicki

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004750UC

; CURRENT APPLICATION NUMBER: US/10/928,926

; CURRENT FILING DATE: 2004-08-27

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/580,015

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-928-926-23

Query Match 88.2%; Score 30; DB 5; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7  
:|||||  
Db 1 QKLVFPA 7

RESULT 57  
US-11-058-757-20  
; Sequence 20, Application US/11058757  
; Publication No. US20050142132A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-004760US  
; CURRENT APPLICATION NUMBER: US/11/058,757  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-11-058-757-20

Query Match 88.2%; Score 30; DB 6; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7  
:|||||  
Db 4 QKLVFPA 10

RESULT 58  
US-11-058-757-21  
; Sequence 21, Application US/11058757  
; Publication No. US20050142132A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152700-004760US

; CURRENT APPLICATION NUMBER: US/11/058,757  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-11-058-757-21

Query Match 88.2%; Score 30; DB 6; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7  
:|||||  
Db 3 QKLVFPA 9

RESULT 59  
US-11-058-757-22  
; Sequence 22, Application US/11058757  
; Publication No. US20050142132A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-004760US  
; CURRENT APPLICATION NUMBER: US/11/058,757  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-11-058-757-22

Query Match 88.2%; Score 30; DB 6; Length 10;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7  
:|||||  
Db 2 QKLVFPA 8

RESULT 60  
US-11-058-757-23  
; Sequence 23, Application US/11058757  
; Publication No. US20050142132A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152700-004760US

```
/ FILE REFERENCE: 15270J-004760US
/ CURRENT APPLICATION NUMBER: US/11/058,757
/ CURRENT FILING DATE: 2005-02-14
/ PRIOR APPLICATION NUMBER: US/09/580,018
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US/09/322,289
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
/ OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
/ OTHER INFORMATION: peptide)
US-11-058-757-23

Query Match      88.2%; Score 30; DB 6; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 61
US-09-988-842-9
/ Sequence 9, Application US/09988842
/ Patent No. US20020143105A1
/ GENERAL INFORMATION:
/ APPLICANT: Johansson, Jan
/ TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
/ TITLE OF INVENTION: OF AMYLOID FORMATION
/ FILE REFERENCE: 12125-002001
/ CURRENT APPLICATION NUMBER: US/09/988,842
/ CURRENT FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: US/60/251,662
/ PRIOR FILING DATE: 2000-12-06
/ PRIOR APPLICATION NUMBER: US/60/253,695
/ PRIOR FILING DATE: 2000-11-20
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match      88.2%; Score 30; DB 3; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 62
US-09-988-842-25
/ Sequence 25, Application US/09988842
/ Patent No. US20020143105A1
/ GENERAL INFORMATION:
/ APPLICANT: Johansson, Jan
/ TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
/ TITLE OF INVENTION: OF AMYLOID FORMATION
/ FILE REFERENCE: 12125-002001
/ CURRENT APPLICATION NUMBER: US/09/988,842
/ CURRENT FILING DATE: 2001-11-19
```

```
/ PRIOR APPLICATION NUMBER: US/60/251,662
/ PRIOR FILING DATE: 2000-12-06
/ PRIOR APPLICATION NUMBER: US/60/253,695
/ PRIOR FILING DATE: 2000-11-20
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match      88.2%; Score 30; DB 3; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 63
US-10-235-483-14
/ Sequence 14, Application US/10235483
/ Publication No. US20030087407A1
/ GENERAL INFORMATION:
/ APPLICANT: SOTO-JARA, Claudio
/ BAUMANN, Marc
/ FRANGIONE, Blas
/ TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
/ COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
/ ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIK
/ DEPOSITS
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 400
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/235,483
/ FILING DATE: 06-Sep-2002
/ CLASSIFICATION: <unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/766,596
/ FILING DATE: <unknown>
/ APPLICATION NUMBER: US/08/630,645
/ FILING DATE: 10-APR-1996
/ APPLICATION NUMBER: US/08/478,326
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: YUN, Allen C.
/ REGISTRATION NUMBER: 37,971
/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
```

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-235-483-14

Query Match 88.2%; Score 30; DB 4; Length 11;  
Best Local Similarity 85.7%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 1 QKLVPFA 7

RESULT 64

US-10-050-200-33  
; Sequence 33, Application US/10050200  
; Publication No. US20030166037A1  
; GENERAL INFORMATION:  
; APPLICANT: Fourie, Anne  
; APPLICANT: Coles, Fawn  
; APPLICANT: Karlsson, Lars  
; TITLE OF INVENTION: Aggrrecanase-1 and -2 Peptide Substrates and Methods  
; FILE REFERENCE: ORT-1417  
; CURRENT APPLICATION NUMBER: US/10/050,200  
; CURRENT FILING DATE: 2002-01-16  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 33  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide substrate  
; US-10-050-200-33

Query Match 88.2%; Score 30; DB 4; Length 11;  
Best Local Similarity 85.7%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 5 QKLVPFA 11

RESULT 65

US-10-464-117-13  
; Sequence 13, Application US/10464117  
; Publication No. US20050014193A1  
; GENERAL INFORMATION:  
; APPLICANT: Palatin Technologies, Inc.  
; APPLICANT: Sharma, Shubh D.  
; APPLICANT: Shi, Yi-Qun  
; TITLE OF INVENTION: Identification of Target-Specific Folding Sites in Peptides and  
; FILE REFERENCE: 70025-UT-50075  
; CURRENT APPLICATION NUMBER: US/10/464,117  
; CURRENT FILING DATE: 2003-06-17  
; PRIOR APPLICATION NUMBER: PCT/US01/50075  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: US 60/256,842  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 60/304,835  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: US 60/327,835  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 171  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 13  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amyloid beta-protein related peptide  
; US-10-464-117-13

Query Match 88.2%; Score 30; DB 5; Length 11;  
Best Local Similarity 85.7%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 2 EKLVPFA 8

RESULT 66

US-10-772-230-9  
; Sequence 9, Application US/10772230  
; Publication No. US20050059084A1  
; GENERAL INFORMATION:  
; APPLICANT: Johansson, Jan  
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION  
; FILE REFERENCE: 12125-002001  
; CURRENT APPLICATION NUMBER: US/10/772,230  
; CURRENT FILING DATE: 2004-02-04  
; PRIOR APPLICATION NUMBER: US/09/988,842  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: US 60/251,662  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 60/253,695  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
; US-10-772-230-9

Query Match 88.2%; Score 30; DB 5; Length 11;  
Best Local Similarity 85.7%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 1 QKLVPFA 7

RESULT 67

US-10-772-230-25  
; Sequence 25, Application US/10772230  
; Publication No. US20050059084A1  
; GENERAL INFORMATION:  
; APPLICANT: Johansson, Jan  
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION  
; FILE REFERENCE: 12125-002001  
; CURRENT APPLICATION NUMBER: US/10/772,230  
; CURRENT FILING DATE: 2004-02-04  
; PRIOR APPLICATION NUMBER: US/09/988,842  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: US 60/251,662  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 60/253,695  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
; US-10-772-230-25

```
Query Match      88.2%; Score 30; DB 5; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 68
US-09-867-847-8
; Sequence 8, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangdi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-8

Query Match      88.2%; Score 30; DB 3; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 69
US-10-810-881A-115
; Sequence 115, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Mercken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5021 NP
; CURRENT APPLICATION NUMBER: US/10/810,881A
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PEPTIDE

Query Match      88.2%; Score 30; DB 5; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 68
US-09-867-847-8
; Sequence 8, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangdi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-8

Query Match      88.2%; Score 30; DB 3; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 69
US-10-810-881A-115
; Sequence 115, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Mercken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5021 NP
; CURRENT APPLICATION NUMBER: US/10/810,881A
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PEPTIDE

Query Match      88.2%; Score 30; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 70
US-10-508-586-2
; Sequence 2, Application US/10508586
; Publication No. US20050164361A1
; GENERAL INFORMATION:
; APPLICANT: EMORY UNIVERSITY
; TITLE OF INVENTION: SELF-ASSEMBLING-PEPTIDE-BASED STRUCTURES AND PROCESSES FOR
; FILE REFERENCE: 050508-2230
; CURRENT APPLICATION NUMBER: US/10/508,586
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-508-586-2

Query Match      88.2%; Score 30; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 71
US-10-508-586-3
; Sequence 3, Application US/10508586
; Publication No. US20050164361A1
; GENERAL INFORMATION:
; APPLICANT: EMORY UNIVERSITY
; TITLE OF INVENTION: SELF-ASSEMBLING-PEPTIDE-BASED STRUCTURES AND PROCESSES FOR
; FILE REFERENCE: 050508-2230
; CURRENT APPLICATION NUMBER: US/10/508,586
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-508-586-3

Query Match      88.2%; Score 30; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 72
US-10-625-854-139
; Sequence 139, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
```

```
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 12
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-139
```

```
Query Match      88.2%; Score 30; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVPFA 7
Db      6 QKLVPFA 12
```

## RESULT 73

```
US-11-012-797A-33
; Sequence 33, Application US/11012797A
; Publication No. US20050164319A1
; GENERAL INFORMATION:
; APPLICANT: FOURIE, ANNE M.
; APPLICANT: KARLSSON, LARS
; APPLICANT: COLES, EAWN
; TITLE OF INVENTION: AGGREGINASE-1 AND -2 PEPTIDE SUBSTRATES AND METHODS
; FILE REFERENCE: ORT-1417-USCWT1
; CURRENT APPLICATION NUMBER: US/11/012,797A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 10/050,200
; PRIOR FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 3.3
; SEQ ID NO 33
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: Aedans-Glu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Dabcyl-Lys
US-11-012-797A-33
```

```
Query Match      88.2%; Score 30; DB 6; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVPFA 7
Db      5 QKLVPFA 11
```

## RESULT 74

```
US-10-281-458-1
; Sequence 1, Application US/10281458
; Publication No. US20030108978A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Ciambrone, Gary J.
; APPLICANT: Gibbons, Ian
; TITLE OF INVENTION: Whole Cell Assay Systems for Cell
; TITLE OF INVENTION: Surface Proteases
; FILE REFERENCE: 50225-8093 US03
; CURRENT APPLICATION NUMBER: US/10/281,458
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/337,641
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/924,692
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-458-1
```

```
Query Match      88.2%; Score 30; DB 4; Length 13;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVPFA 7
Db      5 QKLVPFA 11
```

## RESULT 75

```
US-10-625-854-127
; Sequence 127, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-127
```

```
Query Match      88.2%; Score 30; DB 5; Length 13;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVPFA 7
Db      7 QKLVPFA 13
```

```
Search completed: December 29, 2005, 18:49:35
Job time : 79.3387 secs
```

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 23.371 Seconds  
(without alignments)  
24.763 Million cell updates/sec

Title: US-10-009-122-2

Perfect score: 34

Sequence: 1 KKLFFFA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/pCTUS COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	2	US-09-747-408-2
2	34	100.0	9	2	US-08-766-596A-64
3	34	100.0	34	1	US-08-475-579A-4
4	30	88.2	6	2	US-09-242-724-33
5	30	88.2	7	1	US-08-612-785B-7
6	30	88.2	7	2	US-08-703-675C-30
7	30	88.2	7	2	US-08-617-267C-7
8	30	88.2	8	1	US-08-612-785B-5
9	30	88.2	8	2	US-08-703-675C-28
10	30	88.2	8	2	US-08-617-267C-5
11	30	88.2	9	2	US-08-766-596A-54
12	30	88.2	9	2	US-09-747-408-20
13	30	88.2	10	2	US-09-724-961-21
14	30	88.2	10	2	US-09-724-961-22
15	30	88.2	10	2	US-09-724-961-23
16	30	88.2	10	2	US-09-724-961-24
17	30	88.2	10	2	US-09-580-018-20
18	30	88.2	10	2	US-09-580-018-21
19	30	88.2	10	2	US-09-580-018-22
20	30	88.2	10	2	US-09-580-018-23
21	30	88.2	10	2	US-09-724-551-20
22	30	88.2	10	2	US-09-724-551-21
23	30	88.2	10	2	US-09-724-551-22
24	30	88.2	10	2	US-09-724-551-23
25	30	88.2	10	2	US-09-724-940-20
26	30	88.2	10	2	US-09-724-940-21
27	30	88.2	10	2	US-09-724-940-22

28	88.2	10	2	US-09-724-940-23	Sequence 23, Appl
29	88.2	11	1	US-08-630-645-14	Sequence 14, Appl
30	88.2	11	2	US-08-766-596A-14	Sequence 14, Appl
31	88.2	11	2	US-09-988-842-9	Sequence 9, Appl
32	88.2	11	2	US-09-988-842-25	Sequence 25, Appl
33	88.2	11	4	PCT-US96-10220-14	Sequence 14, Appl
34	88.2	14	2	US-09-594-366-5	Sequence 5, Appl
35	88.2	14	2	US-09-592-800-5	Sequence 5, Appl
36	88.2	15	1	US-08-612-785B-37	Sequence 37, Appl
37	88.2	15	2	US-08-766-596A-56	Sequence 56, Appl
38	88.2	15	2	US-08-766-596A-57	Sequence 57, Appl
39	88.2	15	2	US-08-766-596A-60	Sequence 60, Appl
40	88.2	15	2	US-08-766-596A-61	Sequence 61, Appl
41	88.2	15	2	US-08-766-596A-63	Sequence 63, Appl
42	88.2	15	2	US-08-766-596A-65	Sequence 65, Appl
43	88.2	17	2	US-09-264-709A-2	Sequence 2, Appl
44	88.2	17	2	US-09-594-366-3	Sequence 3, Appl
45	88.2	17	2	US-09-623-548A-950	Sequence 950, App
46	88.2	17	2	US-09-623-548A-983	Sequence 983, App
47	88.2	17	2	US-09-592-800-3	Sequence 3, Appl
48	88.2	17	2	US-09-657-276-950	Sequence 950, App
49	88.2	17	2	US-09-657-276-983	Sequence 983, App
50	88.2	19	2	US-08-970-833-11	Sequence 11, Appl
51	88.2	19	2	US-09-723-384-5	Sequence 5, Appl
52	88.2	19	2	US-09-724-961-75	Sequence 75, Appl
53	88.2	19	2	US-09-724-552-5	Sequence 5, Appl
54	88.2	19	2	US-09-580-018-75	Sequence 75, Appl
55	88.2	19	2	US-09-723-927-5	Sequence 5, Appl
56	88.2	19	2	US-09-724-489-5	Sequence 5, Appl
57	88.2	19	2	US-09-724-477-5	Sequence 5, Appl
58	88.2	19	2	US-09-723-762-5	Sequence 5, Appl
59	88.2	19	2	US-09-201-430-5	Sequence 5, Appl
60	88.2	19	2	US-09-724-551-75	Sequence 75, Appl
61	88.2	19	2	US-10-815-353-5	Sequence 5, Appl
62	88.2	19	2	US-10-816-529-5	Sequence 5, Appl
63	88.2	19	2	US-10-815-391-5	Sequence 5, Appl
64	88.2	19	2	US-10-816-022-5	Sequence 5, Appl
65	88.2	19	2	US-09-724-940-75	Sequence 75, Appl
66	88.2	19	2	US-10-934-609-5	Sequence 5, Appl
67	88.2	19	2	US-10-884-892-5	Sequence 5, Appl
68	88.2	20	2	US-08-970-833-10	Sequence 10, Appl
69	88.2	20	2	US-09-724-953-33	Sequence 33, Appl
70	88.2	20	2	US-09-724-567-33	Sequence 33, Appl
71	88.2	20	2	US-09-979-352-33	Sequence 33, Appl
72	88.2	20	2	US-09-585-817-33	Sequence 33, Appl
73	88.2	26	1	US-08-304-585-7	Sequence 7, Appl
74	88.2	28	1	US-08-346-849-4	Sequence 4, Appl
75	88.2	28	1	US-08-302-808-7	Sequence 7, Appl
76	88.2	28	1	US-08-609-090-2	Sequence 2, Appl
77	88.2	28	1	US-08-986-948-7	Sequence 7, Appl
78	88.2	28	1	US-08-293-284A-4	Sequence 4, Appl
79	88.2	28	1	US-08-461-216-2	Sequence 2, Appl
80	88.2	28	2	US-09-388-890-2	Sequence 2, Appl
81	88.2	28	2	US-09-388-890-3	Sequence 3, Appl
82	88.2	28	2	US-09-388-890-4	Sequence 4, Appl
83	88.2	28	2	US-09-388-890-5	Sequence 5, Appl
84	88.2	28	2	US-09-388-890-6	Sequence 6, Appl
85	88.2	28	2	US-09-388-890-7	Sequence 7, Appl
86	88.2	28	2	US-09-388-890-8	Sequence 8, Appl
87	88.2	28	2	US-09-388-890-9	Sequence 9, Appl
88	88.2	28	2	US-09-388-890-10	Sequence 10, Appl
89	88.2	28	2	US-09-388-890-12	Sequence 12, Appl
90	88.2	28	2	US-09-388-890-13	Sequence 13, Appl
91	88.2	28	2	US-09-388-890-14	Sequence 14, Appl
92	88.2	28	2	US-09-264-709A-1	Sequence 1, Appl
93	88.2	28	2	US-08-723-661B-2	Sequence 2, Appl
94	88.2	28	2	US-09-660-954-2	Sequence 2, Appl
95	88.2	28	2	US-09-660-954-3	Sequence 3, Appl
96	88.2	28	2	US-09-660-954-4	Sequence 4, Appl
97	88.2	28	2	US-09-660-954-5	Sequence 5, Appl
98	88.2	28	2	US-09-660-954-6	Sequence 6, Appl
99	88.2	28	2	US-09-660-954-7	Sequence 7, Appl
100	88.2	28	2	US-09-660-954-8	Sequence 8, Appl



101	30	88.2	28	2	US-09-660-954-9	Sequence 9, Appli	174	30	88.2	40	2	US-09-623-548A-995	Sequence 995, App
102	30	88.2	28	2	US-09-660-954-10	Sequence 10, Appli	175	30	88.2	40	2	US-09-623-548A-1005	Sequence 1005, Ap
103	30	88.2	28	2	US-09-660-954-12	Sequence 12, Appl	176	30	88.2	40	2	US-09-657-276-956	Sequence 956, App
104	30	88.2	28	2	US-09-660-954-13	Sequence 13, Appl	177	30	88.2	40	2	US-09-657-276-962	Sequence 962, App
105	30	88.2	28	2	US-09-660-954-14	Sequence 14, Appl	178	30	88.2	40	2	US-09-657-276-968	Sequence 968, App
106	30	88.2	28	2	US-08-898-300-4	Sequence 4, Appli	179	30	88.2	40	2	US-09-657-276-978	Sequence 978, App
107	30	88.2	28	2	US-08-824-513-4	Sequence 4, Appli	180	30	88.2	40	2	US-09-657-276-989	Sequence 989, App
108	30	88.2	28	2	US-09-623-548A-959	Sequence 959, App	181	30	88.2	40	2	US-09-657-276-995	Sequence 995, App
109	30	88.2	28	2	US-09-623-548A-965	Sequence 965, App	182	30	88.2	40	2	US-09-657-276-1005	Sequence 1005, Ap
110	30	88.2	28	2	US-09-623-548A-976	Sequence 976, App	183	30	88.2	40	2	US-09-962-955D-36	Sequence 36, Appl
111	30	88.2	28	2	US-09-623-548A-992	Sequence 992, App	184	30	88.2	40	4	PCT-US92-06700-1	Sequence 1, Appli
112	30	88.2	28	2	US-09-623-548A-1003	Sequence 1003, Ap	185	30	88.2	41	1	US-07-819-361-1	Sequence 1, Appli
113	30	88.2	28	2	US-09-657-276-959	Sequence 959, App	186	30	88.2	41	1	US-08-302-808-4	Sequence 4, Appli
114	30	88.2	28	2	US-09-657-276-965	Sequence 965, App	187	30	88.2	41	1	US-08-682-245A-3	Sequence 3, Appli
115	30	88.2	28	2	US-09-657-276-976	Sequence 976, App	188	30	88.2	41	1	US-08-986-948-4	Sequence 4, Appli
116	30	88.2	28	2	US-09-657-276-992	Sequence 992, App	189	30	88.2	42	1	US-07-744-767A-2	Sequence 2, Appli
117	30	88.2	28	2	US-09-657-276-1003	Sequence 1003, Ap	190	30	88.2	42	1	US-08-179-574-1	Sequence 1, Appli
118	30	88.2	28	2	US-09-865-294A-66	Sequence 66, Appl	191	30	88.2	42	1	US-08-271-162-5	Sequence 5, Appli
119	30	88.2	30	1	US-08-609-090-3	Sequence 3, Appli	192	30	88.2	42	1	US-08-347-144-1	Sequence 1, Appli
120	30	88.2	30	2	US-09-861-847A-1	Sequence 1, Appli	193	30	88.2	42	1	US-08-462-859A-19	Sequence 19, Appl
121	30	88.2	33	1	US-08-609-090-4	Sequence 4, Appli	194	30	88.2	42	1	US-08-123-659A-19	Sequence 19, Appl
122	30	88.2	35	1	US-08-304-585-6	Sequence 6, Appli	195	30	88.2	42	1	US-08-464-247A-19	Sequence 19, Appl
123	30	88.2	35	1	US-08-612-785B-16	Sequence 16, Appl	196	30	88.2	42	1	US-08-464-248A-19	Sequence 19, Appl
124	30	88.2	35	1	US-08-612-785B-36	Sequence 36, Appl	197	30	88.2	42	1	US-08-476-464A-1	Sequence 1, Appli
125	30	88.2	35	1	US-08-612-785B-38	Sequence 38, Appl	198	30	88.2	42	1	US-08-304-585-2	Sequence 2, Appli
126	30	88.2	35	1	US-08-612-785B-40	Sequence 40, Appl	199	30	88.2	42	1	US-08-302-808-5	Sequence 5, Appli
127	30	88.2	35	2	US-08-617-267C-16	Sequence 16, Appl	200	30	88.2	42	1	US-08-268-348A-1	Sequence 1, Appli
128	30	88.2	35	2	US-09-623-548A-979	Sequence 979, App	201	30	88.2	42	1	US-08-268-348A-2	Sequence 2, Appli
129	30	88.2	35	2	US-09-623-548A-1006	Sequence 1006, Ap	202	30	88.2	42	1	US-08-268-348A-3	Sequence 3, Appli
130	30	88.2	35	2	US-09-657-276-979	Sequence 979, App	203	30	88.2	42	1	US-08-268-348A-4	Sequence 4, Appli
131	30	88.2	35	2	US-09-657-276-1006	Sequence 1006, Ap	204	30	88.2	42	1	US-08-268-348A-5	Sequence 5, Appli
132	30	88.2	36	1	US-08-609-090-6	Sequence 6, Appli	205	30	88.2	42	1	US-08-268-348A-6	Sequence 6, Appli
133	30	88.2	36	2	US-09-861-847A-6	Sequence 6, Appli	206	30	88.2	42	1	US-08-433-734-2	Sequence 2, Appli
134	30	88.2	36	2	US-09-861-847A-11	Sequence 11, Appl	207	30	88.2	42	1	US-08-609-090-9	Sequence 9, Appli
135	30	88.2	38	1	US-08-302-808-1	Sequence 1, Appli	208	30	88.2	42	1	US-07-737-371E-72	Sequence 72, Appl
136	30	88.2	38	1	US-07-737-371E-68	Sequence 68, Appl	209	30	88.2	42	1	US-08-422-333-4	Sequence 4, Appli
137	30	88.2	38	1	US-08-986-948-1	Sequence 1, Appli	210	30	88.2	42	1	US-08-682-245A-4	Sequence 4, Appli
138	30	88.2	38	2	US-09-623-548A-975	Sequence 975, App	211	30	88.2	42	1	US-08-986-948-5	Sequence 5, Appli
139	30	88.2	38	2	US-09-623-548A-1002	Sequence 1002, Ap	212	30	88.2	42	2	US-08-717-551A-2	Sequence 2, Appli
140	30	88.2	38	2	US-09-657-276-975	Sequence 975, App	213	30	88.2	42	2	US-09-388-890-1	Sequence 1, Appli
141	30	88.2	38	2	US-09-657-276-1002	Sequence 1002, Ap	214	30	88.2	42	2	US-09-005-215-20	Sequence 20, Appl
142	30	88.2	39	1	US-08-304-585-5	Sequence 5, Appli	215	30	88.2	42	2	US-09-724-724-23	Sequence 23, Appl
143	30	88.2	39	1	US-08-302-808-2	Sequence 2, Appli	216	30	88.2	42	2	US-08-922-930-2	Sequence 2, Appli
144	30	88.2	39	1	US-08-609-090-7	Sequence 7, Appli	217	30	88.2	42	2	US-09-660-954-1	Sequence 1, Appli
145	30	88.2	39	1	US-08-682-245A-1	Sequence 1, Appli	218	30	88.2	42	2	US-08-923-055-2	Sequence 2, Appli
146	30	88.2	39	1	US-08-986-948-2	Sequence 2, Appli	219	30	88.2	42	2	US-08-922-889-2	Sequence 2, Appli
147	30	88.2	40	1	US-07-744-767A-1	Sequence 1, Appli	220	30	88.2	42	2	US-09-731-460-1	Sequence 1, Appli
148	30	88.2	40	1	US-08-235-400-2	Sequence 2, Appli	221	30	88.2	42	2	US-09-133-866-2	Sequence 2, Appli
149	30	88.2	40	1	US-08-476-464A-2	Sequence 2, Appli	222	30	88.2	42	2	US-09-723-384-1	Sequence 1, Appli
150	30	88.2	40	1	US-08-304-585-1	Sequence 1, Appli	223	30	88.2	42	2	US-09-724-961-42	Sequence 42, Appl
151	30	88.2	40	1	US-08-304-585-8	Sequence 8, Appli	224	30	88.2	42	2	US-09-724-552-1	Sequence 1, Appli
152	30	88.2	40	1	US-08-302-808-3	Sequence 3, Appli	225	30	88.2	42	2	US-10-455-218-2	Sequence 2, Appli
153	30	88.2	40	1	US-08-433-734-1	Sequence 1, Appli	226	30	88.2	42	2	US-09-723-927-1	Sequence 1, Appli
154	30	88.2	40	1	US-08-609-090-8	Sequence 8, Appli	227	30	88.2	42	2	US-09-724-489-1	Sequence 1, Appli
155	30	88.2	40	1	US-07-737-371E-69	Sequence 69, Appl	228	30	88.2	42	2	US-09-723-767-1	Sequence 1, Appli
156	30	88.2	40	1	US-08-682-245A-2	Sequence 2, Appli	229	30	88.2	42	2	US-09-724-477-1	Sequence 1, Appli
157	30	88.2	40	1	US-08-986-948-3	Sequence 3, Appli	230	30	88.2	42	2	US-09-723-472-1	Sequence 1, Appli
158	30	88.2	40	1	US-08-461-216-1	Sequence 1, Appli	231	30	88.2	42	2	US-09-201-430-1	Sequence 1, Appli
159	30	88.2	40	2	US-08-959-148-1	Sequence 1, Appli	232	30	88.2	42	2	US-09-724-551-42	Sequence 42, Appl
160	30	88.2	40	2	US-09-242-724-22	Sequence 22, Appl	233	30	88.2	42	2	US-10-815-353-1	Sequence 1, Appli
161	30	88.2	40	2	US-08-723-661B-1	Sequence 1, Appli	234	30	88.2	42	2	US-10-278-181-1	Sequence 1, Appli
162	30	88.2	40	2	US-09-062-365-3	Sequence 3, Appli	235	30	88.2	42	2	US-10-816-529-1	Sequence 1, Appli
163	30	88.2	40	2	US-09-133-866-1	Sequence 1, Appli	236	30	88.2	42	2	US-09-623-548A-955	Sequence 955, App
164	30	88.2	40	2	US-09-861-847A-7	Sequence 7, Appli	237	30	88.2	42	2	US-09-623-548A-961	Sequence 961, App
165	30	88.2	40	2	US-09-861-847A-8	Sequence 8, Appli	238	30	88.2	42	2	US-08-623-548A-967	Sequence 967, App
166	30	88.2	40	2	US-09-988-842-3	Sequence 3, Appli	239	30	88.2	42	2	US-09-623-548A-988	Sequence 988, App
167	30	88.2	40	2	US-10-455-218-1	Sequence 1, Appli	240	30	88.2	42	2	US-09-623-548A-994	Sequence 994, App
168	30	88.2	40	2	US-10-151-614-1	Sequence 1, Appli	241	30	88.2	42	2	US-10-815-391-1	Sequence 1, Appli
169	30	88.2	40	2	US-09-623-548A-956	Sequence 956, App	242	30	88.2	42	2	US-10-816-022-1	Sequence 1, Appli
170	30	88.2	40	2	US-09-623-548A-962	Sequence 962, App	243	30	88.2	42	2	US-09-724-953-34	Sequence 34, Appl
171	30	88.2	40	2	US-09-623-548A-968	Sequence 968, App	244	30	88.2	42	2	US-09-657-276-955	Sequence 955, App
172	30	88.2	40	2	US-09-623-548A-978	Sequence 978, App	245	30	88.2	42	2	US-09-657-276-961	Sequence 961, App
173	30	88.2	40	2	US-09-623-548A-989	Sequence 989, App	246	30	88.2	42	2	US-09-657-276-967	Sequence 967, App



```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: polypeptide
US-09-242-724-33

Query Match      88.2%; Score 30; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
Db      1 KKLVEFA 7

RESULT 3
US-08-475-579A-4
; Sequence 4, Application US/08475579A
; Patent No. 5854215
; GENERAL INFORMATION:
; APPLICANT: Mark A. Findeis et al.
; TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "Symbol")-Amyloid Peptide Aggrega
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,579A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,831
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: PPI-002CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-475-579A-4

Query Match      100.0%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
Db      9 KKLVEFA 15

RESULT 4
US-09-242-724-33
; Sequence 33, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
; APPLICANT: Solomon, Michael E.
; APPLICANT: Rich, Daniel H.
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
; FILE REFERENCE: Cyclosporin Analogs
; CURRENT APPLICATION NUMBER: US/09/242,724
; CURRENT FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT

```

```
RESULT 6
US-08-703-675C-30
; Sequence 30, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findexis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-703-675C-30

Query Match      88.2%; Score 30; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches      6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVFPA 7
Db      1 QKLVFPA 7

RESULT 7
US-08-617-267C-7
; Sequence 7, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findexis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts

Query Match      88.2%; Score 30; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches      6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVFPA 7
Db      1 QKLVFPA 7

RESULT 8
US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findexis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
```

```
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-617-267C-7

Query Match      88.2%; Score 30; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches      6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVFPA 7
Db      1 QKLVFPA 7

RESULT 8
US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findexis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
```

```
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-5

Query Match 88.2%; Score 30; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db :|||||
2 QKLVPFA 8

RESULT 9
US-08-703-675C-28
; Sequence 28, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-5

Query Match 88.2%; Score 30; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db :|||||
2 QKLVPFA 8

Aggregation Comprising D-

US-08-703-675C-28
; Sequence 28, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-5

Query Match 88.2%; Score 30; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db :|||||
2 QKLVPFA 8

RESULT 11
US-08-766-596A-54
```

```
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-703-675C-28

Query Match 88.2%; Score 30; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db :|||||
2 QKLVPFA 8

RESULT 10
US-08-617-267C-5
; Sequence 5, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-617-267C-5

Query Match 88.2%; Score 30; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db :|||||
2 QKLVPFA 8

RESULT 11
US-08-766-596A-54
```

; Sequence 54, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATIONS WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSIT  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-766-596A-54

Query Match 88.2%; Score 30; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6  
Db 1 KKLVPFF 6

RESULT 12  
US-09-747-408-20  
; Sequence 20, Application US/09747408  
; Patent No. 6670399  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-747-408-20

Query Match 88.2%; Score 30; DB 2; Length 9;  
Best Local Similarity 85.7%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 7  
Db 3 OKLVFFA 9

RESULT 13  
US-09-724-961-20  
; Sequence 20, Application US/09724961  
; Patent No. 6743427  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,961  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
; US-09-724-961-20

Query Match 88.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 7  
Db 4 OKLVFFA 10

RESULT 14  
US-09-724-961-21  
; Sequence 21, Application US/09724961  
; Patent No. 6743427  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC

```
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-21

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
      :|||||
DB      3 QKLVPFA 9

RESULT 15
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-22

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
      :|||||
DB      3 QKLVPFA 9
```

```
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
      :|||||
DB      2 QKLVPFA 8

RESULT 16
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-23

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
      :|||||
DB      1 QKLVPFA 7

RESULT 17
US-09-580-018-20
; Sequence 20, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
```

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-20

Query Match 88.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 4 QKLVPFA 10

RESULT 18  
US-09-580-018-21  
; Sequence 21, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-21

Query Match 88.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 3 QKLVPFA 9

RESULT 19  
US-09-580-018-22  
; Sequence 22, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-22

Query Match 88.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 2 QKLVPFA 8

RESULT 20  
US-09-580-018-23  
; Sequence 23, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-23

Query Match 88.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
:|||||  
Db 1 QKLVPFA 7

RESULT 21  
US-09-724-551-20  
; Sequence 20, Application US/09724551  
; Patent No. 6787637  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/724,551  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid



```
; OTHER INFORMATION: peptide)
US-09-724-551-20

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 4 QKLVPFA 10

RESULT 22
US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 3 QKLVPFA 9

RESULT 23
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 3 QKLVPFA 9

RESULT 24
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 1 QKLVPFA 7

RESULT 25
US-09-724-940-20
; Sequence 20, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
```

; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-20

Query Match 88.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 4 QKLVPFA 10

## RESULT 26

US-09-724-940-21  
; Sequence 21, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC

; CURRENT APPLICATION NUMBER: US/09/724,940

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US/09/580,015

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07

; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)  
US-09-724-940-21

Query Match 88.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 3 QKLVPFA 9

## RESULT 27

US-09-724-940-22

; Sequence 22, Application US/09724940  
; Patent No. 6905686

; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004750UC

; CURRENT APPLICATION NUMBER: US/09/724,940

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US/09/580,015

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07

; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)  
US-09-724-940-22

Query Match 88.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 2 QKLVPFA 8

## RESULT 28

US-09-724-940-23

; Sequence 23, Application US/09724940

; Patent No. 6905686

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vasquez, Nicki

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004750UC

; CURRENT APPLICATION NUMBER: US/09/724,940

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US/09/580,015

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07

; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

```
/ ; FEATURE:
/ ; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
/ ; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
/ ; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 29
US-08-630-645-14
/ ; Sequence 14, Application US/08630645
/ ; Patent No. 5948763
/ ; GENERAL INFORMATION:
/ ; APPLICANT: SOTO-JARA, Claudio
/ ; APPLICANT: BAUMANN, Marc
/ ; APPLICANT: FRANGIONE, Blas
/ ; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
/ ; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
/ ; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
/ ; NUMBER OF SEQUENCES: 26
/ ; CORRESPONDENCE ADDRESS:
/ ; ADDRESSEE: BROWDY AND NEIMARK
/ ; STREET: 419 Seventh Street, N.W., Suite 400
/ ; CITY: Washington
/ ; STATE: D.C.
/ ; COUNTRY: USA
/ ; ZIP: 20004
/ ; COMPUTER READABLE FORM:
/ ; MEDIUM TYPE: Floppy disk
/ ; COMPUTER: IBM PC compatible
/ ; OPERATING SYSTEM: PC-DOS/MS-DOS
/ ; SOFTWARE: PatentIn Release #1.0, Version #1.30
/ ; CURRENT APPLICATION DATA:
/ ; APPLICATION NUMBER: US/08/630,645
/ ; FILING DATE:
/ ; CLASSIFICATION: 530
/ ; PRIOR APPLICATION NUMBER:
/ ; APPLICATION NUMBER: US 08/478,326
/ ; FILING DATE: 06-JUN-1995
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: YUN, Allen C.
/ ; REGISTRATION NUMBER: 37,971
/ ; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: 202-628-5197
/ ; TELEFAX: 202-737-3528
/ ; INFORMATION FOR SEQ ID NO: 14:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 11 amino acids
/ ; TYPE: amino acid
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: peptide
US-08-630-645-14

Query Match      88.2%; Score 30; DB 1; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 30
US-08-766-596A-14
```

```
/ ; Sequence 14, Application US/08766596A
/ ; Patent No. 6462171
/ ; GENERAL INFORMATION:
/ ; APPLICANT: SOTO-JARA, Claudio
/ ; APPLICANT: BAUMANN, Marc
/ ; APPLICANT: FRANGIONE, Blas
/ ; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
/ ; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
/ ; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
/ ; TITLE OF INVENTION: DEPOSITS
/ ; NUMBER OF SEQUENCES: 69
/ ; CORRESPONDENCE ADDRESS:
/ ; ADDRESSEE: BROWDY AND NEIMARK
/ ; STREET: 419 Seventh Street, N.W., Suite 400
/ ; CITY: Washington
/ ; STATE: D.C.
/ ; COUNTRY: USA
/ ; ZIP: 20004
/ ; COMPUTER READABLE FORM:
/ ; MEDIUM TYPE: Floppy disk
/ ; COMPUTER: IBM PC compatible
/ ; OPERATING SYSTEM: PC-DOS/MS-DOS
/ ; SOFTWARE: PatentIn Release #1.0, Version #1.30
/ ; CURRENT APPLICATION DATA:
/ ; APPLICATION NUMBER: US/08/766,596A
/ ; FILING DATE:
/ ; CLASSIFICATION: 435
/ ; PRIOR APPLICATION NUMBER:
/ ; APPLICATION NUMBER: US 08/630,645
/ ; FILING DATE: 10-APR-1996
/ ; PRIOR APPLICATION DATA:
/ ; APPLICATION NUMBER: US 08/478,326
/ ; FILING DATE: 06-JUN-1995
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: YUN, Allen C.
/ ; REGISTRATION NUMBER: 37,971
/ ; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: 202-628-5197
/ ; TELEFAX: 202-737-3528
/ ; INFORMATION FOR SEQ ID NO: 14:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 11 amino acids
/ ; TYPE: amino acid
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: peptide
US-08-766-596A-14

Query Match      88.2%; Score 30; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 31
US-09-988-842-9
/ ; Sequence 9, Application US/09988842
/ ; Patent No. 6716589
/ ; GENERAL INFORMATION:
/ ; APPLICANT: Johansson, Jan
/ ; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
/ ; TITLE OF INVENTION: OF AMYLOID FORMATION
/ ; FILE REFERENCE: 12125-002001
/ ; CURRENT APPLICATION NUMBER: US/09/988,842
/ ; CURRENT FILING DATE: 2001-11-19
/ ; PRIOR APPLICATION NUMBER: US 60/251,662
/ ; PRIOR FILING DATE: 2000-12-06
/ ; PRIOR APPLICATION NUMBER: US 60/253,695
/ ; PRIOR FILING DATE: 2000-11-20
```

```
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match      88.2%; Score 30; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 32
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johanson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCES: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match      88.2%; Score 30; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 33
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEROP FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; NUMBER OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match      88.2%; Score 30; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 34
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCES: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-5

Query Match      88.2%; Score 30; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 6.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 3 QKLVPFA 9

RESULT 35
US-09-992-800-5
; Sequence 5, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCES: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
```

;/ CURRENT FILING DATE: 2001-11-06  
;/ PRIOR APPLICATION NUMBER: 09/594,366  
;/ PRIOR FILING DATE: 2000-06-15  
;/ PRIOR APPLICATION NUMBER: 60/139,408  
;/ PRIOR FILING DATE: 1999-06-16  
;/ NUMBER OF SEQ ID NOS: 7  
;/ SOFTWARE: Patentin Ver. 2.0  
;/ SEQ ID NO 5  
;/ LENGTH: 14  
;/ TYPE: PRT  
;/ ORGANISM: Homo sapiens  
US-09-992-800-5

Query Match 88.2%; Score 30; DB 2; Length 14;  
Best Local Similarity 85.7%; Pred. No. 6.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
Db 3 QKLVFFA 9

RESULT 36  
US-08-612-785B-37  
;/ Sequence 37, Application US/08612785B  
;/ Patent No. 5854204  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Findeis, Mark A. et al.  
;/ TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
;/ NUMBER OF INVENTIONS: Aggregation  
;/ NUMBER OF SEQUENCES: 40  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: LAHIVE & COCKFIELD  
;/ STREET: 28 State Street, Suite 510  
;/ CITY: Boston  
;/ STATE: Massachusetts  
;/ COUNTRY: USA  
;/ ZIP: 02109-1875  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patentin Release #1.0, Version #1.25  
;/ CURRENT APPLICATION NUMBER: US/08/612,785B  
;/ FILING DATE: Herewith  
;/ CLASSIFICATION: 514  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: USSN 08/404,831  
;/ FILING DATE: 14-MAR-1995  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: USSN 08/475,579  
;/ FILING DATE: 07-JUN-1995  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: USSN 08/548,998  
;/ FILING DATE: 27-OCT-1995  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: DeConti, Giulio A.  
;/ REGISTRATION NUMBER: 31,503  
;/ REFERENCE/DOCKET NUMBER: PPI-002CP3  
;/ TELEPHONE: (617)227-7400  
;/ TELEFAX: (617)742-4214  
;/ INFORMATION FOR SEQ ID NO: 37:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 15 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ FRAGMENT TYPE: internal  
US-08-612-785B-37

Query Match 88.2%; Score 30; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 7.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKLVFFA 7  
Db 5 QKLVFFA 11  
RESULT 37  
US-08-766-596A-56  
;/ Sequence 56, Application US/08766596A  
;/ Patent No. 6462171  
;/ GENERAL INFORMATION:  
;/ APPLICANT: SOTO-JARA, Claudio  
;/ APPLICANT: BAUMANN, Marc  
;/ APPLICANT: FRANGIONE, Blas  
;/ TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
;/ TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
;/ TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
;/ NUMBER OF INVENTIONS: DEPOSITS  
;/ NUMBER OF SEQUENCES: 69  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: BROWDY AND NEIMARK  
;/ STREET: 419 Seventh Street, N.W., Suite 400  
;/ CITY: Washington  
;/ STATE: D.C.  
;/ COUNTRY: USA  
;/ ZIP: 20004  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patentin Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/766,596A  
;/ FILING DATE:  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/630,645  
;/ FILING DATE: 10-APR-1996  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/478,326  
;/ FILING DATE: 06-JUN-1995  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: YUN, Allen C.  
;/ REGISTRATION NUMBER: 37,971  
;/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 202-628-5197  
;/ TELEFAX: 202-737-3528  
;/ INFORMATION FOR SEQ ID NO: 56:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 15 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
US-08-766-596A-56

Query Match 88.2%; Score 30; DB 2; Length 15;  
Best Local Similarity 85.7%; Pred. No. 7.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
Db 4 QKLVFFA 10

RESULT 38  
US-08-766-596A-57  
;/ Sequence 57, Application US/08766596A  
;/ Patent No. 6462171  
;/ GENERAL INFORMATION:

APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
TITLE OF INVENTION: DEPOSITS  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-57

Query Match 88.2%; Score 30; DB 2; Length 15;  
Best Local Similarity 85.7%; Pred. No. 7.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7  
:|||||  
Db 4 QKLVFFA 10

RESULT 39  
US-08-766-596A-60  
Sequence 60, Application US/08766596A  
Patent No. 6462171  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
TITLE OF INVENTION: DEPOSITS  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.

COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-60

Query Match 88.2%; Score 30; DB 2; Length 15;  
Best Local Similarity 85.7%; Pred. No. 7.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7  
:|||||  
Db 4 QKLVFFA 10

RESULT 40  
US-08-766-596A-61  
Sequence 61, Application US/08766596A  
Patent No. 6462171  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
TITLE OF INVENTION: DEPOSITS  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645

;; FILING DATE: 10-APR-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/478,326  
;; FILING DATE: 06-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: YUN, Allen C.  
;; REGISTRATION NUMBER: 37,971  
;; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; INFORMATION FOR SEQ ID NO: 61:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-766-596A-61

Query Match 88.2%; Score 30; DB 2; Length 15;  
Best Local Similarity 85.7%; Pred. No. 7.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
DB 4 QKLVPFA 10

RESULT 41  
US-08-766-596A-63  
; Sequence 63, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-61

;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-766-596A-63

Query Match 88.2%; Score 30; DB 2; Length 15;  
Best Local Similarity 85.7%; Pred. No. 7.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
DB 4 QKLVPFA 10

RESULT 42  
US-08-766-596A-65  
; Sequence 65, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/766,596A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/478,326  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-65

Query Match 88.2%; Score 30; DB 2; Length 15;  
Best Local Similarity 85.7%; Pred. No. 7.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7  
DB 4 QKLVPFA 10

Db 4 QKLVFFA 10

## RESULT 43

US-09-264-709A-2  
; Sequence 2, Application US/09264709A  
; Patent No. 6320024  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, Eugene  
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and  
; TITLE OF INVENTION: Improve the Quality of Life  
; FILE REFERENCE: 2124-310  
; CURRENT APPLICATION NUMBER: US/09/264,709A  
; CURRENT FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: 08/797,782  
; PRIOR FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-264-709A-2

Query Match 88.2%; Score 30; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 8.2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
:|||||  
Db 4 QKLVFFA 10

## RESULT 44

US-09-594-366-3  
; Sequence 3, Application US/09594366  
; Patent No. 6582945  
; GENERAL INFORMATION:  
; APPLICANT: Rago, Victor  
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO  
; FILE REFERENCE: BBRI-2004  
; CURRENT APPLICATION NUMBER: US/09/594,366  
; CURRENT FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/139,408  
; PRIOR FILING DATE: 1999-06-16  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-594-366-3

Query Match 88.2%; Score 30; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 8.2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
:|||||  
Db 7 QKLVFFA 13

## RESULT 45

US-09-623-548A-950  
; Sequence 950, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen

; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 950  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-950

Query Match 88.2%; Score 30; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 8.2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
:|||||  
Db 4 QKLVFFA 10

## RESULT 46

US-09-623-548A-983  
; Sequence 983, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 983  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-983

Query Match 88.2%; Score 30; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 8.2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
:|||||  
Db 4 QKLVFFA 10



```
RESULT 47
US-09-992-800-3
; Sequence 3, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-3

Query Match      88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
DB      7 QKLVPFA 13

RESULT 48
US-09-657-276-950
; Sequence 950, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudreau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 950
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-950

Query Match      88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
DB      7 QKLVPFA 13

RESULT 49
US-09-657-276-983
; Sequence 983, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudreau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 983
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-983

Query Match      88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
DB      4 QKLVPFA 10

RESULT 50
US-08-970-833-11
; Sequence 11, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Kiessling, Laura L.
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
```

```

; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-970-833-11

```

Query Match 88.2%; Score 30; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
:  
Db 9 QKLVEFA 15

```

RESULT 51
US-09-723-384-5
; Sequence 5, Application US/09723384
; Patent No. 6710226
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: NeuraLab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/09/723,384
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-384-5

```

Query Match 88.2%; Score 30; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 9;  
Matches 6: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	KKLVFFA	7
		:	
Db	3	QKLVFFA	9

RESULT 52  
US-09-724-961-75  
; Sequence 75, Application US/09724961  
; Patent No. 6743427  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,961  
; CURRENT FILING DATE: 2000-11-28

```

1  ; PRIORITY APPLICATION NUMBER: US 09/580,015
2  ;
3  ; PRIORITY FILING DATE: 2000-05-26
4  ;
5  ; PRIORITY APPLICATION NUMBER: US 09/322,289
6  ;
7  ; PRIORITY FILING DATE: 1999-05-28
8  ;
9  ; PRIORITY APPLICATION NUMBER: US 09/201,430
10 ;
11 ; PRIORITY FILING DATE: 1998-11-30
12 ;
13 ; PRIORITY APPLICATION NUMBER: WO PCT/US00/14810
14 ;
15 ; PRIORITY FILING DATE: 1998-11-30
16 ;
17 ; PRIORITY APPLICATION NUMBER: US 60/080,970
18 ;
19 ; PRIORITY FILING DATE: 1998-04-07
20 ;
21 ; PRIORITY APPLICATION NUMBER: US 60/067,740
22 ;
23 ; PRIORITY FILING DATE: 1997-12-02
24 ;
25 ; NUMBER OF SEQ ID NOS: 77
26 ;
27 ; SOFTWARE: PatentIn Ver. 2.1
28 ;
29 ; SEQ ID NO 75
30 ;
31 ; LENGTH: 19
32 ;
33 ; TYPE: PRT
34 ;
35 ; ORGANISM: Artificial Sequence
36 ;
37 ; FEATURE:
38 ;
39 ; OTHER INFORMATION: Description of Artificial Sequence: Abeta 13-28
40 ;
41 ; OTHER INFORMATION: Peptide with two Gly residues added and inserted
42 ;
43 ; OTHER INFORMATION: Cys residue
44 ;
45 ; NAME/KEY: MOD RES
46 ;
47 ; LOCATION: (1)
48 ;
49 ; OTHER INFORMATION: Xaa = N-acetyl His
50 ;
51 ; 09-724-961-75
52 ;

```

```
Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches         6: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	KKLVFFA	7
		:	
D <sub>b</sub>	3	QKLVFFA	9

```

RESULT 53
US-09-724-552-5
; Sequence 5, Application US/09724552
; Patent No. 6750324
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/09/724,552
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,019A
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-552-5

```

```
Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 KKL VFFA 7  
: |||||

Db 3 QKLVFFA 9

```
RESULT 54
US-09-580-018-75
; Sequence 75, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:beta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-580-018-75
```

Query Match 88.2%; Score 30; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
:|||||  
Db 3 QKLVFFA 9

```
RESULT 55
US-09-723-927-5
; Sequence 5, Application US/09723927
; Patent No. 6787138
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/723,927
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:beta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-927-5
```

Query Match 88.2%; Score 30; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
:|||||  
Db 3 QKLVFFA 9

```
RESULT 56
US-09-724-489-5
; Sequence 5, Application US/09724489
; Patent No. 6787140
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/724,489
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-489-5
```

Query Match 88.2%; Score 30; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7  
:|||||  
Db 3 QKLVFFA 9

```
RESULT 57
US-09-724-477-5
; Sequence 5, Application US/09724477
; Patent No. 6787143
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/724,477
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-477-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 QKLVFPA 9

RESULT 58
US-09-723-762-5
; Sequence 5, Application US/09723762
; Patent No. 6787144
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/723,762
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-762-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 QKLVFPA 9

RESULT 59
US-09-201-430-5
; Sequence 5, Application US/09201430
; Patent No. 6787523
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/201,430
; CURRENT FILING DATE: 1998-11-30
```

```
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-201-430-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 QKLVFPA 9

RESULT 60
US-09-724-551-75
; Sequence 75, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; OTHER INFORMATION: Cys residue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-724-551-75

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 QKLVFPA 9

RESULT 61
US-10-815-353-5
; Sequence 5, Application US/10815353
; Patent No. 6808712
```

```
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/815,353
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-815-353-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KKLVEFA 7
Db  3 QKLVEFA 9

RESULT 62
US-10-816-529-5
; Sequence 5, Application US/10816529
; Patent No. 6818218
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/816,529
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-816-529-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KKLVEFA 7
Db  3 QKLVEFA 9

RESULT 64
US-10-816-022-5
; Sequence 5, Application US/10816022
; Patent No. 6866850
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/816,022
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-816-022-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KKLVEFA 7
Db  3 QKLVEFA 9

RESULT 66
US-10-816-022-5
; Sequence 5, Application US/10816022
; Patent No. 6866850
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/816,022
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-816-022-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-10-816-022-5

Query Match 88.2%; Score 30; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 3 QKLVPFA 9

## RESULT 65

US-09-724-940-75  
; Sequence 75, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 75  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28  
; OTHER INFORMATION: peptide with two Gly residues added and inserted  
; OTHER INFORMATION: Cys residue  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = N-acetyl His  
US-09-724-940-75

Query Match 88.2%; Score 30; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 3 QKLVPFA 9

## RESULT 66

US-10-934-609-5  
; Sequence 5, Application US/10934609  
; Patent No. 6946135  
; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004720US  
; CURRENT APPLICATION NUMBER: US/10/934,609  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US/09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-10-934-609-5

Query Match 88.2%; Score 30; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
:|||||  
Db 3 QKLVPFA 9

## RESULT 67

US-10-884-892-5  
; Sequence 5, Application US/10884892  
; Patent No. 6962707  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004720US  
; CURRENT APPLICATION NUMBER: US/10/884,892  
; CURRENT FILING DATE: 2004-07-01  
; PRIOR APPLICATION NUMBER: US/09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-10-884-892-5

Query Match 88.2%; Score 30; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 KKLVEFA 7
Db 3 QKLVEFA 9

RESULT 68
US-08-970-833-10
; Sequence 10, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Klessling, Laura L.
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 13..14
; OTHER INFORMATION: /note= "amino caproate should
; OTHER INFORMATION: appear between residues 13 and 14."
US-08-970-833-10

Query Match 88.2%; Score 30; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 9.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
Db 2 QKLVEFA 8

RESULT 69
US-09-724-953-33
; Sequence 33, Application US/09724953
; Patent No. 6875434
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Elan Pharmaceuticals
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Diseases
; FILE REFERENCE: 015270-005913US
; CURRENT APPLICATION NUMBER: US/09/724,953
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/585,817

; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,010
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Beta 13-28
; OTHER INFORMATION: peptide with Cys added
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl-asparagine
US-09-724-567-33

Query Match 88.2%; Score 30; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 9.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
Db 4 QKLVEFA 10

RESULT 71
US-09-979-952-33
; Sequence 33, Application US/09979952
; Patent No. 6913745
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Elan Pharmaceuticals
```

```
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-0059150S
; CURRENT APPLICATION NUMBER: US/09/979,952
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: WO PCT/US00/25239
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,010
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta 13-28
; OTHER INFORMATION: peptide with Cys added
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl-asparagine
US-09-979-952-33

Query Match      88.2%; Score 30; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 9.5; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

Qy      1 KKLVPFA 7
       :|||||
Db      4 QKLVPFA 10

RESULT 72
US-09-585-817-33
; Sequence 33, Application US/09585817
; Patent No. 6923964
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Elan Pharmaceuticals
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Diseases
; FILE REFERENCE: 015270-005910US
; CURRENT APPLICATION NUMBER: US/09/585,817
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: WO PCT/US00/25239
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,010
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta 13-28
; OTHER INFORMATION: peptide with Cys added
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl-asparagine
US-09-585-817-33

Query Match      88.2%; Score 30; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 9.5; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

Qy      1 KKLVPFA 7
       :|||||
Db      4 QKLVPFA 10

RESULT 73
US-08-304-585-7
```

```
; Sequence 7, Application US/08304585
; Patent No. 5721166
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: .peptide
US-08-304-585-7

Query Match      88.2%; Score 30; DB 1; Length 26;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVPFA 7
       :|||||
Db      6 QKLVPFA 12

RESULT 74
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```



SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/346,849  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/973,326  
FILING DATE: 28 DECEMBER 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: MIT-6008  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-346-849-4

Query Match 88.2%; Score 30; DB 1; Length 28;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
:|||||  
Db 15 QKLVEFA 21

RESULT 75  
US-08-302-808-7  
Sequence 7, Application US/08302808  
Patent No. 5750349  
GENERAL INFORMATION:  
APPLICANT: SUZUKI, No. 5750349uhiro  
APPLICANT: ODAKA, Asano  
APPLICANT: KITADA, Chieko  
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
DERIVATIVES AND USE THEREOF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02019  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/302,808  
FILING DATE: 15-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/00089  
FILING DATE: 24-JAN-1994  
APPLICATION NUMBER: 010132/1993  
FILING DATE: 25-JAN-1993  
APPLICATION NUMBER: 019035/1993  
FILING DATE: 05-FEB-1993  
APPLICATION NUMBER: 286985/1993  
FILING DATE: 16-NOV-1993  
APPLICATION NUMBER: 334773/1993  
FILING DATE: 28-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 44631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: 200291 STRE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-302-808-7

Query Match 88.2%; Score 30; DB 1; Length 28;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7  
:|||||  
Db 15 QKLVEFA 21

Search completed: December 29, 2005, 17:52:32  
Job time : 24.471 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 91.2258 Seconds  
(without alignments)  
54.137 Million cell updates/sec

Title: US-10-009-122-2  
Perfect score: 34  
Sequence: 1 KKLVFFA 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	137	2 QUPR1	RHOBA
2	34	100.0	493	2 Q5K4D5	9POTV
3	33	97.1	284	2 Q4ZXZ2	PSESY
4	32	94.1	387	2 Q81FHS	BACCR
5	31	91.2	51	2 Q72A51	DESVH
6	31	91.2	137	2 Q74E04	GEOSL
7	31	91.2	176	2 Q4QLX3	HAB18
8	31	91.2	183	2 Q9RQ09	BACTIN
9	31	91.2	314	2 Q9PUW1	METMA
10	31	91.2	362	2 Q4HSJ7	CAMUP
11	31	91.2	387	2 Q9K110	BACCE
12	31	91.2	387	2 Q4MT39	BACCE
13	31	91.2	387	2 Q63DD4	BACZ
14	31	91.2	387	2 Q6HKU6	BACHK
15	31	91.2	387	2 Q73AP3	BACCI
16	31	91.2	387	2 Q81SK9	BACAN
17	31	91.2	447	2 Q59243	PRHO
18	31	91.2	488	2 Q37931	9POTV
19	31	91.2	488	2 Q37932	9POTV
20	31	91.2	488	2 Q37933	9POTV
21	31	91.2	488	2 Q37934	9POTV
22	31	91.2	697	2 Q5AU77	EMENI
23	31	91.2	3222	2 Q563A1	RCMVN
24	30	88.2	33	2 Q9UC33	HUMAN
25	30	88.2	34	2 Q9XQRS	PEA
26	30	88.2	42	2 Q56JJ6	GRAGR
27	30	88.2	42	2 Q56JJ7	TURTR
28	30	88.2	42	2 Q7M088	CAVPO
29	30	88.2	52	2 Q8WZ99	HUMAN
30	30	88.2	57	1 A4 URSMA	
31	30	88.2	58	1 A4 CANFA	

32	30	88.2	58	1 A4 RABIT	Q28748 o alzheimer
33	30	88.2	58	1 A4 SHEEP	Q28757 o alzheimer
34	30	88.2	59	1 A4 BOVIN	Q28053 b alzheimer
35	30	88.2	79	2 Q35463	CRIGR
36	30	88.2	94	2 Q5XD67	STRP6
37	30	88.2	94	2 Q9A0W1	STRPY
38	30	88.2	94	2 Q7CNF7	STRP8
39	30	88.2	94	2 Q8PIX8	STRP3
40	30	88.2	113	2 Q8JH58	CHESE
41	30	88.2	125	2 Q5TUI4	ANOAG
42	30	88.2	150	1 FAB2	DESPS
43	30	88.2	165	2 Q6CX11	KLULA
44	30	88.2	187	2 Q4TUZ7	MAIZE
45	30	88.2	214	2 Q64NE8	BACFR
46	30	88.2	218	2 Q8BPV5	MOUSE
47	30	88.2	228	2 Q64MC9	BACFR
48	30	88.2	270	2 Q7MV75	PORGI
49	30	88.2	336	2 Q74HY9	LACJO
50	30	88.2	346	2 Q9PMW9	CAMJE
51	30	88.2	357	2 Q8UUI8	BRARE
52	30	88.2	359	1 MLTA	BUCAI
53	30	88.2	380	2 Q67225	AQUAE
54	30	88.2	384	2 Q8BPC7	MOUSE
55	30	88.2	426	2 Q83DX9	COXBU
56	30	88.2	472	2 Q8UUS0	BRARE
57	30	88.2	479	2 Q9X152	ARATH
58	30	88.2	481	2 Q8L731	ARATH
59	30	88.2	493	2 Q5K4D4	9POTV
60	30	88.2	534	2 Q93296	CHICK
61	30	88.2	569	2 Q9PVL1	CHICK
62	30	88.2	572	2 Q75JL6	DICDI
63	30	88.2	586	1 RPOCL	EUGGR
64	30	88.2	612	2 Q919E7	BRARE
65	30	88.2	639	2 Q8LD58	ARATH
66	30	88.2	645	2 Q9ZT08	ARATH
67	30	88.2	647	2 Q9LV16	ARATH
68	30	88.2	655	2 Q9LP77	ARATH
69	30	88.2	678	2 Q7ZT11	BRARE
70	30	88.2	693	2 Q98SG0	XENLA
71	30	88.2	694	2 Q6Y2W9	MAIZE
72	30	88.2	695	2 Q5R477	PONPY
73	30	88.2	695	2 Q6RH29	CANFA
74	30	88.2	695	2 Q56JK3	CANFA
75	30	88.2	695	2 Q6GR78	MOUSE
76	30	88.2	695	2 Q9DGJ8	CHICK
77	30	88.2	695	2 Q98SF9	XENLA
78	30	88.2	695	2 Q7ZXQ0	XENLA
79	30	88.2	702	2 Q4WT56	ASPTU
80	30	88.2	714	2 Q56JK4	CANFA
81	30	88.2	733	2 Q6P605	RAT
82	30	88.2	737	1 A4 FUGRU	
83	30	88.2	738	2 Q6NUZ1	BRARE
84	30	88.2	738	2 Q9W28	BRARE
85	30	88.2	747	2 Q91963	9PIPI
86	30	88.2	749	2 Q56JK2	STECO
87	30	88.2	749	2 Q6NRR1	XENLA
88	30	88.2	750	2 Q6DJB6	XENTR
89	30	88.2	751	1 A4 SAISC	
90	30	88.2	751	2 Q6GSC0	HUMAN
91	30	88.2	751	2 Q6RH28	CANFA
92	30	88.2	751	2 Q56JK5	CANFA
93	30	88.2	751	2 Q4R4R8	MACFA
94	30	88.2	751	2 Q9DGJ7	CHICK
95	30	88.2	754	2 Q4RX33	TETNG
96	30	88.2	759	2 Q4S0J4	TETNG
97	30	88.2	770	1 A4 CAVFO	
98	30	88.2	770	1 A4 HUMAN	
99	30	88.2	770	1 A4 MACFA	
100	30	88.2	770	1 A4 MOUSE	
101	30	88.2	770	1 A4 PANTR	
102	30	88.2	770	1 A4 PIG	
103	30	88.2	770	1 A4 RAT	
104	30	88.2	770	2 Q6RH30	CANFA

105	30	88.2	770	2	Q56JK6_CANFA	Q56JK6 canis famil	178	29	85.3	809	2	Q9N3K6_CABEL	Q9N3K6 caenorthabdi
106	30	88.2	770	2	Q53ZT3_MOUSE	Q53zt3 mus musculu	179	29	85.3	866	2	Q4YAT8_PLABE	Q4yat8 plasmodium
107	30	88.2	770	2	Q547B7_RAT	Q547b7 rattus norv	180	29	85.3	911	2	Q6MUF5_MYCMS	Q6muf5 mycoplasma
108	30	88.2	780	1	A4_TETFL	Q73683 tetraodon f	181	29	85.3	962	2	Q4NTK2_0ELT	Q4ntk2 anaeromyxob
109	30	88.2	955	2	Q8QRZ2_9POTV	Q80rz2 calla lily	182	29	85.3	970	2	Q758X5_ASHGO	Q758x5 ashbya goss
110	30	88.2	1678	2	Q6BUD9_DEBHA	Q6bud9 debaryomyce	183	29	85.3	1016	2	Q05912_9POTV	Q05912 zucchini ye
111	30	88.2	3105	2	Q70XR2_9POTV	Q70xr2 soybean mos	184	29	85.3	1056	2	Q6FKH6_CANGA	Q6fkh6 candida gla
112	30	88.2	4664	2	Q4QFY9_LEIMA	Q4qfy9 leishmania	185	29	85.3	1293	2	Q55A32_DfCYD	Q55a32 dictyosteli
113	30	88.2	5808	2	Q4UFB3_THEAN	Q4ufb3 theileria a	186	29	85.3	1492	2	Q83Y21_PEWBP	Q83y21 peanut wic
114	29	85.3	34	2	Q8GJC8_CAMJE	Q8gjc8 campylobact	187	29	85.3	1916	2	Q8QKU4_9POTV	Q8qku4 zucchini ye
115	29	85.3	45	2	Q4XF00_PLACH	Q4xf00 plasmodium	188	29	85.3	3080	1	POLG_ZYMVC	P1g479 z genome po
116	29	85.3	96	1	IFIC_TOBAC	P12136 nicotiana t	189	29	85.3	3080	2	Q6WN47_9POTV	Q6wn47 zucchini ye
117	29	85.3	104	2	Q9G8Z7_OCHDN	Q9g8z7 ochromonas	190	29	85.3	3080	2	Q6WN48_9POTV	Q6wn48 zucchini ye
118	29	85.3	109	2	Q9X292_THEMA	Q9x292 thermotoga	191	29	85.3	3080	2	Q6WN49_9POTV	Q6wn49 zucchini ye
119	29	85.3	127	2	Q4XF83_PLACH	Q4xf83 plasmodium	192	29	85.3	3080	2	Q6Y2U7_9POTV	Q6y2u7 zucchini ye
120	29	85.3	149	2	Q6AIF8_DESPS	Q6aif8 desulfotale	193	29	85.3	3080	2	Q7T908_9POTV	Q7t908 zucchini ye
121	29	85.3	152	2	Q9STZ9_ATH	Q9stz9 arabidopsis	194	29	85.3	3080	2	Q7T914_9POTV	Q7t914 zucchini ye
122	29	85.3	158	2	Q4EPG2_9RICK	Q4epg2 candidatus	195	29	85.3	3083	1	POLG_ZYMVS	Q3g979 z genome po
123	29	85.3	176	1	NRFX_HABIN	P44943 haemophilus	196	28	82.4	26	2	Q4XGPI_PLACH	Q4xgpi plasmodium
124	29	85.3	177	2	Q5LD66_BACFN	Q5ld66 bacteroides	197	28	82.4	46	2	Q4Y2T9_PLABE	Q4y2t9 plasmodium
125	29	85.3	177	2	Q64U86_BACFR	Q64u86 bacteroides	198	28	82.4	46	2	Q8EXM4_LBPIN	Q8exm4 leptospira
126	29	85.3	229	2	Q8VY56_ATH	Q8vy56 arabidopsis	199	28	82.4	51	2	Q7RF81_PLAYO	Q7rf81 plasmodium
127	29	85.3	230	2	Q7RDM9_PLAYO	Q7rdm9 plasmodium	200	28	82.4	66	2	Q7Z8FO_DESVH	Q7z8fo desulfovibr
128	29	85.3	231	2	Q9SV79_ATH	Q9sv79 arabidopsis	201	28	82.4	72	2	Q4HSS4_CAMUP	Q4hss4 campylobact
129	29	85.3	258	2	Q65K48_BACLD	Q65k48 bacillus li	202	28	82.4	79	2	Q8FAZ7_ECOL6	Q8faz7 escherichia
130	29	85.3	268	2	Q6YPU1_ONYPE	Q6ypu1 onion yello	203	28	82.4	88	2	Q4LBQ8_SODGL	Q4lbq8 sodalis glo
131	29	85.3	275	2	Q5SE89_DICDI	Q5se89 dictyosteli	204	28	82.4	105	2	Q64CV5_9ARCH	Q64cv5 uncultured
132	29	85.3	283	2	Q7R9D9_PLAYO	Q7r9d9 plasmodium	205	28	82.4	109	2	Q8XQ19_RALSO	Q8xq19 ralstonia s
133	29	85.3	294	2	Q4XEU4_PLACH	Q4xeu4 plasmodium	206	28	82.4	118	2	Q5ZDNC_ORYSA	Q5zdn6 cryza sativ
134	29	85.3	296	2	Q5NQG3_ZYMMO	Q5ngq3 zymomonas m	207	28	82.4	118	2	Q8Y1S2_RALSO	Q8y1s2 ralstonia s
135	29	85.3	296	2	Q8F385_LEPIN	Q8f385 leptospira	208	28	82.4	123	2	Q97WV1_SULSO	Q97wv1 sulfolobus
136	29	85.3	296	2	Q7ZSD7_LEPIC	Q7zsd7 leptospira	209	28	82.4	130	1	Y613_PASMU	Y613 PASMU
137	29	85.3	316	2	Q8Y985_LISMO	Q8y985 listeria mo	210	28	82.4	133	2	Q8KKG9_HELPU	Q8kkg9 helicobacte
138	29	85.3	316	2	Q9ZEL0_LISIN	Q9zel0 listeria in	211	28	82.4	141	2	Q5LGT9_BACFN	Q5lgt9 bacteroides
139	29	85.3	316	2	Q7Z2Q1_LISMP	Q7z2q1 listeria mo	212	28	82.4	141	2	Q8XPI1_BACFR	Q8xpi1 bacteroides
140	29	85.3	324	2	Q4Y0J6_PLACH	Q4y0j6 plasmodium	213	28	82.4	143	2	Q8EMC6_OCEIH	Q8emc6 oceanobacil
141	29	85.3	352	2	Q9XGY6_SIMCH	Q9xgy6 simmondsia	214	28	82.4	144	2	Q67K60_SYMTH	Q67k60 symbiobacte
142	29	85.3	357	2	Q8U460_PYRFU	Q8u460 pyrococcus	215	28	82.4	165	2	Q5NX98_AZOSE	Q5nx98 azoarcus sp
143	29	85.3	366	2	Q8PPL1_XANAC	Q8ppl1 xanthomonas	216	28	82.4	176	2	Q6AM23_DESPS	Q6am23 desulfotale
144	29	85.3	380	2	Q7VJCI_HELHP	Q7vici helicobacte	217	28	82.4	182	2	Q5OY54_ENTHI	Q5oy54 entamoeba h
145	29	85.3	381	2	Q5LIA8_GEOKA	Q5lia8 geobacillus	218	28	82.4	182	2	Q5NSY6_ENTHI	Q5nsy6 entamoeba h
146	29	85.3	386	2	Q6Z7Y5_CABER	Q6z7y5 caenorthabdi	219	28	82.4	196	2	Q7RCT7_PLAYO	Q7rct7 plasmodium
147	29	85.3	386	2	Q45308_BACME	Q45308 bacillus me	220	28	82.4	207	2	Q4HDT2_CAMCO	Q4hdt2 campylobact
148	29	85.3	391	2	Q4NSU7_THEPA	Q4nsu7 theileria p	221	28	82.4	214	2	Q9LZV2_ATH	Q9lzy2 arabidopsis
149	29	85.3	403	2	Q5L117_GEOKA	Q5l117 geobacillu	222	28	82.4	218	2	Q9WZ39_THEMEA	Q9wz39 thermotoga
150	29	85.3	404	2	Q4UY55_XANCP	Q4uy55 xanthomonas	223	28	82.4	220	2	Q79A00_STRPY	Q79a00 streptococc
151	29	85.3	404	2	Q8P597_XANCP	Q8p597 xanthomonas	224	28	82.4	236	2	P97163_STRPY	P97163 streptococc
152	29	85.3	421	2	Q9LH60_ATH	Q9lh60 arabidopsis	225	28	82.4	236	2	Q54779_STRPY	Q54779 streptococc
153	29	85.3	421	2	Q9PNU9_CAMJE	Q9pnu9 campylobact	226	28	82.4	236	2	Q57453_STRPY	Q57453 streptococc
154	29	85.3	421	2	Q5HUH1_CAMJR	Q5huhi campylobact	227	28	82.4	243	2	Q4V613_DROME	Q4v613 drosophila
155	29	85.3	423	2	Q59MK9_CANAL	Q59mk9 candida alb	228	28	82.4	244	2	Q9VQ40_DROME	Q9vq40 drosophila
156	29	85.3	428	2	Q9M1Q8_ATH	Q9m1q8 arabidopsis	229	28	82.4	245	1	VITO_BACSU	V06752 bacillus su
157	29	85.3	461	2	Q89329_9POTV	Q89329 zucchini ye	230	28	82.4	248	2	Q5L384_GROKA	Q5l384 geobacillus
158	29	85.3	470	2	Q7T910_9POTV	Q7t910 zucchini ye	231	28	82.4	251	1	SPEA_STRPB	P63561 streptococc
159	29	85.3	484	1	Y1062_METUA	Q58462 methanococc	232	28	82.4	251	1	SPEA_STRPB	P63561 streptococc
160	29	85.3	485	2	Q4F982_9POTV	Q4f982 serratia v	233	28	82.4	251	2	Q9YWB3_MSEPV	Q9ywb3 streptococc
161	29	85.3	488	2	Q52NV6_9POTV	Q52nv6 zucchini ye	234	28	82.4	254	2	Q9YWB3_MSEPV	Q9ywb3 streptococc
162	29	85.3	490	2	Q7T911_9POTV	Q7t911 zucchini ye	235	28	82.4	266	2	Q6FY12_BARQU	Q6fy12 bartonella
163	29	85.3	490	2	Q7T912_9POTV	Q7t912 zucchini ye	236	28	82.4	273	2	Q4L2R4_BARQU	Q4l2r4 bartonella
164	29	85.3	502	2	Q5LUS5_GEOKA	Q5lus5 geobacillus	237	28	82.4	273	2	Q4HSP7_CAMUP	Q4hsp7 campylobact
165	29	85.3	508	2	Q5GVS5_XANOR	Q5gvs5 xanthomonas	238	28	82.4	275	2	Q7SDV7_NEUCR	Q7sdv7 neurospora
166	29	85.3	533	2	Q975B3_SULTO	Q975b3 sulfolobus	239	28	82.4	275	2	Q5K2M1_BACLI	Q5k2m1 bacillus li
167	29	85.3	610	2	Q21604_CABEL	Q21604 caenorthabdi	240	28	82.4	275	2	Q5WTR1_LSGPL	Q5wtr1 legionella
168	29	85.3	615	2	Q5OZ85_ENTHI	Q5oz85 entamoeba h	241	28	82.4	275	2	Q5X1Y6_LSGPA	Q5x1y6 legionella
169	29	85.3	636	2	Q6CHB2_YARLI	Q6chb2 yarrowia li	242	28	82.4	276	2	Q7Q835_GIALA	Q7q835 giardia lam
170	29	85.3	638	2	Q5B2V4_EMENI	Q5b2v4 aspergillus	243	28	82.4	276	2	Q5E2G2_VIBF1	Q5e2g2 vibrio fisc
171	29	85.3	675	2	Q8H811_ORYSA	Q8h811 oryza sativ	244	28	82.4	276	2	Q9KT31_VIECH	Q9kt31 vibrio chol
172	29	85.3	686	2	Q7RBQ7_ORYSA	Q7rbq7 oryza sativ	245	28	82.4	293	1	Y844_ARCFU	Y844 ARCFU
173	29	85.3	716	2	Q7RBQ0_PLAYO	Q7rbq0 plasmodium	246	28	82.4	293	1	Q5ZSH6_LRGPH	Q5zsh6 legionella
174	29	85.3	743	2	Q6BM34_DEBHA	Q6bm34 debaryomyce	247	28	82.4	294	2	Q97XW2_SULSO	Q97xw2 sulfolobus
175	29	85.3	763	2	Q9CH71_LACLA	Q9ch71 lactococcus	248	28	82.4	301	2	Q8EB34_SHEON	Q8eb34 shewanella
176	29	85.3	774	2	Q64777_ATH	Q64777 arabidopsis	249	28	82.4	306	2	Q4YZW0_PLABE	Q4yzw0 plasmodium
177	29	85.3	804	2	Q64770_ATH	Q64770 arabidopsis	250	28	82.4	310	2	Q6R7D4_9HERP	Q6r7d4 ostreid her

251 28 82.4 315 2 065532 AQUAE  
 252 28 82.4 320 2 Q59DR9\_DROME  
 253 28 82.4 321 1 Y189 RICPR  
 254 28 82.4 326 2 Q627D1 CAEBR  
 255 28 82.4 327 2 Q7Q914 ANOAG  
 256 28 82.4 330 2 Q8ZU32 PYRAE  
 257 28 82.4 333 2 P72489 STRPN  
 258 28 82.4 333 2 Q77SK3\_STRPN  
 259 28 82.4 334 2 Q81KN3\_PLAF7  
 260 28 82.4 339 2 Q5FNR0\_GLUOX  
 261 28 82.4 343 2 Q9V531\_DROSOPHILA  
 262 28 82.4 355 2 Q8DR72\_STRR6  
 263 28 82.4 367 2 Q4FR77\_9GAMM  
 264 28 82.4 370 2 Q65SJI\_MANSW  
 265 28 82.4 371 2 Q6C6Q0\_YARLI  
 266 28 82.4 372 2 Q6D7U3\_ERWCT  
 267 28 82.4 383 2 Q8YYZ5\_ANASP  
 268 28 82.4 403 2 Q5CTP3\_CRYPV  
 269 28 82.4 423 2 Q6C1K6\_YARLI  
 270 28 82.4 434 2 Q89YS3\_BACTN  
 271 28 82.4 463 2 Q8ESN1\_OCEIH  
 272 28 82.4 464 2 Q4S4T5\_TETNG  
 273 28 82.4 465 2 Q82YV5\_ENTPA  
 274 28 82.4 469 2 Q4Y318\_PLACH  
 275 28 82.4 473 2 Q5UPQ3\_MINIV  
 276 28 82.4 479 2 Q9QDU5\_9POTV  
 277 28 82.4 479 2 Q4F979\_9POTV  
 278 28 82.4 480 2 Q4N8N8\_THEPA  
 279 28 82.4 488 2 Q52NV7\_9POTV  
 280 28 82.4 496 2 Q5K4D0\_9POTV  
 281 28 82.4 504 2 Q4H3G7\_CIOIN  
 282 28 82.4 505 2 Q474G0\_GEOSL  
 283 28 82.4 528 2 Q9P7P2\_SCHPO  
 284 28 82.4 542 2 Q6FTN7\_CANGA  
 285 28 82.4 542 2 Q8X0Z5\_CANGA  
 286 28 82.4 557 2 Q4UG24\_THEAN  
 287 28 82.4 559 2 Q4XZR3\_PLACH  
 288 28 82.4 562 2 Q7NNW2\_CHRVO  
 289 28 82.4 605 2 Q9TYX2\_CABEL  
 290 28 82.4 605 2 Q6MPZ3\_BDEBA  
 291 28 82.4 606 2 Q1V1V5\_MOUSE  
 292 28 82.4 614 2 Q7P291\_ANOAG  
 293 28 82.4 624 2 Q7SDS8\_NEUCR  
 294 28 82.4 648 2 Q6C0N6\_YARLI  
 295 28 82.4 652 2 Q9F531\_ECOLI  
 296 28 82.4 655 2 Q7R9H2\_PLAYO  
 297 28 82.4 663 2 Q6RUU2\_MOUSE  
 298 28 82.4 685 1 M0L1\_CANAL  
 299 28 82.4 685 2 Q5A951\_CANAL  
 300 28 82.4 704 2 Q65J18\_BACLD

## ALIGNMENTS

RESULT 1  
 Q7UPR1\_RHOBA PRELIMINARY; PRT; 137 AA.  
 ID Q7UPR1\_RHOBA PRELIMINARY;  
 AC Q7UPR1\_RHOBA PRELIMINARY;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocusNames=RB6777;  
 OS Rhodospirillum rubrum  
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Pirellula.  
 OX NCBI\_TaxID=1117;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=1;  
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;  
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,

RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,  
 RA Schleiner H., Anann R., Reinhardt R.;  
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
 strain 1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).  
 DR EMBL; BX294144; CAD75000.1; -; Genomic DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 137 AA; 15530 MW; 5DCCL33B06CC5FC0 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 137;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
 Db 84 KKLVPFA 90

## RESULT 2

Q5K4D5\_9POTV PRELIMINARY; PRT; 493 AA.  
 ID Q5K4D5\_9POTV PRELIMINARY;  
 AC Q5K4D5\_9POTV PRELIMINARY;  
 DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
 DE Polyprotein (fragment).  
 DE Soybean mosaic virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 OX NCBI\_TaxID=12222;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=P;  
 RX PubMed=15449140; DOI=10.1007/s00705-004-0390-z;  
 RA Shi Y.H., Hong X.Y., Chen J., Adams M.J., Zheng H.Y., Lin L.,  
 RA Qing B.X., Chen J.;  
 RT "Further molecular characterisation of potyviruses infecting aroid  
 plants for medicinal use in China.";  
 RL Arch. Virol. 150:125-135(2005).  
 DR EMBL; AJ628751; CAF32241.1; -; Genomic RNA.  
 DR GO; GO:0019028; C:Viral capsid; IEA.  
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
 DR GO; GO:0019079; P:Viral genome replication; IEA.  
 DR InterPro; IPR001592; Poty coat.  
 DR InterPro; IPR001205; RNA\_pol\_P3D.  
 DR InterPro; IPR007094; RNA\_pol\_P5vir.  
 DR Pfam; PF00767; Poty coat; 1.  
 DR Pfam; PF00680; RdRP\_1; 1.  
 KW Capsid protein; Polyprotein. Nib protein.  
 FT CHAIN <1 211 coat protein.  
 FT CHAIN 212 493  
 FT NON TER 1 1  
 SQ SEQUENCE 493 AA; 55866 MW; 6D50976B5C7DF5F3 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 493;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
 Db 37 KKLVPFA 43

## RESULT 3

Q4ZXZ2\_PSESY PRELIMINARY; PRT; 284 AA.  
 ID Q4ZXZ2\_PSESY PRELIMINARY;  
 AC Q4ZXZ2\_PSESY PRELIMINARY;  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
 DE Glycosyl transferase, family 2 precursor.  
 GN ORFNames=Psyt\_0922;  
 OS Pseudomonas syringae pv. syringae B728a.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=205918;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B728a;  
 RG DOE Joint Genome Institute;  
 RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,  
 RA Nolan M., Goltermann E., Thiel J., Malfatti S., Lapidus A., Dettler J.C.,  
 RA Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;  
 RT "Comparison of two complete genome sequences of Pseudomonas syringae  
 RT pv. syringae B728a and pv. tomato DC3000";  
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B728a;  
 RA Loper J.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B728a;  
 RA Feil H., Feil W.S., Lindow S.E.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CF000075; AY35980.1; -; Genomic DNA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 KW Signal; Transferase.  
 FT SIGNAL 284 284 Potential.  
 SQ SEQUENCE 284 AA; 30871 MW; 37921A81C4BB728D CRC64;  
 Query Match 97.1%; Score 33; DB 2; Length 284;  
 Best Local Similarity 85.7%; Pred. No. 37;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db 2 KKLIFPA 8  
 RESULT 4  
 ID Q81FH5\_BACCR PRELIMINARY; PRT; 387 AA.  
 AC Q81FH5;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Na+/H+ antiporter NapA (inosine-dependent germination).  
 GN OrderedLocNames=BC1612;  
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=226900;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;  
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candellon B.,  
 RA Kapral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,  
 RA Chu L., Mazur M., Goldstein E., Larsen N., D'Souza M., Walunas T.,  
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,  
 RA Overbeek R., Kyrpides N.C.;  
 RT "Genome sequence of Bacillus cereus and comparative analysis with  
 RT Bacillus anthracis";  
 RL Nature 423:97-91(2003).  
 RL EMBL; AB017003; AAP08591.1; -; Genomic DNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0008324; F:cation transporter activity; IEA.  
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR GO; GO:0006885; P:regulation of pH; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR004771; K eff.  
 DR InterPro; IPR006153; Na/H porter.  
 DR Pfam; PF00999; Na\_H\_Exchange; 1.  
 DR TIGRFAMs; TIGR00932; 2a37; 1.

KW Complete proteome; Transmembrane; Transport.  
 SQ SEQUENCE 387 AA; 41037 MW; 907C03E6BA150B4A CRC64;  
 Query Match 94.1%; Score 32; DB 2; Length 387;  
 Best Local Similarity 85.7%; Pred. No. 84;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db 183 KKLVPFA 189  
 RESULT 5  
 ID Q72A51\_DESVH PRELIMINARY; PRT; 51 AA.  
 AC Q72A51;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocNames=DVU2146;  
 OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB  
 OS 8303).  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;  
 OC Desulfovibrionaceae; Desulfovibrio.  
 OX NCBI\_TaxID=882;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15077118; DOI=10.1038/nbt959;  
 RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,  
 RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,  
 RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,  
 RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,  
 RA Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,  
 RA Dimitrov G., Hance W., Tran K., Khouri H.M., Gill J., Utterback T.R.,  
 RA Feldblyum T.V., Wall J.D., Voordouw G., Frazer C.M.;  
 RT "The genome sequence of the anaerobic, sulfate-reducing bacterium  
 RT Desulfovibrio vulgaris Hildenborough";  
 RL Nat. Biotechnol. 22:554-559(2004).  
 DR EMBL; AE017316; AAS96619.1; -; Genomic DNA.  
 DR TIGR; DVU2146; -;  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 51 AA; 6205 MW; E7F69C0D8432B7F5 CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 51;  
 Best Local Similarity 85.7%; Pred. No. 24;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db 17 KKLVPFA 23  
 RESULT 6  
 ID Q74E04\_GEOSL PRELIMINARY; PRT; 137 AA.  
 AC Q74E04;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocNames=GSU1160;  
 OS Geobacter sulfurreducens.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;  
 OC Geobacteraceae; Geobacter.  
 OX NCBI\_TaxID=35554;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PCA / ATCC 51573;  
 RX PubMed=14671304; DOI=10.1126/science.1088727;  
 RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,  
 RA Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J.,  
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,

RA	Gwinn M.L., Kolonay J.P., Sullivan S.A., Haft D.H., Selengut J., Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.; "Genome of Geobacter sulfurreducens: metal reduction in subsurface environments."; Science 302:1967-1969(2003).
RL	Science 302:1967-1969(2003).
RN	EMBL; AB017180; AAC34536.1; -; Genomic_DNA.
DR	TIGR; GSU1160; -;
DR	GO; GO:0042597; C:periplasmic space; IEA.
DR	GO; GO:0016491; P:oxidoreductase activity; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
KW	Complete proteome; Copper; Hypothetical protein; Metal-binding; Oxidoreductase; Periplasmic.
KX	Oxidoreductase; Periplasmic.
SQ	SEQUENCE 137 AA; 15272 MW; 3C3F00FFDD6B2FC7 CRC64;
Query Match	91.2%; Score 31; DB 2; Length 137;
Best Local Similarity	85.7%; Pred. No. 57;
Matches	6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KGLVFFA 7    :
Dd	116 KGLLFFA 122
RESULT 7	
Q4QLX3_HAEI8	
ID	Q4QLX3_HAEI8 PRELIMINARY; PRT; 176 AA.
AC	Q4QLX3;
DT	13-SEP-2005 (TrEMBLrel. 31, Created)
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE	Probable thiol-disulfide interchange protein Debe.
GN	Name:dsb2; OrderedLocNames:NTH1106;
OS	Haemophilus influenzae (strain 86-028NP).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC	Pasteurellaceae; Haemophilus.
OX	NCBI_TaxID=281310;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	PubMed:1968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA	Harrison A., Dyer D.W., Gillespy A., Ray W.C., Mungur R., Carson M.B., Zhong H., Gipson J.J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O., Munson R.S. Jr.; "Genomic sequence of an otitis media isolate of nontypeable Haemophilus influenzae: comparative study with H. influenzae serotype d, strain KW20." J. Bacteriol. 187:4627-4636(2005).
CC	-1- FUNCTION: Involved in disulfide bond formation. Catalyzes a late, reductive step in the assembly of periplasmic c-type cytochromes, probably the reduction of disulfide bonds of the apocytochrome c to allow covalent linkage with the heme. Possible subunit of a heme lyase (by similarity).
CC	-1- SUBCELLULAR LOCATION: Mostly periplasmic; anchored in the inner membrane (By similarity).
CC	EMBL; CP000057; AAX87974.1; -; Genomic_DNA.
DR	InterPro; IPR004799; DabE.
DR	InterPro; IPR006662; Thiorred.
DR	InterPro; IPR006663; Thiorredoxin_dom2.
DR	InterPro; IPR012336; Thiorredoxin-like.
DR	InterPro; IPR011594; Thiorredoxin_like.
DR	PRINTS; PR00421; THIORREDOXIN.
DR	ProDom; PD003679; Thiorredoxin_like; 1.
DR	TIGRFAMs; TIGR003185; dabE; 1.
DR	PROSITE; PS00194; THIORREDOXIN; UNKNOWN_1.
KW	Complete proteome; Cytochrome c-type biogenesis; Inner membrane; Membrane; Redox-active center; Transmembrane.
KX	Membrane; Redox-active center; Transmembrane.
SQ	SEQUENCE 176 AA; 19783 MW; 19A38F868C161582 CRC64;
Query Match	91.2%; Score 31; DB 2; Length 176;
Best Local Similarity	85.7%; Pred. No. 71;
Matches	6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

RC STRAIN=Coel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINS=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartesch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Waezler A., Baumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Mechanosarcina mazeli: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AS013463; AM31913.1; -: Genomic DNA.
DR GO; GO:0005794; C:Golgi apparatus; IEA.
DR InterPro; IPR001173; Glyco_transf_2; 1.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 314 AA; 36354 MW; A8BAB274A44808B7 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 314;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 158 KKLVPFS 164
|||||:

RESULT 10
Q4HSJ7 CAMUP
ID Q4HSJ7_CAMUP PRELIMINARY; PRT; 362 AA.
AC Q4HSJ7_
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hydrogenase expression/formation protein Hypd.
GN Name=hypd; ORFNames=CUP0294;
OS Campylobacter upsaliensis RM3195.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306264;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM3195;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFJ01000002; FAL5713.1; -: Genomic DNA.
SQ SEQUENCE 362 AA; 40365 MW; 15B0A8B12B60C8AD CRC64;

Query Match 91.2%; Score 31; DB 2; Length 362;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 131 KKIIFPA 137
|||||:

RESULT 11
Q9K110_BACCE
ID Q9K110_BACCE PRELIMINARY; PRT; 387 AA.
AC Q9K110;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GerN.

```

```

GN Name=gerN;
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1396;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC10876;
RX MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;
RA Thackray P.D., Bhargava J., Southworth T.W., Moir A.;
RT "GerN, an antiporter homologue important in germination of Bacillus
RT cereus endospores.";
RL J. Bacteriol. 183:476-482(2001).
DR EMBL; AF246294; AAF91326.1; -: Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41093 MW; 40DE45B71B715D01 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 183 KKVFFA 189
|||||:

RESULT 12
Q4MT39_BACCE
ID Q4MT39_BACCE PRELIMINARY; PRT; 387 AA.
AC Q4MT39;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Na+/H+ antiporter.
GN ORFNames=BCE_G9241_1647;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maitland M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAER01000008; FAL15336.1; -: Genomic DNA.
SQ SEQUENCE 387 AA; 41122 MW; 15CC136E9B1C38 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 183 KKVFFA 189
|||||:

```



Db 183 KKVFFFA 189

# RESULT 13

ID Q63DD4\_BACCCZ  
AC Q63DD4\_BACCCZ PRELIMINARY; PRT; 387 AA.  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Na+/H+ exchanger family protein.  
GN Name=gerN;  
OS Bacillus cereus (strain ZK).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=288681;  
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RT "Complete genome sequence of Bacillus cereus ZK.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CP000001; AYL18770.1; -; Genomic\_DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0008324; C:cation transporter activity; IEA.  
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006885; P:regulation of pH; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR004771; K\_eff.  
DR InterPro; IPR006153; Na\_H\_porter.  
DR Pfam; PF00999; Na\_H\_Exchange; 1.  
DR TIGRFAMs; TIGR00932; 2a37; 1.  
KW Complete proteome; Transmembrane; Transport.  
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;  
Best Local Similarity 85.7%; Pred. NO. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7

Db 183 KKVFFFA 189

# RESULT 14

ID Q6HKU6\_BACHK  
AC Q6HKU6\_BACHK PRELIMINARY; PRT; 387 AA.  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Na+/H+ exchanger family protein.  
GN Name=gerN; OrderedLocusNames=B79727\_1493;  
OS Bacillus thuringiensis (subsp. konkukian).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=180856;  
RN [1]

# NUCLEOTIDE SEQUENCE.

RP STRAIN=97-27;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB017355; AAT63168.1; -; Genomic\_DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0008324; C:cation transporter activity; IEA.  
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006885; P:regulation of pH; IEA.

DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR004771; K\_eff.  
DR InterPro; IPR006153; Na\_H\_porter.  
DR Pfam; PF00999; Na\_H\_Exchange; 1.  
DR TIGRFAMs; TIGR00932; 2a37; 1.  
KW Complete proteome; Transmembrane; Transport.  
SQ SEQUENCE 387 AA; 41076 MW; DFPECAD90985P951 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;  
Best Local Similarity 85.7%; Pred. NO. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7

Db 183 KKVFFFA 189

# RESULT 15

ID Q73AP3\_BACCI PRELIMINARY; PRT; 387 AA.  
AC Q73AP3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Germination protein gerN.  
DE OrderedLocusNames=BCE1729;  
GN OrderedLocusNames=BCE1729;  
OS Bacillus cereus (strain ATCC 10987).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=22523;  
RN [1]

# NUCLEOTIDE SEQUENCE.

RP PubMed=14960714; DOI=10.1093/nar/gkh258;  
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,  
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,  
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;  
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1.";  
RL Nucleic Acids Res. 32:1977-988(2004).  
DR EMBL; AE017269; AAS40658.1; -; Genomic\_DNA.  
DR TIGR; BCE1729; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0008324; C:cation transporter activity; IEA.  
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006885; P:regulation of pH; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR004771; K\_eff.  
DR InterPro; IPR006153; Na\_H\_porter.  
DR Pfam; PF00999; Na\_H\_Exchange; 1.  
DR TIGRFAMs; TIGR00932; 2a37; 1.  
KW Complete proteome; Transmembrane; Transport.  
SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FEB33 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;  
Best Local Similarity 85.7%; Pred. NO. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7

Db 183 KKVFFFA 189

# RESULT 16

ID Q81SK9\_BACAN  
AC Q81SK9\_BACAN PRELIMINARY; PRT; 387 AA.  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Germination protein gerN.  
DE OrderedLocusNames=BA1639;  
OS Bacillus anthracis.



OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=1392;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Ames / isolate Porton;  
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;  
 RA Read T.D., Peterson S.N., Toutsse N.J., Bailie L.W., Paulsen I.T.,  
 RA Nelson K.E., Tettelin H., Fouts D.B., Eisen J.A., Gill S.R.,  
 RA Kolczapple E.K., Oksad O.A., Helgason E., Rilstone J., Wu M.,  
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,  
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
 RA Nelson W.C., Peterson J.D., Pop M., Knouri H.M., Radune D.,  
 RA Benson J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,  
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,  
 RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,  
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;  
 RA "The genome sequence of *Bacillus anthracis* Ames and comparison to  
 RT closely related bacteria.";  
 RL Nature 423:81-86(2003).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Ames / isolate 0581;  
 RX Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,  
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,  
 RA Fraser C.M.;  
 RT "Bacillus anthracis comparative genomics.";  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Sterne;  
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
 RA Richardson P., Rubin E., Tice H.;  
 RT "Complete genome sequence of *Bacillus anthracis* Sterne.";  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AS017029; AAP25572.1; -; Genomic DNA.  
 DR EMBL; AS017334; AAT30749.1; -; Genomic DNA.  
 DR EMBL; AS017225; AAT53839.1; -; Genomic DNA.  
 DR TIGR; BA1639; -;  
 DR TIGR; GAA1639; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0008324; F:cation transporter activity; IEA.  
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR GO; GO:0006885; P:regulation of pH; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR004771; K\_eff.  
 DR InterPro; IPR006153; Na\_H\_porter.  
 DR Pfam; PF00999; Na\_H\_Exchange; 1.  
 DR TIGRFAMS; TIGR00932; 2a37; 1.  
 KW Complete proteome; Transmembrane; Transport.  
 SQ SEQUENCE 387 AA; 40932 MW; D59F6A08A283BCA3 CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 387;  
 Best Local Similarity 85.7%; Pred. NO. 1.4e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVEFA 7  
 Db 183 KKVVEFA 189  
 RESULT 17  
 OS0243 PYRHO  
 ID 059243 PYRHO PRELIMINARY; PRT; 447 AA.  
 AC 059243;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein PH1606.  
 GN Ordered locus names=PH1606;

OS Pyrococcus horikoshii.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID=53953;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=OT3;  
 RX MEDLINE=98344137; PubMed=9679194;  
 RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,  
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
 RA Masuchi Y., Shizuya H., Kikuchi H.;  
 RT "Complete sequence and gene organization of the genome of a hyper-  
 thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";  
 RL DNA Res. 5:55-76(1998).  
 DR EMBL; BA000001; BAA30718.1; -; Genomic DNA.  
 DR FIR; F71039; F71039.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005355; F:glucose transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR000803; Gluc transporter.  
 DR PRINTS; PR00172; GLUCTRNSPORT.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;  
 Query Match 91.2%; Score 31; DB 2; Length 447;  
 Best Local Similarity 71.4%; Pred. NO. 1.6e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVEFA 7  
 Db 206 KXIIFFA 212  
 RESULT 18  
 OS07931 9POTV  
 ID 037931 9POTV PRELIMINARY; PRT; 488 AA.  
 AC 037931;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Polypeptide (Fragment).  
 GN Name=Nib/CP;  
 OS Ceratobium mosaic potyvirus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 OX NCBI\_TaxID=66702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CerMV-13;  
 RX MEDLINE=98309067; PubMed=9645197; DOI=10.1007/s007050050341;  
 RA Mackenzie A.M., Nolan M., Wei K.J., Clements M.A., Gowanlock D.,  
 RA Wallace B.J., Gibbs A.J.;  
 RT "Ceratobium mosaic potyvirus: another virus from orchids.";  
 RL Arch. Virol. 143:903-914(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CerMV-13;  
 RA Gibbs A., Mackenzie A., Blanchfield A., Cross P., Wilson C.,  
 RA Kitajima E., Nightingale M., Clements M.;  
 RT "Viruses of orchids in Australia: their identification, biology and  
 RT control.";  
 RL Aust. Orchid Rev. 65:10-21(2000).  
 DR EMBL; AF022442; AAC59610.1; -; Genomic DNA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0004386; F:helicase activity; IEA.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 DR GO; GO:0019079; P:viral genome replication; IEA.

```

DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR001205; RNA_pol_P3D.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00767; Poty_coat; 1.
DR Pfam; PF00680; RdRP_1; 1.
DR KW Polyprotein. <1 211 NIB polymerase.
FT CHAIN 212 488 coat protein.
FT NON TER 1
SQ SEQUENCE 488 AA; 56094 MW; 86C48176140FBAE9 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 488;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGLVFFA 7
Db 37 KRLVFFA 43

RESULT 19
O37932_9POTV PRELIMINARY; PRT; 488 AA.
AC O37932;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
GN Name=NIB/CP;
OS Ceratobium mosaic potyvirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=66702;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CerMV-1;
RX MEDLINE=98309067; PubMed=9645197; DOI=10.1007/s007050050341;
RA Mackenzie A.M., Nolan M., Wei K.J., Clements M.A., Gowanlock D.,
Wallace B.J., Gibbs A.J.;
RT "Ceratobium mosaic potyvirus: another virus from orchids.";
RL Arch. Virol. 143:903-914(1998).
RN 2
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CerMV-1;
RA Gibbs A., Mackenzie A., Blanchfield A., Cross P., Wilson C.,
Kitajima E., Nightingale M., Clements M.;
RT "Viruses of orchids in Australia: their identification, biology and
control.";
RL Aust. Orchid Rev. 65:10-21(2000).
DR EMBL; AF022443; AAC59611.1; -; Genomic DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transcription; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR001205; RNA_pol_P3D.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00767; Poty_coat; 1.
DR Pfam; PF00680; RdRP_1; 1.
DR KW Polyprotein. <1 211 NIB polymerase.
FT CHAIN 212 488 coat protein.
FT NON TER 1
SQ SEQUENCE 488 AA; 55976 MW; 4D693009D3E5F83 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 488;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGLVFFA 7
Db 37 KRLVFFA 43

RESULT 21
O37934_9POTV PRELIMINARY; PRT; 488 AA.
AC O37934;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
GN Name=NIB/CP;
OS Ceratobium mosaic potyvirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.

```

```

Db 37 KRLVFFA 43

RESULT 20
O37933_9POTV PRELIMINARY; PRT; 488 AA.
AC O37933;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
GN Name=NIB/CP;
OS Ceratobium mosaic potyvirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=66702;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CerMV-6;
RX MEDLINE=98309067; PubMed=9645197; DOI=10.1007/s007050050341;
RA Mackenzie A.M., Nolan M., Wei K.J., Clements M.A., Gowanlock D.,
Wallace B.J., Gibbs A.J.;
RT "Ceratobium mosaic potyvirus: another virus from orchids.";
RL Arch. Virol. 143:903-914(1998).
RN 2
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CerMV-6;
RA Gibbs A., Mackenzie A., Blanchfield A., Cross P., Wilson C.,
Kitajima E., Nightingale M., Clements M.;
RT "Viruses of orchids in Australia: their identification, biology and
control.";
RL Aust. Orchid Rev. 65:10-21(2000).
DR EMBL; AF022444; AAC59612.1; -; Genomic DNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transcription; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR001205; RNA_pol_P3D.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00767; Poty_coat; 1.
DR Pfam; PF00680; RdRP_1; 1.
DR KW Polyprotein. <1 211 NIB polymerase.
FT CHAIN 212 488 coat protein.
FT NON TER 1
SQ SEQUENCE 488 AA; 56036 MW; 03514055B96B64F CRC64;

Query Match 91.2%; Score 31; DB 2; Length 488;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGLVFFA 7
Db 37 KRLVFFA 43

RESULT 21
O37934_9POTV PRELIMINARY; PRT; 488 AA.
AC O37934;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
GN Name=NIB/CP;
OS Ceratobium mosaic potyvirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.

```

```

OX NCBI_TaxID=66702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CerMV-18;
RX MEDLINE=98309067; PubMed=9645197; DOI=10.1007/s007050050341;
RA Mackenzie A.M., Nolan M., Wei K.J., Clements M.A., Gowanlock D.,
RA Wallace B.J., Gibbs A.J.;
RT "Ceratobium mosaic potyvirus: another virus from orchids.";
RL Arch. Virol. 143:903-914(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CerMV-19;
RA Gibbs A., Mackenzie A., Blanchfield A., Cross P., Wilson C.,
RA Kitajima E., Nightingale M., Clements M.;
RT "Viruses of orchids in Australia: their identification, biology and
RT control.";
RL Aust. Orchid Rev. 65:10-21(2000).
DR EMBL: AF022445; AAC59613.1; -; Genomic_DNA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0004386; F:helicase activity; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR GO: GO:0019079; P:viral genome replication; IEA.
DR InterPro: IPR001592; Poty coat.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_P5vir.
DR Pfam: PF00767; Poty coat; 1.
DR Pfam: PF00680; RdRP_1; 1.
KW Polyprotein.
FT CHAIN <1 211 Nib polymerase.
FT CHAIN 212 488 coat protein.
FT NON_TER 1 1
SQ SEQUENCE 488 AA; 55976 MW; 1DCAEF91D1813C8 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 488;
Best Local Similarity 85.7%; Pred. NO. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 37 KRLVPFA 43

RESULT 22
QSAU77 EMENI
ID Q5AU77_EMENI PRELIMINARY; PRT; 697 AA.
AC Q5AU77;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN8153.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collimore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gierke S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt T., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

```

```

RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AAC001000141; EAA59175.1; -; Genomic_DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR InterPro: IPR003593; AAA_ATPase_cent.
DR InterPro: IPR003959; AAA_ATPase_cent.
DR Pfam: PF00004; AAA; 1.
DR SMART: SM00382; AAA; 1.
KW ATP-binding; Hypothetical protein; Nucleotide-binding.
SQ SEQUENCE 697 AA; 78657 MW; DED32691DD5754A CRC64;

Query Match 91.2%; Score 31; DB 2; Length 697;
Best Local Similarity 85.7%; Pred. NO. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 123 KKLVPFA 129

RESULT 23
Q563A1 BCMVN
ID Q563A1 BCMVN PRELIMINARY; PRT; 3222 AA.
AC Q563A1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Polyprotein.
OS Peanut stripe virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=28353;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang H.L., Chang Y.Y.;
RT "Molecular sequencing and analysis of the viral genome of Peanut
RT stripe virus Ts strain.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY968604; AAX82171.1; -; Genomic_RNA.
KW Polyprotein.
FT CHAIN 1 443 P1 protein.
FT CHAIN 444 900 HC-Pro protein.
FT CHAIN 901 1247 P3 protein.
FT CHAIN 1248 1299 6K1 protein.
FT CHAIN 1934 1986 6K2 protein.
FT CHAIN 1987 2176 VPg protein.
FT CHAIN 2177 2419 NIa protein.
FT CHAIN 2420 2935 Nib protein.
FT CHAIN 2936 3222 coat protein.
SQ SEQUENCE 3222 AA; 365455 MW; AC20BF23721EC338 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 3222;
Best Local Similarity 85.7%; Pred. NO. 9.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 2761 KKLVPFA 2767

RESULT 24

```

```
Q9UC33_HUMAN
ID Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RA MDLINE=3024877; PubMed=1406936; DOI=10.1038/359325a0;
RX Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RX Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids".
RL Nature 359:325-327(1992).
DR HSP; Q16019; 1BA4.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS; PR0204; BETAAMYLOID.
SQ SEQUENCE 33 AA; 3674 MW; B1DEFE2F4167ABD0 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 33;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 15 QKLVPFA 21

RESULT 25
Q9XQR5_PEA
ID Q9XQR5_PEA PRELIMINARY; PRT; 34 AA.
AC Q9XQR5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Pisum sativum (Garden pea).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lehbeck J., Stummann B.M., Henningsen K.W.;
RT "Nucleotide sequence of the 5.6 kbp psbB operon of pea chloroplast
RT DNA.".
RL Physiol. Plantarum 76:57-64(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lehbeck J., Stummann B.M., Henningsen K.W.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF153442; AA041885.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009539; C:photosystem II reaction center; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro: IPR001743; PSII_PsbT.
DR Pfam: PF01405; PsbT; 1.
DR ProDom: PD004453; PSII_PsbT; 1.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 34 AA; 4005 MW; F99C563A18BD170 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 13 KKLVPFA 19

RESULT 26
Q56J36_GRAGR
ID Q56J36_GRAGR PRELIMINARY; PRT; 42 AA.
AC Q56J36;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926589; AAX81918.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 15 QKLVPFA 21

RESULT 27
Q56J37_TURTR
ID Q56J37_TURTR PRELIMINARY; PRT; 42 AA.
AC Q56J37;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926588; AAX81917.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 15 QKLVPFA 21

RESULT 28
```

Q7M088\_CAVPO  
 ID Q7M088\_CAVPO PRELIMINARY; PRT; 42 AA.  
 AC Q7M088;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Beta-amyloid protein (Fragment).  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 OC Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=93290653; PubMed=76855598;  
 RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,  
 RA Kamiya H., Ohno M.;  
 RT "Receptor-mediated specific biological activity of a beta-amyloid  
 RT protein fragment for NK-1 substance p receptors.";  
 RL Biochem. Biophys. Res. Commun. 193:624-630(1993).  
 DR PIR; P05112; P0512.  
 DR HSSP; Q16019; ILYT.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 42  
 SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;  
 Query Match 88.2%; Score 30; DB 2; Length 42;  
 Best Local Similarity 85.7%; Pred. No. 34;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db :|||||  
 15 QKLVPFA 21

Q8WZ99\_HUMAN  
 ID Q8WZ99\_HUMAN PRELIMINARY; PRT; 52 AA.  
 AC Q8WZ99;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Amyloid protein (Fragment).  
 GN NamesAPP;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;  
 RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,  
 RA Ninomiya H., Saido TC., Hashimoto T., Iwatsubo T., Nakashima K.;  
 RT "Novel amyloid precursor protein gene missense mutation (D678N) in  
 RT Probable familial Alzheimer's disease.";  
 RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).  
 DR EMBL; AB066441; BAB71958.2; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 52  
 SQ SEQUENCE 52 AA; 5597 MW; 3F0E8E9EC18011AD CRC64;  
 Query Match 88.2%; Score 30; DB 2; Length 52;

Q7M088\_CAVPO PRELIMINARY; PRT; 42 AA.  
 AC Q7M088;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Beta-amyloid protein (Fragment).  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 OC Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=93290653; PubMed=76855598;  
 RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,  
 RA Kamiya H., Ohno M.;  
 RT "Receptor-mediated specific biological activity of a beta-amyloid  
 RT protein fragment for NK-1 substance p receptors.";  
 RL Biochem. Biophys. Res. Commun. 193:624-630(1993).  
 DR PIR; P05112; P0512.  
 DR HSSP; Q16019; ILYT.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 42  
 SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;  
 Query Match 88.2%; Score 30; DB 2; Length 42;  
 Best Local Similarity 85.7%; Pred. No. 34;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db :|||||  
 15 QKLVPFA 21

Q8WZ99\_HUMAN PRELIMINARY; PRT; 52 AA.  
 AC Q8WZ99;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Amyloid protein (Fragment).  
 GN NamesAPP;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;  
 RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,  
 RA Ninomiya H., Saido TC., Hashimoto T., Iwatsubo T., Nakashima K.;  
 RT "Novel amyloid precursor protein gene missense mutation (D678N) in  
 RT Probable familial Alzheimer's disease.";  
 RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).  
 DR EMBL; AB066441; BAB71958.2; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 52  
 SQ SEQUENCE 52 AA; 5597 MW; 3F0E8E9EC18011AD CRC64;  
 Query Match 88.2%; Score 30; DB 2; Length 52;

Best Local Similarity 85.7%; Pred. No. 42;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLVPFA 7  
 Db :|||||  
 15 QKLVPFA 21

RESULT 30  
 A4 URSMA  
 ID A4 URSMA STANDARD; PRT; 57 AA.  
 AC Q29149;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-  
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);  
 DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase  
 DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal  
 DE fragment 57)] (Fragment).  
 GN Name=APP;  
 OS Ursus maritimus (Polar bear) (Thalarcos maritimus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;  
 OC Ursus.  
 OX NCBI\_TaxID=29073;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -!- FUNCTION: Functional neuronal receptor which couples to  
 CC intracellular signaling pathway through the GTP-binding protein  
 CC G(O) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X56128; CAA39593.1; -; mRNA.  
 DR PIR; B60045; B60045.  
 DR HSSP; P08592; INMJ.  
 DR InterPro; IPR008155; A4 APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR PROSITE; PS00319; A4 EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4 INTRA; PARTIAL.  
 KW Amyloid; Transmembrane.  
 FT CHAIN <1 5 Soluble APP-beta (By similarity).  
 FT CHAIN 6 >57 CTF-alpha (By similarity).  
 FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).  
 FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).  
 FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).  
 FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).  
 FT TOPO\_DOM <1 33 Extracellular (Potential).  
 FT TRANSMEM 34 57 Potential.  
 FT NON\_TER 1  
 FT NON\_TER 57  
 SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;  
 Query Match 88.2%; Score 30; DB 1; Length 57;  
 Best Local Similarity 85.7%; Pred. No. 45;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFA 7  
:|||||  
Db 20 QKLVEFA 26

```

RESULT 31
A4_CANFA STANDARD; PRT; 58 AA.
ID_A4_CANFA
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN NUCLEOTIDE SEQUENCE.
[1]
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G1O (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
-----
This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
EMBL; X56125; CRA39590.1; -; mRNA.
DR HSP; P08592; INMJ.
DR Ensembl; ENSGAF00000008557; Canis familiaris.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >58 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
Query Match 88.2%; Score 30; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 KKLVEFA 7  
:|||||  
Db 20 QKLVEFA 26

```

RESULT 32
A4_RABIT STANDARD; PRT; 58 AA.
ID_A4_RABIT
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN NUCLEOTIDE SEQUENCE.
[1]
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G1O (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
-----
This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
EMBL; X56129; CRA39594.1; -; mRNA.
DR HSP; P08592; INMJ.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
Query Match 88.2%; Score 30; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 33
A4 SHEEP
ID_ A4 SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56130; CAA39595.1; -, mRNA.
DR HSSP; P08592; INMU.
DR InterPro; IPR008155; A4_APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 88.2%; Score 30; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
Db 20 QKLVEFA 26

RESULT 34
A4 BOVIN
ID_ A4 BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56124; CAA39589.1; -, mRNA.
DR EMBL; X56126; CAA39591.1; -, mRNA.
DR HSSP; P08592; INMU.
DR InterPro; IPR008155; A4_APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >59 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >59 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >59 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT TOPO_DOM 59 >59 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 88.2%; Score 30; DB 1; Length 59;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
Db 21 QKLVEFA 27

RESULT 35

```



Query Match	88.2%;	Score 30;	DB 2;	Length 94;
Best Local Similarity	85.7%;	Pred. No. 70;		
Matches	6; Conservative	1; Mismatches	0; Indels	0; Gaps
Query Match	88.2%;	Score 30;	DB 2;	Length 94;
Best Local Similarity	85.7%;	Pred. No. 70;		
Matches	6; Conservative	1; Mismatches	0; Indels	0; Gaps



```
RESULT 39
QB1X8 STRP3
ID QB1X8 STRP3 PRELIMINARY; PRT; 94 AA.
AC QB1X8_07CF33;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein SP61439 (Hypothetical protein spyM3_0416).
GN OrderedLocusNames=SP61439, spyM3_0416;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301448;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSI-1 / Serotype M3;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Berra S.B., Sylva G.B., Barbian K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
DR EMBL; BA000034; BAC64534.1; -; Genomic DNA.
DR EMBL; AB014144; AAM79023.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 94 AA; 10579 MW; FE5064A8B849FED0 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 94;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
DB 38 KSLVFFA 44
|:|||||

RESULT 40
QB1H58 CHESE
ID QB1H58 CHESE PRELIMINARY; PRT; 113 AA.
AC QB1H58;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Ocylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AAN04908.1; -; mRNA.
DR HSSP; Q16019; IIYT.
```

```
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00204; BETAAMYLOID.
FT NON TER 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
DB 29 QRLVFFA 35
|:|||||

RESULT 41
Q5TUI4 ANOGA
ID Q5TUI4 ANOGA PRELIMINARY; PRT; 125 AA.
AC Q5TUI4;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE ENGANGP0000025864 (Fragment).
GN Name=CTL2; ORFNames=ENGANGG0000022826;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008848; EAL41080.1; -; Genomic DNA.
DR GO; GO:0005529; F: sugar binding; IEA.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; Lectin C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
FT NON TER 1
FT NON TER 125
SQ SEQUENCE 125 AA; 14081 MW; F4BC758D6262EA7F CRC64;

Query Match 88.2%; Score 30; DB 2; Length 125;
Best Local Similarity 85.7%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
DB 7 KKLTFFA 13
|:|||||

RESULT 42
FABZ DESPS
ID FABZ DESPS STANDARD; PRT; 150 AA.
AC Q6AJ07;
DT 10-MAY-2005 (Rel. 47, Created)
```

DT 10-MAY-2005 (Rel. 47, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE (3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase (BC 4.2.1.1.-)  
 DE (3R)-hydroxymyristoyl ACP dehydratase)  
 GN Name=fabZ; OrderedLocusNames=DP2944;  
 OS Desulfotalea psychrophila  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;  
 OC Desulfobulbaceae; Desulfotalea  
 OX NCBI\_TaxID=84980;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=LSV54 / DSM 12343;  
 RX PubMed=15305914; DOI=10.1101/1462-2920.2004.00665.x;  
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Partmann B., Stark M.,  
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,  
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,  
 RA Klenk H.-P.;  
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium  
 RT from permanently cold Arctic sediments.";  
 RL Environ. Microbiol. 6:887-902(2004).  
 CC -1- FUNCTION: Involved in saturated fatty acids biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; CR522870; CAG37673.1; -, Genomic\_DNA.  
 DR HAMAP; MP 00406; -, 1.  
 DR InterPro; IPR010084; FabZ.  
 DR TIGRPFAMs; TIGR01750; fabZ; 1.  
 KW Complete proteome; Lipid A biosynthesis; Lipid synthesis; Lyase.  
 FT ACT\_SITE 56 56 By similarity  
 FT ACT\_SITE 56 56 By similarity  
 SQ SEQUENCE 150 AA; 16687 MW; 37FA4FC716389219 CRC64;  
  
 Query Match 88.2%; Score 30; DB 1; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 1 KKLVPFA 7  
 Db 90 KKLAPFA 96  
 ||| |||  
  
 RESULT 43  
 Q6CKL1\_KLUJL  
 ID Q6CKL1\_KLUJL PRELIMINARY; PRT; 165 AA.  
 AC Q6CKL1;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Similar to sp|Q12322 Saccharomyces cerevisiae YOL114c singleton.  
 GN OrderedLocusNames=KLUJL007381g;  
 OS Kluyveromyces lactis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC PubMed=15229592; DOI=10.1038/nature02579;  
 RX DuJong B., Sherman D., Fischer G., Durrien P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neugebauer C., Talia E.,  
 RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boisdame A., Boyer J., Catholico L., Confanioli F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantraye P., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicaud J.-M., Nikolski M., Ozcas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,

RA Swennen D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Bach J.,  
 RA Bouchier C., Caudion B., Scarpetti C., Gallardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in yeasts.";  
 RL Nature 430:35-44(2004).  
 DR EMBL; CR182121; CAH02916.1; -, Genomic DNA.  
 DR GO; GO:0003747; P:translation release factor activity; IEA.  
 DR GO; GO:0006415; P:translational termination; IEA.  
 DR InterPro; IPR000352; Pep\_rel\_factor\_1.  
 DR Pfam; PF00472; RF-1; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 165 AA; 19350 MW; EEDF94B5004EFD93 CRC64;  
  
 Query Match 88.2%; Score 30; DB 2; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 KKLVPF 6  
 Db 117 KKLVPF 122  
 |||||  
  
 RESULT 44  
 Q4TUZ7\_MAIZE  
 ID Q4TUZ7\_MAIZE PRELIMINARY; PRT; 187 AA.  
 AC Q4TUZ7;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Atypical receptor-like kinase MARK (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Ohtsu K., Hake S.C., Schnable P.S.;  
 RT "SAM control genes.";  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; DQ056240; AAY57565.1; -, mRNA.  
 KW Kinase; Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 187 187  
 SQ SEQUENCE 187 AA; 18072 MW; E5291DD1F65F8FB8 CRC64;  
  
 Query Match 88.2%; Score 30; DB 2; Length 187;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 KKLVPF 6  
 Db 152 KKLVPF 157  
 |||||  
  
 RESULT 45  
 Q64ME8\_BACFR  
 ID Q64ME8\_BACFR PRELIMINARY; PRT; 214 AA.  
 AC Q64ME8;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocusNames=BFP0012;  
 OS Bacteroides fragilis.  
 OC Bacteroidetes; Bacteroidales; Bacteroidia; Bacteroidaceae; Bacteroides.  
 OX NCBI\_TaxID=817;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=YCH46;

```

RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuwaha S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RL inversions regulating cell surface adaptation.";
RA Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924 (2004).
DR EMBL; AF006842; BAD51339.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 214 AA; 25216 MW; CESD86CD4212ADC8 CRC64;

Query Match      88.2%; Score 30; DB 2; Length 214;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
DB 2 KKLIFS 8

RESULT 46
QBPPV5 MOUSE
ID Q8BPV5 MOUSE PRELIMINARY; PRT; 218 AA.
AC Q8BPV5
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
DE library, clone: D430025B14 product: amyloid beta (A4) protein, full
DE insert sequence. (Fragment).
GN Name: App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga M., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald W., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

```

```

RL Nature 420:563-573 (2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayase N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Harada A.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara S., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK052448; BAC34997.1; -; mRNA.
DR HSP; P08592; 1NMJ.
DR MGI; MGI:88059; App.
DR GO; GO:0016021; C: integral to membrane; IDA.
DR GO; GO:0016020; C: membrane; TAS.
DR GO; GO:0005515; F: protein binding; IPI.
DR GO; GO:0030198; F: extracellular matrix organization and bioge. .; IGI.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;

Query Match      88.2%; Score 30; DB 2; Length 218;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
DB 134 QKLVFFA 140

RESULT 47
Q84MC9 BACFR PRELIMINARY; PRT; 228 AA.
AC Q84MC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BFP0031;

```

```

OS Bacteroides fragilis.
OG Plasmid pBFY46.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
ON NCBI_TaxID=817;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924 (2004).
RW EMBL; AP006842; BAD51358.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 228 AA; 25837 MW; 2A53B2BB05742631 CRC64;

Query Match      88.2%; Score 30; DB 2; Length 228;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
DB 2 KKLIFPS 8

RESULT 48
Q7MV75_PORGI
ID Q7MV75_PORGI PRELIMINARY; PRT; 270 AA.
AC Q7MV75;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lipoprotein protein, putative.
GN OrderedLocusNames=FG1215;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
ON NCBI_TaxID=837;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601 (2003).
RW EMBL; AB017176; AAQ66305.1; -; Genomic_DNA.
RX TIGR; FG1215; -.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like helical.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 270 AA; 31551 MW; DA058B9B99FF6A5D CRC64;

Query Match      78.2%; Score 30; DB 2; Length 270;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
DB 4 KKLIFPA 10

RESULT 49
Q74HY9_LACJO
ID Q74HY9_LACJO PRELIMINARY; PRT; 336 AA.
AC Q74HY9;

```

```

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=LJ0670;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
ON NCBI_TaxID=33959;
RX [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 533;
RX PubMed=14983040; DOI=10.1073/pnas.0307327101;
RA Pridmore R.D., Berger B., Desiere P., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).
RW EMBL; AB017205; AAS09551.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 336 AA; 37650 MW; F97C983851FBF1CC CRC64;

Query Match      88.2%; Score 30; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFF 6
DB 258 KKLVFF 263

RESULT 50
Q9PMW9_CAMJE
ID Q9PMW9_CAMJE PRELIMINARY; PRT; 346 AA.
AC Q9PMW9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative fucose synthetase.
GN Names=fcl; OrderedLocusNames=Cj1428c;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
ON NCBI_TaxID=197;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Kettle J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RW EMBL; AL139078; CAB73852.1; -; Genomic_DNA.
RX Nature 403:665-668 (2000).
DR EMBL; D81288; D81288.
DR HSP; P32055; IE6U.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 346 AA; 39431 MW; DF7D95EB5630FC3 CRC64;

Query Match      88.2%; Score 30; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFF 6
DB 100 KKLVFF 105

```

```

RESULT 51
Q8UUI8 BRARE
ID Q8UUI8 BRARE PRELIMINARY; PRT; 357 AA.
AC Q8UUI8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative membrane protein (Fragment).
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole embryo;
RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
RA Musa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
RT APP gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ315637; CAC85734.1; -; mRNA.
DR HSSP; Q16019; IHZ3.
DR SMR; Q8UUI8; 62-170.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:Binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF03494; Beta_APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 357 AA; 40962 MW; 07D99BEF6C55B2D8 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 357;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 273 QKLVPFA 279

RESULT 52
MLTA_BUCAI
ID MLTA_BUCAI STANDARD; PRT; 359 AA.
AC P57531;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Membrane-bound lytic murein transglycosylase A homolog (EC 3.2.1.-)
DE (Murein hydrolase A).
DE (Murein hydrolase A).
GN Name=mlta; OrderedLocNames=BU458;
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077; DOI=10.1038/35024074;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -!- FUNCTION: Murein-degrading enzyme. May play a role in recycling of
CC muropeptides during cell elongation and/or cell division (By
CC similarity).

```

```

CC -!- CATALYTIC ACTIVITY: Cleavage of the beta-1,4-glycosidic bond
CC between N-acetylmuramic acid and N-acetylglucosamine residues,
CC thereby conserving the energy in a newly synthesized 1,6-
CC anhydrobond in the muramic acid residue.
CC -!- SUBCELLULAR LOCATION: In closeley related bacteria this protein is
CC attached to the outer membrane by a lipid anchor. This is
CC apparently not the case here.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000003; BAB13155.1; -; Genomic_DNA.
CC InterPro; IPR010611; 3D.
CC InterPro; IPR005300; MltA.
CC Pfam; PF06725; 3D; 1.
CC Pfam; PF03562; MltA; 1.
KW Cell wall; Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 359 AA; 41773 MW; 24E12A2778D351AB CRC64;

Query Match 88.2%; Score 30; DB 1; Length 359;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 196 KKLIPFS 202

RESULT 53
O67225 AQUAE
ID O67225 AQUAE PRELIMINARY; PRT; 380 AA.
AC O67225;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hydrogenase expression/formation protein HypD.
DE Name=hypd; OrderedLocNames=AQ_1157;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AE000726; AAC07185.1; -; Genomic_DNA.
DR PIR; F70399; F70399.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrgn_mat_hypd; 1.
DR TIGRFAMs; TIGR00075; hypd; 1.
KW Complete proteome.
SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 380;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 140 KKLVPFA 146

RESULT 54
Q8BPC7_MOUSE

```

```

ID QBBPCT_MOUSE PRELIMINARY; PRT; 384 AA.
AC QBBPCT;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
DE library, clone:483432109 product:amyloid beta (A4) protein, full
DE insert sequence. (Fragment).
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Ishii Y., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Orawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

```

```

RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagata T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK076506; BAC36369.1; -, mRNA.
DR HSSP; P08592; INMJ.
DR SNR; Q8BPC7; 74-183.
DR MGI; MGI:88059; App.
DR GO; GO:0016021; C:integral to membrane; IDA.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0030198; P:extracellular matrix organization and biogenesis; IGI.
DR InterPro; IPR008155; A4_APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR0203; AMYLOIDA4.
DR PRINTS; PR0204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 384;
Best Local Similarity 85.7%; Pred.No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 300 QKLVPFA 306

RESULT 55
Q83DX9 COXBU
ID Q83DX9 COXBU PRELIMINARY; PRT; 426 AA.
AC Q83DX9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=CBU0562;
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Nine Mile phase I / RSA 493;
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA Sehadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Daviden T.M., Beanan M.J.,
RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
RT burnetii.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
DR EMBL; AE016961; AA090106.1; -, Genomic_DNA.
DR TIGR; CBU0562; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 426 AA; 49687 MW; 0BA2844C7E052CB2 CRC64;

```

```

Query Match      88.2%; Score 30; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 6
DB      237 KKLVPFF 242

RESULT 56
Q8U50_BRARE
ID Q8U50_BRARE PRELIMINARY; PRT; 472 AA.
AC Q8U50;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative membrane protein (Fragment).
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
RA Musa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
  APP gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ315636; CAC85733.1; -; mRNA.
DR HSP; Q16019; 1H23.
DR SMR; Q8U50; 177-285.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; ANYLOID4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 472 AA; 53787 MW; 24F7128BE3356550 CRC64;

Query Match      88.2%; Score 30; DB 2; Length 472;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 7
DB      388 KKLVPFF 394

RESULT 57
Q9X152_ARATH
ID Q9X152_ARATH PRELIMINARY; PRT; 479 AA.
AC Q9X152;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F9L1.11 protein.
GN Name=F9L1.11;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
KW Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
  Vysotskaia I., Luros J., Gonzalez A.,
  Altafi H., Araujo R., Brooks S., Buehler E., Chao Q., Conn L.,
  Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C.,
  Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R.,
  Pederspiel N.A., Theologis A.,
  Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007591; AAD39644.1; -; Genomic_DNA.
DR PIR; F86285; F86285.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:antipporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; F:multidrug transport; IEA.
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; MatE; 2.
DR TIGRFAMs; TIGR00797; matE; 1.
SQ SEQUENCE 479 AA; 52123 MW; 05D2044C9331806B CRC64;

Query Match      88.2%; Score 30; DB 2; Length 479;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 7
DB      36 KKLIFFA 42

RESULT 58
Q8L731_ARATH
ID Q8L731_ARATH PRELIMINARY; PRT; 481 AA.
AC Q8L731;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein Atg15170.
GN Name=Atg15170;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
  Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
  Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
  Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
  Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
  Ecker J., Theologis A., Davis R.W.;
  Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RP NUCLEOTIDE SEQUENCE.
RA Palm C.J., Davis R.W.;
  Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
  Dale J.M., Hayashizaki Y., Huan V.W., Ishida J., Jones T., Kamiya A.,
  Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
  Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
  Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
  Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
  Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY139985; AAM38128.1; -; mRNA.
DR EMBL; BT006616; AAP31960.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:antipporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; F:multidrug transport; IEA.
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; MatE; 2.
DR TIGRFAMs; TIGR00797; matE; 1.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52188 MW; 47876B51B57CE760 CRC64;

```



Query Match 88.2%; Score 30; DB 2; Length 491;  
 Best Local Similarity 71.4%; Pred. No. 3e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
 Db 36 KRLIFFA 42

RESULT 59  
 Q5K4D4\_9POTV PRELIMINARY; PRT; 493 AA.  
 AC Q5K4D4;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Polypeptide (Fragment).  
 OS Soybean mosaic virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 OC NCBI\_TaxID=12222;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=P;  
 RX PubMed=15449140; DOI=10.1007/s00705-004-0390-z;  
 RA Shi Y.H., Hong X.Y., Chen J., Adams M.J., Zheng H.Y., Lin L.,  
 RA Qing B.X., Chen J.;  
 RT "Further molecular characterisation of potyviruses infecting aroid  
 plants for medicinal use in China.";  
 RL Arch. Virol. 150:125-135(2005).  
 DR EMBL; AJ628752; C: viral capsid; IEA.  
 DR GO; GO:0019028; C: viral capsid; IEA.  
 DR GO; GO:0003968; F: RNA-directed RNA polymerase activity; IEA.  
 DR GO; GO:0019079; F: viral genome replication; IEA.  
 DR InterPro; IPR001592; Poty. coat.  
 DR InterPro; IPR001205; RNA\_pol\_PSD.  
 DR InterPro; IPR007094; RNA\_pol\_PSD.  
 DR Pfam; PF00676; Poty. coat; 1.  
 DR Pfam; PF00680; RdRp\_1; 1.  
 KW Capsid protein; Polyprotein.  
 FT CHAIN <1 211  
 FT CHAIN 212 493 coat protein.  
 FT NON TER 1  
 SQ SEQUENCE 493 AA; 55921 MW; 0898559BD4C19F6F CRC64;

Query Match 88.2%; Score 30; DB 2; Length 493;  
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
 Db 37 EKLVPFA 43

RESULT 60  
 O93296\_CHICK PRELIMINARY; PRT; 534 AA.  
 AC O93296;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Amyloid protein (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98337885; PubMed=9671674;  
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
 RA Milligan C.E.;

RT "Increased production of amyloid precursor protein provides a  
 substrate for caspase-3 in dying motoneurons.";  
 RL J. Neurosci. 18:5869-5880(1998).  
 DR EMBL; AF042098; AAC25052.1; -; mRNA.  
 DR HSP; Q16019; IYT.  
 DR SNR; O93296; 224-333.  
 DR Ensembl; ENSGALG0000015770; Gallus gallus.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0005488; F: binding; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAMYLOID.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON TER 1  
 SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 534;  
 Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7  
 Db 450 QKLVPFA 456

RESULT 61  
 Q9PVL1\_CHICK PRELIMINARY; PRT; 569 AA.  
 AC Q9PVL1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Amyloid protein (Fragment).  
 GN Name=APP;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RA Coulson E.J., Pálga K., Beyreuther K., Masters C.L.;  
 RT "What the evolution of the amyloid protein precursor supergene family  
 tells us about its function.";  
 RL Neurochem. Int. 0:0-0(2000).  
 DR EMBL; AF030341; AAF12698.1; -; mRNA.  
 DR HSP; Q16019; IYT.  
 DR SNR; Q9PVL1; 1-64, 260-369.  
 DR Ensembl; ENSGALG0000015770; Gallus gallus.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0005488; F: binding; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAMYLOID.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON TER 1  
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 88.2%; Score 30; DB 2; Length 569;  
 Best Local Similarity 85.7%; Pred. No. 3.5e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



```

QY 1 KKLVPFA 7
DB 486 OKLVFFA 492

RESULT 62
Q75JL6_DICDI
ID Q75JL6_DICDI PRELIMINARY; PRT; 572 AA.
AC Q75JL6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Similar to Lelishmania major. Lail.4 (Hypothetical protein).
GN ORFNames=DD0169466;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafarski K., Pachebat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baugart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzter M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
RL Nature 418:79-85(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baugart C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Kerriman M., Song J., Olsen R., Szafarski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Pey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren B., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegue H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzter M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0(2005).
RL EMBL; AC116979; AAS38717.1; -; Genomic DNA.
DR EMBL; AAF10100032; BAF6934.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 572 AA; 63642 MW; 7B9158ADA5020D1 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 572;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 3 KKLIFFS 9

RESULT 63
RPOC1_EUGGR
ID RPOC1_EUGGR STANDARD; PRT; 586 AA.
AC F23560;

QY 1 KKLVPFA 6
DB 564 KKLVPFF 569

Query Match 88.2%; Score 30; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6
DB 564 KKLVPFF 569

RESULT 64
Q919E7_BRARE
ID Q919E7_BRARE PRELIMINARY; PRT; 612 AA.

```

DR	InterPro; IPR000560; HisAc_phsptase.	
DR	InterPro; IPR001611; LRR.	
DR	InterPro; IPR007090; LRR_plant.	
DR	InterPro; IPR000719; Prot_kinase.	
DR	Pfam; PF00560; LRR_1; 4.	
DR	Pfam; PF00069; PKinase; 1.	
DR	PRINTS; PR00019; LEURICHRPT.	
DR	ProDom; PD000001; Prot_kinase; 1.	
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
KW	Kinase; Receptor.	
QW	SEQUENCE 639 AA; 69564 MW; EOASFEBS87D8DB80 CRC64;	
QY	1 KKLVPF 6	
DB	338 KKLVPF 343	
<p>Query Match 88.2%; Score 30; DB 2; Length 639;        Best Local Similarity 100.0%; Pred.No. 3.9e+02;        Matches 6; Conservative 0; Mismatches 0; Indels 0; Gap</p>		
<p>RESULT 66</p> <p>Q9ZT08_ARATH PRELIMINARY; PRT; 645 AA.</p> <p>AC Q9ZT08;</p> <p>DT 01-MAY-1999 (TREMBLrel. 10, Created)</p> <p>DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)</p> <p>DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)</p> <p>DR Receptor-like protein kinase.</p> <p>GN Names=RKL1;</p> <p>OS Arabidopsis thaliana (Mouse-ear cress).</p> <p>OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.</p> <p>OC NCBI_Taxid=3702;</p> <p>OX [1]</p> <p>RN NUCLEOTIDE SEQUENCE.</p> <p>RP MEDLINE=20550477; PubMed=11100776; DOI=10.1093/pcp/pcd028;</p> <p>RX Ohtake Y., Takahashi T., Kameda Y.</p> <p>RA "Salicylic acid induces the expression of a number of receptor-like kinase genes in Arabidopsis thaliana.";</p> <p>RL Plant Cell Physiol. 41:1038-1044(2000).</p> <p>DR EMBL; AF084034; AAC95351.1; -; Genomic_DNA.</p> <p>DR GO; GO:0005524; F:ATP binding; IEA.</p> <p>DR GO; GO:0004672; F:protein kinase activity; IEA.</p> <p>DR GO; GO:0004872; F:receptor activity; IEA.</p> <p>DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.</p> <p>DR InterPro; IPR000560; HisAc_phsptase.</p> <p>DR InterPro; IPR001611; LRR.</p> <p>DR InterPro; IPR007090; LRR_plant.</p> <p>DR InterPro; IPR000719; Prot_kinase.</p> <p>DR Pfam; PF00560; LRR_1; 5.</p> <p>DR PRINTS; PR00019; LEURICHRPT.</p> <p>DR ProDom; PD000001; Prot_kinase; 1.</p> <p>DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.</p> <p>DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.</p> <p>DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.</p> <p>KW Kinase; Receptor.</p> <p>QW SEQUENCE 645 AA; 69917 MW; 7769E171D5A1600E CRC64;</p> <p>QY 1 KKLVPF 6</p> <p>DB 342 KKLVPF 347</p>		
<p>Query Match 88.2%; Score 30; DB 2; Length 645;        Best Local Similarity 100.0%; Pred.No. 3.9e+02;        Matches 6; Conservative 0; Mismatches 0; Indels 0; Gap</p>		
<p>RESULT 67</p> <p>Q9LV16_ARATH</p>		

ID Q9LV16\_ARATH PRELIMINARY; PRT; 647 AA.  
 AC Q9LV16;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Probable receptor-like protein kinase protein (AT3917840/NEBS\_6).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
 RT clones."; DNA Res. 7:131-135 (2000).  
 RL [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.B., Sakurai T., Satou M.,  
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,  
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
 RA Quach H.B., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,  
 RA Toriumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G.,  
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB019230; BAB02707.1; -; Genomic\_DNA.  
 DR EMBL; AY095994; RAN19950.1; -; mRNA.  
 DR EMBL; BT002283; RAN72294.1; -; mRNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004672; F:protein kinase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000560; Hisac\_phsphtse.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR007090; LRR\_plant.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR Pfam; PF00560; LRR 1; 4.  
 DR Pfam; PF0069; Pkinase; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR PRODOM; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Kinase; Receptor.  
 SQ SEQUENCE 647 AA; 70406 MW; 1FF91B013B75A1DA CRC64;  
  
 Query Match 88.2%; Score 30; DB 2; Length 647;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 KKLVEF 6  
 Db 346 KKLVEF 351

RESULT 68  
 Q9LP77\_ARATH PRELIMINARY; PRT; 655 AA.  
 AC Q9LP77;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE T1N15.9.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,  
 RA Shinn P., Altafi H., Bei Q., Chin C., Chioi J., Choi E., Conn L.,  
 RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,  
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N., Nguyen M.,  
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
 RA Ecker J.R.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chioi J., Choi E.,  
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howng B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 RA Theologis A., Ecker J.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC020889; BAF79696.1; -; Genomic\_DNA.  
 DR FIR; G96524; G96524.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004672; F:protein kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000560; Hisac\_phsphtse.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR007090; LRR\_plant.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR Pfam; PF00560; LRR 1; 5.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR PRODOM; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 SQ SEQUENCE 655 AA; 71131 MW; 734B4A7D2E956456 CRC64;  
  
 Query Match 88.2%; Score 30; DB 2; Length 655;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 KKLVEF 6  
 Db 352 KKLVEF 357

RESULT 69  
 Q7ZT1\_BRARE PRELIMINARY; PRT; 678 AA.  
 AC Q7ZT1;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Amyloid protein a variant 2.  
 GN Name:appa;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Cypriniformes;  
 OC Cyprinidae; Danio.

```
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Groth C., Lardelli M.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RE EMBL; AY271746; AAP22958.1; -, mRNA.
RS HSP; Q16019; 1HZ3.
DR SMR; Q72ZT1; 29-124, 393-491.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4 EXTRA; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
SQ SEQUENCE 678 AA; 76755 MW; 94163778444FD0BC CRC64;

Query Match 88.2%; Score 30; DB 2; Length 678;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLVFFA 7
Db 594 QKLVFFA 600

RESULT 70
Q98SG0 XENLA PRELIMINARY; PRT; 693 AA.
AC Q98SG0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Beta-amyloid precursor protein A.
GN Name=app;
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21610087; PubMed=11744158; DOI=10.1016/S0169-328X(01)00279-0;
RA Van den Hurk W.H., Bloemen M., Martens G.J.M.;
RT "Expression of the gene encoding the beta-amyloid precursor protein
  APP in Xenopus laevis.";
RL Brain Res. Mol. Brain Res. 97:13-20(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences, University of
  Nijmegen, Nijmegen, Netherlands.
RE EMBL; AJ298150; CAC37193.1; -, mRNA.
RS HSP; Q16019; 1HZ3.
DR SMR; Q98SG0; 27-122, 393-492.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4 EXTRA; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.

OY 1 KKLVFFA 7
Db 594 QKLVFFA 600

RESULT 70
Q98SG0 XENLA PRELIMINARY; PRT; 693 AA.
AC Q98SG0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid precursor protein A.
GN Name=app;
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21610087; PubMed=11744158; DOI=10.1016/S0169-328X(01)00279-0;
RA Van den Hurk W.H., Bloemen M., Martens G.J.M.;
RT "Expression of the gene encoding the beta-amyloid precursor protein
  APP in Xenopus laevis.";
RL Brain Res. Mol. Brain Res. 97:13-20(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22995821; PubMed=12966093; DOI=10.1074/jbc.M307482200;
RA Llompart B., Castells E., Rio A., Roca R., Ferrando A., Stiefel V.,
  Puigdomenech P., Casacuberta J.M.;
RT "The direct activation of M1K, a germinal center kinase (GCK)-like
  kinase, by MARK, a maize atypical receptor kinase, suggests a new
  mechanism for signaling through kinase-dead receptors.";
RL J. Biol. Chem. 278:48105-48111(2003).
RE EMBL; AY188755; AA083390.1; -, mRNA.
DR GRAMENE; Q6Y2W9; -.
DR GO; GO:0005524; F: ATP binding; IEA.
DR GO; GO:0004674; F: protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F: protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0006468; P: protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 4.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc_1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Kinase; Receptor.
SQ SEQUENCE 694 AA; 71924 MW; 49883823202B6B5 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 694;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLVEP 6
Db 373 KKLVEP 378

RESULT 72
Q5R477_PONPY PRELIMINARY; PRT; 695 AA.
ID Q5R477_PONPY PRELIMINARY;
```

```

AC QSR477;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459D212.
GN Name=DKFZp459D212;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR861380; CAH93439.1; -; mRNA.
DR SMR; QSR477; 28-123, 124-189, 385-494.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0008118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome_c_r.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Hypothetical protein.
SQ SEQUENCE 695 AA; 78626 MW; 0BF5DD9BA2213E49 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 611 QKLVPFA 617

RESULT 73
QSRH29_CANFA
ID Q6RH29_CANFA PRELIMINARY; PRT; 695 AA.
AC Q6RH29;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta amyloid protein isoform APP695.
GN Name=Beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY498707; IBA4.
DR HSP; Q16019; IBA4.
DR SMR; Q6RH29; 28-123, 124-189, 385-494.
DR Ensembl; ENSCAF00000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.

```

```

DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F9B6C10 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 611 QKLVPFA 617

RESULT 74
Q56JK3_CANFA
ID Q56JK3_CANFA PRELIMINARY; PRT; 695 AA.
AC Q56JK3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Beta-amyloid protein 695.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926582; AAX81911.1; -; mRNA.
SQ SEQUENCE 695 AA; 78748 MW; 5A253E0DB677875A CRC64;

Query Match 88.2%; Score 30; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 611 QKLVPFA 617

RESULT 75
Q6GR78_MOUSE
ID Q6GR78_MOUSE PRELIMINARY; PRT; 695 AA.
AC Q6GR78;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta (A4) protein.
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

```

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC070409; AAH70409.1; -; mRNA.  
 SQ SEQUENCE 695 AA; 78442 MW; 0DE93FA56FB20F3A CRC64;  
  
 Query Match 88.2%; Score 30; DB 2; Length 695;  
 Best Local Similarity 85.7%; Pred. No. 4.1e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 KKLVFFA 7  
 Db 611 QKLVFFA 617  
 :|||||  
 :|||||

Search completed: December 29, 2005, 17:46:58  
 Job time : 99.2258 secs

**THIS PAGE BLANK (USPTO)**

Fri Dec 30 10:25:28 2005

us-10-009-122-7.ra1

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds  
(without alignments)  
24.763 Million cell updates/sec

Title: US-10-009-122-7

Perfect score: 29

Sequence: 1 KAVFPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/H COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/PCITUS COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	2	US-09-747-408-7
2	29	100.0	6	2	US-09-747-408-15
3	29	100.0	74	2	US-09-194-468A-19
4	29	100.0	74	2	US-09-194-468A-25
5	29	100.0	108	2	US-09-194-468A-20
6	29	100.0	108	2	US-09-194-468A-26
7	29	100.0	193	2	US-09-194-468A-18
8	29	100.0	193	2	US-09-194-468A-24
9	29	100.0	222	2	US-09-194-468A-17
10	29	100.0	228	2	US-09-194-468A-23
11	29	100.0	429	2	US-09-194-468A-45
12	29	100.0	631	2	US-08-448-489-17
13	29	100.0	631	2	US-09-689-730-17
14	29	100.0	660	2	US-08-704-711A-18
15	29	100.0	660	2	US-08-521-220-18
16	29	100.0	660	2	US-09-391-104-19
17	29	100.0	660	2	US-09-917-254-89
18	29	100.0	660	2	US-09-949-016-6512
19	29	100.0	660	2	US-09-949-016-7937
20	29	100.0	660	2	US-10-153-185-14
21	29	100.0	663	2	US-09-194-468A-30
22	26	89.7	65	2	US-09-471-276-1595
23	26	89.7	128	2	US-09-540-236-2808
24	26	89.7	295	2	US-09-248-796A-18333
25	26	89.7	334	2	US-09-205-258-348
26	26	89.7	334	2	US-10-004-860-348
27	26	89.7	494	2	US-09-328-352-7729

28	89.7	535	2	US-09-902-540-10002	Sequence 10002, A
29	89.7	1507	2	US-08-929-329-5	Sequence 5, Appli
30	86.2	5	2	US-09-095-106A-40	Sequence 40, Appli
31	86.2	6	2	US-09-747-408-9	Sequence 9, Appli
32	86.2	6	2	US-09-747-408-17	Sequence 17, Appli
33	86.2	28	1	US-08-461-216-4	Sequence 4, Appli
34	86.2	77	2	US-09-513-999C-6921	Sequence 6921, Ap
35	86.2	80	2	US-09-248-796A-27785	Sequence 27785, A
36	86.2	142	2	US-09-270-767-33756	Sequence 33756, A
37	86.2	142	2	US-09-270-767-48973	Sequence 48973, A
38	86.2	261	2	US-09-270-767-43456	Sequence 43456, A
39	86.2	281	2	US-09-252-991A-29199	Sequence 29199, A
40	86.2	282	2	US-09-845-713A-2	Sequence 2, Appli
41	86.2	306	2	US-09-303-518D-676	Sequence 676, App
42	86.2	306	2	US-09-303-518D-678	Sequence 678, App
43	86.2	307	2	US-09-303-518D-680	Sequence 680, App
44	86.2	322	2	US-09-495-406-34	Sequence 34, Appl
45	86.2	322	2	US-09-816-028A-48	Sequence 48, Appl
46	86.2	322	2	US-10-303-162-48	Sequence 48, Appl
47	86.2	322	2	US-10-303-134-48	Sequence 48, Appl
48	86.2	322	2	US-10-303-118-48	Sequence 48, Appl
49	86.2	322	2	US-10-303-128-48	Sequence 48, Appl
50	86.2	334	2	US-09-270-767-43522	Sequence 43522, A
51	86.2	337	2	US-09-438-185A-960	Sequence 960, App
52	86.2	347	2	US-08-749-816-3	Sequence 3, Appli
53	86.2	347	2	US-09-144-914-6	Sequence 6, Appli
54	86.2	375	2	US-09-489-039A-11261	Sequence 11261, A
55	86.2	421	2	US-09-543-681A-5731	Sequence 5731, Ap
56	86.2	430	2	US-09-272-960-2	Sequence 2, Appli
57	86.2	430	2	US-10-058-636-2	Sequence 2, Appli
58	86.2	462	2	US-09-583-110-3587	Sequence 3587, Ap
59	86.2	473	2	US-09-107-433-3273	Sequence 3273, Ap
60	86.2	474	2	US-09-489-039A-13140	Sequence 13140, A
61	86.2	532	1	US-08-288-405A-10	Sequence 10, Appl
62	86.2	532	2	US-10-162-012-13	Sequence 13, Appl
63	86.2	547	2	US-09-605-703B-2398	Sequence 2398, Ap
64	86.2	560	1	US-08-594-031-90	Sequence 90, Appl
65	86.2	560	2	US-09-643-597-225	Sequence 225, App
66	86.2	560	2	US-09-480-884A-225	Sequence 225, App
67	86.2	560	2	US-09-542-615A-225	Sequence 225, App
68	86.2	560	2	US-09-606-421B-225	Sequence 225, App
69	86.2	560	2	US-09-476-496A-225	Sequence 225, App
70	86.2	560	2	US-09-630-940B-225	Sequence 225, App
71	86.2	560	2	US-09-943-075A-6	Sequence 6, Appli
72	86.2	560	2	US-10-039-272A-2	Sequence 2, Appli
73	86.2	560	2	US-10-007-700-225	Sequence 225, App
74	86.2	560	5	US-09-985-799-90	Sequence 90, Appl
75	86.2	560	5	US-09-977-371-90	Sequence 90, Appl
76	86.2	591	2	US-09-489-039A-12837	Sequence 12837, A
77	86.2	605	2	US-08-693-214-8	Sequence 8, Appli
78	86.2	945	2	US-09-198-452A-1030	Sequence 1030, Ap
79	86.2	1144	1	US-08-147-812-5	Sequence 5, Appli
80	86.2	1144	1	US-08-319-866-12	Sequence 12, Appl
81	86.2	1144	2	US-09-123-708-2	Sequence 2, Appli
82	86.2	1144	2	US-09-123-624-2	Sequence 2, Appli
83	86.2	1144	2	US-09-661-258-5	Sequence 5, Appli
84	86.2	1144	2	US-08-809-917-12	Sequence 12, Appl
85	86.2	1144	2	US-09-419-371-12	Sequence 12, Appl
86	86.2	2343	2	US-09-324-867-2	Sequence 2, Appli
87	82.8	5	1	US-08-612-785B-25	Sequence 25, Appl
88	82.8	5	2	US-08-703-675C-38	Sequence 38, Appl
89	82.8	5	2	US-08-617-267C-25	Sequence 25, Appl
90	82.8	6	1	US-08-612-785B-9	Sequence 9, Appli
91	82.8	6	2	US-08-703-675C-32	Sequence 32, Appl
92	82.8	6	2	US-08-617-267C-9	Sequence 9, Appli
93	82.8	6	2	US-09-747-408-1	Sequence 1, Appli
94	82.8	6	2	US-09-747-408-3	Sequence 3, Appli
95	82.8	6	2	US-09-747-408-10	Sequence 10, Appl
96	82.8	6	2	US-09-747-408-11	Sequence 11, Appl
97	82.8	7	1	US-08-127-904-14	Sequence 14, Appl
98	82.8	7	1	US-08-612-785B-7	Sequence 7, Appli
99	82.8	7	2	US-08-703-675C-30	Sequence 30, Appl
100	82.8	7	2	US-08-617-267C-7	Sequence 7, Appli



101	24	82.8	7	2	US-09-264-709A-13	Sequence 13, Appl	174	24	82.8	19	2	US-10-815-353-5	Sequence 5, Appl
102	24	82.8	7	2	US-09-747-408-2	Sequence 2, Appl	175	24	82.8	19	2	US-10-816-529-5	Sequence 5, Appl
103	24	82.8	7	2	US-09-747-408-18	Sequence 18, Appl	176	24	82.8	19	2	US-10-815-391-5	Sequence 5, Appl
104	24	82.8	7	2	US-09-747-408-19	Sequence 19, Appl	177	24	82.8	19	2	US-10-816-022-5	Sequence 5, Appl
105	24	82.8	7	4	PCT-US94-10475-14	Sequence 14, Appl	178	24	82.8	19	2	US-09-724-940-75	Sequence 75, Appl
106	24	82.8	8	1	US-08-612-785B-5	Sequence 5, Appl	179	24	82.8	19	2	US-10-934-609-5	Sequence 5, Appl
107	24	82.8	8	1	US-08-630-645-1	Sequence 1, Appl	180	24	82.8	19	2	US-10-884-892-5	Sequence 5, Appl
108	24	82.8	8	2	US-08-703-675C-28	Sequence 28, Appl	181	24	82.8	20	2	US-08-970-833-10	Sequence 10, Appl
109	24	82.8	8	2	US-08-617-267C-5	Sequence 5, Appl	182	24	82.8	20	2	US-09-724-953-33	Sequence 33, Appl
110	24	82.8	8	2	US-09-095-106A-44	Sequence 44, Appl	183	24	82.8	20	2	US-09-724-567-33	Sequence 33, Appl
111	24	82.8	8	2	US-08-766-596A-1	Sequence 1, Appl	184	24	82.8	20	2	US-09-979-952-33	Sequence 33, Appl
112	24	82.8	8	2	US-08-766-596A-1	Sequence 73, Appl	185	24	82.8	20	2	US-09-585-817-33	Sequence 33, Appl
113	24	82.8	8	4	PCT-US96-10220-1	Sequence 1, Appl	186	24	82.8	26	1	US-08-304-585-7	Sequence 7, Appl
114	24	82.8	9	2	US-08-766-596A-50	Sequence 50, Appl	187	24	82.8	28	1	US-08-346-849-4	Sequence 4, Appl
115	24	82.8	9	2	US-08-766-596A-64	Sequence 64, Appl	188	24	82.8	28	1	US-08-302-808-7	Sequence 7, Appl
116	24	82.8	9	2	US-09-747-408-20	Sequence 20, Appl	189	24	82.8	28	1	US-08-609-090-2	Sequence 2, Appl
117	24	82.8	9	2	US-10-014-658-15	Sequence 15, Appl	190	24	82.8	28	1	US-08-986-948-7	Sequence 7, Appl
118	24	82.8	10	2	US-08-970-833-3	Sequence 3, Appl	191	24	82.8	28	1	US-08-293-284A-4	Sequence 4, Appl
119	24	82.8	10	2	US-09-724-961-20	Sequence 20, Appl	192	24	82.8	28	1	US-08-461-216-2	Sequence 2, Appl
120	24	82.8	10	2	US-09-724-961-21	Sequence 21, Appl	193	24	82.8	28	2	US-09-388-890-2	Sequence 2, Appl
121	24	82.8	10	2	US-09-724-961-22	Sequence 22, Appl	194	24	82.8	28	2	US-09-388-890-3	Sequence 3, Appl
122	24	82.8	10	2	US-09-724-961-23	Sequence 23, Appl	195	24	82.8	28	2	US-09-388-890-4	Sequence 4, Appl
123	24	82.8	10	2	US-09-724-961-24	Sequence 24, Appl	196	24	82.8	28	2	US-09-388-890-5	Sequence 5, Appl
124	24	82.8	10	2	US-09-580-018-20	Sequence 20, Appl	197	24	82.8	28	2	US-09-388-890-6	Sequence 6, Appl
125	24	82.8	10	2	US-09-580-018-21	Sequence 21, Appl	198	24	82.8	28	2	US-09-388-890-7	Sequence 7, Appl
126	24	82.8	10	2	US-09-580-018-22	Sequence 22, Appl	199	24	82.8	28	2	US-09-388-890-8	Sequence 8, Appl
127	24	82.8	10	2	US-09-580-018-23	Sequence 23, Appl	200	24	82.8	28	2	US-09-388-890-9	Sequence 9, Appl
128	24	82.8	10	2	US-09-580-018-24	Sequence 24, Appl	201	24	82.8	28	2	US-09-388-890-10	Sequence 10, Appl
129	24	82.8	10	2	US-09-724-551-20	Sequence 20, Appl	202	24	82.8	28	2	US-09-388-890-12	Sequence 12, Appl
130	24	82.8	10	2	US-09-724-551-21	Sequence 21, Appl	203	24	82.8	28	2	US-09-388-890-13	Sequence 13, Appl
131	24	82.8	10	2	US-09-724-551-22	Sequence 22, Appl	204	24	82.8	28	2	US-09-388-890-14	Sequence 14, Appl
132	24	82.8	10	2	US-09-724-551-23	Sequence 23, Appl	205	24	82.8	28	2	US-09-264-709A-1	Sequence 1, Appl
133	24	82.8	10	2	US-09-724-551-24	Sequence 24, Appl	206	24	82.8	28	2	US-08-723-661B-2	Sequence 2, Appl
134	24	82.8	10	2	US-09-724-940-20	Sequence 20, Appl	207	24	82.8	28	2	US-09-660-954-2	Sequence 2, Appl
135	24	82.8	10	2	US-09-724-940-21	Sequence 21, Appl	208	24	82.8	28	2	US-09-660-954-3	Sequence 3, Appl
136	24	82.8	10	2	US-09-724-940-22	Sequence 22, Appl	209	24	82.8	28	2	US-09-660-954-4	Sequence 4, Appl
137	24	82.8	10	2	US-09-724-940-23	Sequence 23, Appl	210	24	82.8	28	2	US-09-660-954-5	Sequence 5, Appl
138	24	82.8	10	2	US-09-724-940-24	Sequence 24, Appl	211	24	82.8	28	2	US-09-660-954-6	Sequence 6, Appl
139	24	82.8	11	1	US-08-630-645-14	Sequence 14, Appl	212	24	82.8	28	2	US-09-660-954-7	Sequence 7, Appl
140	24	82.8	11	2	US-08-766-596A-14	Sequence 14, Appl	213	24	82.8	28	2	US-09-660-954-8	Sequence 8, Appl
141	24	82.8	11	2	US-09-988-842-9	Sequence 9, Appl	214	24	82.8	28	2	US-09-660-954-9	Sequence 9, Appl
142	24	82.8	11	2	US-09-988-842-25	Sequence 25, Appl	215	24	82.8	28	2	US-09-660-954-10	Sequence 10, Appl
143	24	82.8	11	4	PCT-US96-10220-14	Sequence 14, Appl	216	24	82.8	28	2	US-09-660-954-12	Sequence 12, Appl
144	24	82.8	14	2	US-09-594-366-5	Sequence 5, Appl	217	24	82.8	28	2	US-09-660-954-13	Sequence 13, Appl
145	24	82.8	14	2	US-09-992-800-5	Sequence 5, Appl	218	24	82.8	28	2	US-09-660-954-14	Sequence 14, Appl
146	24	82.8	15	1	US-08-612-785B-14	Sequence 14, Appl	219	24	82.8	28	2	US-08-898-300-4	Sequence 4, Appl
147	24	82.8	15	1	US-08-612-785B-37	Sequence 37, Appl	220	24	82.8	28	2	US-08-824-513-4	Sequence 4, Appl
148	24	82.8	15	2	US-08-617-267C-14	Sequence 14, Appl	221	24	82.8	28	2	US-09-623-548A-959	Sequence 959, App
149	24	82.8	15	2	US-08-766-596A-56	Sequence 56, Appl	222	24	82.8	28	2	US-09-623-548A-965	Sequence 965, App
150	24	82.8	15	2	US-08-766-596A-57	Sequence 57, Appl	223	24	82.8	28	2	US-09-623-548A-976	Sequence 976, App
151	24	82.8	15	2	US-08-766-596A-58	Sequence 58, Appl	224	24	82.8	28	2	US-09-623-548A-992	Sequence 992, App
152	24	82.8	15	2	US-08-766-596A-60	Sequence 60, Appl	225	24	82.8	28	2	US-09-623-548A-1003	Sequence 1003, App
153	24	82.8	15	2	US-08-766-596A-61	Sequence 61, Appl	226	24	82.8	28	2	US-09-657-276-959	Sequence 959, App
154	24	82.8	15	2	US-08-766-596A-63	Sequence 63, Appl	227	24	82.8	28	2	US-09-657-276-965	Sequence 965, App
155	24	82.8	15	2	US-08-766-596A-65	Sequence 65, Appl	228	24	82.8	28	2	US-09-657-276-976	Sequence 976, App
156	24	82.8	17	2	US-09-264-709A-2	Sequence 2, Appl	229	24	82.8	28	2	US-09-657-276-992	Sequence 992, App
157	24	82.8	17	2	US-09-594-366-3	Sequence 3, Appl	230	24	82.8	28	2	US-09-657-276-1003	Sequence 1003, App
158	24	82.8	17	2	US-09-623-548A-950	Sequence 950, App	231	24	82.8	28	2	US-09-865-294A-66	Sequence 66, Appl
159	24	82.8	17	2	US-09-623-548A-983	Sequence 983, App	232	24	82.8	30	1	US-08-609-090-3	Sequence 3, Appl
160	24	82.8	17	2	US-09-992-800-3	Sequence 3, Appl	233	24	82.8	30	1	US-09-861-847A-1	Sequence 1, Appl
161	24	82.8	17	2	US-09-657-276-950	Sequence 950, App	234	24	82.8	33	1	US-08-609-090-4	Sequence 4, Appl
162	24	82.8	17	2	US-09-657-276-983	Sequence 983, App	235	24	82.8	34	1	US-08-475-579A-4	Sequence 4, Appl
163	24	82.8	19	2	US-08-970-833-11	Sequence 11, Appl	236	24	82.8	35	1	US-08-304-585-6	Sequence 6, Appl
164	24	82.8	19	2	US-09-723-384-5	Sequence 5, Appl	237	24	82.8	35	1	US-08-612-785B-16	Sequence 16, Appl
165	24	82.8	19	2	US-09-724-961-75	Sequence 75, Appl	238	24	82.8	35	1	US-08-612-785B-36	Sequence 36, Appl
166	24	82.8	19	2	US-09-724-552-5	Sequence 5, Appl	239	24	82.8	35	1	US-08-612-785B-38	Sequence 38, Appl
167	24	82.8	19	2	US-09-580-018-75	Sequence 75, Appl	240	24	82.8	35	1	US-08-612-785B-40	Sequence 40, Appl
168	24	82.8	19	2	US-09-723-927-5	Sequence 5, Appl	241	24	82.8	35	2	US-08-617-267C-16	Sequence 16, Appl
169	24	82.8	19	2	US-09-724-489-5	Sequence 5, Appl	242	24	82.8	35	2	US-09-623-548A-979	Sequence 979, App
170	24	82.8	19	2	US-09-724-477-5	Sequence 5, Appl	243	24	82.8	35	2	US-09-623-548A-1006	Sequence 1006, App
171	24	82.8	19	2	US-09-723-762-5	Sequence 5, Appl	244	24	82.8	35	2	US-09-657-276-979	Sequence 979, App
172	24	82.8	19	2	US-09-201-430-5	Sequence 5, Appl	245	24	82.8	35	2	US-09-657-276-1006	Sequence 1006, App
173	24	82.8	19	2	US-09-724-551-75	Sequence 75, Appl	246	24	82.8	36	1	US-08-609-090-6	Sequence 6, Appl

```

247 24 82.8 36 2 US-09-861-847A-6
248 24 82.8 36 2 US-09-861-847A-11
249 24 82.8 38 1 US-08-302-808-1
250 24 82.8 38 1 US-07-737-371E-68
251 24 82.8 38 1 US-08-986-948-1
252 24 82.8 38 2 US-09-623-548A-975
253 24 82.8 38 2 US-09-623-548A-1002
254 24 82.8 38 2 US-09-657-276-975
255 24 82.8 38 2 US-09-657-276-1002
256 24 82.8 39 1 US-08-304-585-5
257 24 82.8 39 1 US-08-302-808-2
258 24 82.8 39 1 US-08-609-090-7
259 24 82.8 39 1 US-08-682-245A-1
260 24 82.8 39 1 US-08-986-948-2
261 24 82.8 40 1 US-07-744-767A-1
262 24 82.8 40 1 US-08-235-400-2
263 24 82.8 40 1 US-08-476-464A-2
264 24 82.8 40 1 US-08-304-585-1
265 24 82.8 40 1 US-08-304-585-8
266 24 82.8 40 1 US-08-302-808-3
267 24 82.8 40 1 US-08-433-734-1
268 24 82.8 40 1 US-08-609-090-8
269 24 82.8 40 1 US-07-737-371E-69
270 24 82.8 40 1 US-08-682-245A-2
271 24 82.8 40 1 US-08-986-948-3
272 24 82.8 40 1 US-08-461-216-1
273 24 82.8 40 2 US-08-959-148-1
274 24 82.8 40 2 US-09-242-724-22
275 24 82.8 40 2 US-08-723-661B-1
276 24 82.8 40 2 US-09-062-365-3
277 24 82.8 40 2 US-09-133-866-1
278 24 82.8 40 2 US-09-861-847A-7
279 24 82.8 40 2 US-09-861-847A-8
280 24 82.8 40 2 US-09-988-842-3
281 24 82.8 40 2 US-10-455-218-1
282 24 82.8 40 2 US-10-151-614-1
283 24 82.8 40 2 US-09-623-548A-956
284 24 82.8 40 2 US-09-623-548A-962
285 24 82.8 40 2 US-09-623-548A-968
286 24 82.8 40 2 US-09-623-548A-978
287 24 82.8 40 2 US-09-623-548A-989
288 24 82.8 40 2 US-09-623-548A-995
289 24 82.8 40 2 US-09-623-548A-1005
290 24 82.8 40 2 US-09-657-276-956
291 24 82.8 40 2 US-09-657-276-962
292 24 82.8 40 2 US-09-657-276-968
293 24 82.8 40 2 US-09-657-276-978
294 24 82.8 40 2 US-09-657-276-989
295 24 82.8 40 2 US-09-657-276-995
296 24 82.8 40 2 US-09-657-276-1005
297 24 82.8 40 2 US-09-962-955D-36
298 24 82.8 40 4 PCT-US92-06700-1
299 24 82.8 41 1 US-07-819-361-1
300 24 82.8 41 1 US-08-302-808-4

```

# ALIGNMENTS

```

RESULT 1
US-09-747-408-7
; Sequence 7, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

```

```

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-7

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 2
US-09-747-408-15
; Sequence 15, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-15

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 3
US-09-194-468A-19
; Sequence 19, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Chereah, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 19
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-19

```

Query Match 100.0%; Score 29; DB 2; Length 74;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
Db 64 KAVFFA 69

RESULT 4  
US-09-194-468A-25  
; Sequence 25, Application US/09194468A  
; Patent No. 6500924  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheresch, David A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/09/194,468A  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-194-468A-25

Query Match 100.0%; Score 29; DB 2; Length 74;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
Db 64 KAVFFA 69

RESULT 5  
US-09-194-468A-20  
; Sequence 20, Application US/09194468A  
; Patent No. 6500924  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheresch, David A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/09/194,468A  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-194-468A-20

Query Match 100.0%; Score 29; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 38;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAVFFA 6  
Db 64 KAVFFA 69

RESULT 6  
US-09-194-468A-26  
; Sequence 26, Application US/09194468A  
; Patent No. 6500924  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheresch, David A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/09/194,468A  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-194-468A-26

Query Match 100.0%; Score 29; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
Db 64 KAVFFA 69

RESULT 7  
US-09-194-468A-18  
; Sequence 18, Application US/09194468A  
; Patent No. 6500924  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheresch, David A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/09/194,468A  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-194-468A-18

Query Match 100.0%; Score 29; DB 2; Length 193;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 64 KAVFFA 69  
|||||

RESULT 8  
US-09-194-468A-24  
; Sequence 24, Application US/09194468A  
; Patent No. 6500924  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; TITLE OF INVENTION: ANGIOGENESIS  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/09/194,468A  
; CURRENT FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-194-468A-24

Query Match 100.0%; Score 29; DB 2; Length 193;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|||||

Db 64 KAVFFA 69

RESULT 9  
US-09-194-468A-17  
; Sequence 17, Application US/09194468A  
; Patent No. 6500924  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; TITLE OF INVENTION: ANGIOGENESIS  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/09/194,468A  
; CURRENT FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-194-468A-17

Query Match 100.0%; Score 29; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|||||

Db 93 KAVFFA 98

RESULT 10

US-09-194-468A-23  
; Sequence 23, Application US/09194468A  
; Patent No. 6500924  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; TITLE OF INVENTION: ANGIOGENESIS  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/09/194,468A  
; CURRENT FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-194-468A-23

Query Match 100.0%; Score 29; DB 2; Length 228;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|||||

Db 99 KAVFFA 104

RESULT 11

US-09-194-468A-45  
; Sequence 45, Application US/09194468A  
; Patent No. 6500924  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; TITLE OF INVENTION: ANGIOGENESIS  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/09/194,468A  
; CURRENT FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 429  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-194-468A-45

Query Match 100.0%; Score 29; DB 2; Length 429;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|||||

Db 300 KAVFFA 305

RESULT 12  
US-08-448-489-17

; Sequence 17, Application US/08448489  
; Patent No. 6184022  
; GENERAL INFORMATION:  
; APPLICANT: SEIKI, Motoharu  
; APPLICANT: SATO, Hiroshi  
; APPLICANT: SHINAGAWA, Akira  
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
; FILE REFERENCE: 55-290P  
; CURRENT APPLICATION NUMBER: US/08/448,489  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 631  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Known Member of  
; OTHER INFORMATION: Matrix Metalloproteinase Family  
US-08-448-489-17

Query Match 100.0%; Score 29; DB 2; Length 631;  
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 KAVFFA 6  
|||||  
DB 502 KAVFFA 507

RESULT 13  
US-09-689-730-17  
; Sequence 17, Application US/09689730  
; Patent No. 6825024  
; GENERAL INFORMATION:  
; APPLICANT: SEIKI, Motoharu  
; APPLICANT: SATO, Hiroshi  
; APPLICANT: SHINAGAWA, Akira  
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
; FILE REFERENCE: 55-290P  
; CURRENT APPLICATION NUMBER: US/09/689,730  
; CURRENT FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: US/08/448,489  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 631  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Known Member of  
; OTHER INFORMATION: Matrix Metalloproteinase Family  
US-09-689-730-17

Query Match 100.0%; Score 29; DB 2; Length 631;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||  
DB 502 KAVFFA 507

RESULT 14  
US-08-704-711A-18  
; Sequence 18, Application US/08704711A  
; Patent No. 6114159  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; APPLICANT: HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE

; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/704,711A  
; FILING DATE: 20-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/DE95/00357  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4438838.1  
; FILING DATE: 21-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4409663.1  
; FILING DATE: 17-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 26083/124  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 660 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-704-711A-18

Query Match 100.0%; Score 29; DB 2; Length 660;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||  
DB 531 KAVFFA 536

RESULT 15  
US-09-521-220-18  
; Sequence 18, Application US/09521220  
; Patent No. 6399348  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; APPLICANT: HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/521,220  
/ FILING DATE: 08-Mar-2000  
/ CLASSIFICATION: <Unknown>  
/ 21-OCT-1994  
/ 17-MAR-1994  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/704,711  
/ FILING DATE: <Unknown>  
/ APPLICATION NUMBER: DE 4438838.1  
/ FILING DATE: 21-OCT-1994  
/ APPLICATION NUMBER: DE 4409663.1  
/ FILING DATE: 17-MAR-1994  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: GRANADOS, Patricia D.  
/ REGISTRATION NUMBER: 33,683  
/ REFERENCE/DOCKET NUMBER: 26083/124  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (202)672-5300  
/ TELEFAX: (202)672-5399  
/ TELEX: 904136  
/ INFORMATION FOR SEQ ID NO: 18:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 660 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-521-220-18

Query Match 100.0%; Score 29; DB 2; Length 660;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 531 KAVFFA 536

RESULT 16  
US-09-391-104-19  
/ Sequence 19, Application US/09391104  
/ Patent No. 6399371  
/ GENERAL INFORMATION:  
/ APPLICANT: Abbott Laboratories  
/ APPLICANT: Falduto, Michael T.  
/ APPLICANT: Magnuson, Scott R.  
/ APPLICANT: Morgan, Douglas W.  
/ TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,  
/ TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
/ TITLE OF INVENTION: OF USING SAME  
/ FILE REFERENCE: 6073.US.P1  
/ CURRENT APPLICATION NUMBER: US/09/391,104  
/ CURRENT FILING DATE: 1999-09-07  
/ PRIOR APPLICATION NUMBER: US 08/814,394  
/ PRIOR FILING DATE: 1997-03-11  
/ NUMBER OF SEQ ID NOS: 35  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 19  
/ LENGTH: 660  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-391-104-19

Query Match 100.0%; Score 29; DB 2; Length 660;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 531 KAVFFA 536

RESULT 17  
US-09-917-254-89  
/ Sequence 89, Application US/09917254  
/ Patent No. 6703204  
/ GENERAL INFORMATION:  
/ APPLICANT: Mutter, George  
/ APPLICANT: Baak, Jan  
/ TITLE OF INVENTION: Prognostic Classification of Breast Cancer  
/ FILE REFERENCE: B0801/7224(JRV)  
/ CURRENT APPLICATION NUMBER: US/09/917,254  
/ CURRENT FILING DATE: 2001-07-27  
/ PRIOR APPLICATION NUMBER: US 60/222,093  
/ PRIOR FILING DATE: 2000-07-28  
/ NUMBER OF SEQ ID NOS: 102  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 89  
/ LENGTH: 660  
/ TYPE: PRT  
/ ORGANISM: Homo Sapiens  
US-09-917-254-89

Query Match 100.0%; Score 29; DB 2; Length 660;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 531 KAVFFA 536

RESULT 18  
US-09-949-016-6512  
/ Sequence 6512, Application US/09949016  
/ Patent No. 6812339  
/ GENERAL INFORMATION:  
/ APPLICANT: VENTER, J. Craig et al.  
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
/ FILE REFERENCE: CL001307  
/ CURRENT APPLICATION NUMBER: US/09/949,016  
/ CURRENT FILING DATE: 2000-04-14  
/ PRIOR APPLICATION NUMBER: 60/241,755  
/ PRIOR FILING DATE: 2000-10-20  
/ PRIOR APPLICATION NUMBER: 60/237,768  
/ PRIOR FILING DATE: 2000-10-03  
/ PRIOR APPLICATION NUMBER: 60/231,498  
/ PRIOR FILING DATE: 2000-09-08  
/ NUMBER OF SEQ ID NOS: 207012  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 6512  
/ LENGTH: 660  
/ TYPE: PRT  
/ ORGANISM: Human  
US-09-949-016-6512

Query Match 100.0%; Score 29; DB 2; Length 660;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 531 KAVFFA 536

RESULT 19  
US-09-949-016-7937  
/ Sequence 7937, Application US/09949016  
/ Patent No. 6812339  
/ GENERAL INFORMATION:  
/ APPLICANT: VENTER, J. Craig et al.  
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
/ FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7937  
; LENGTH: 660  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7937

Query Match 100.0%; Score 29; DB 2; Length 660;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||  
Db 531 KAVFFA 536

RESULT 20  
US-10-153-185-14  
; Sequence 14, Application US/10153185  
; Patent No. 6906036  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Stephen  
; APPLICANT: Malik, Sohail  
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds  
; FILE REFERENCE: 1443.034US1  
; CURRENT APPLICATION NUMBER: US/10/153,185  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US 10/032,376  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 660  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-153-185-14

Query Match 100.0%; Score 29; DB 2; Length 660;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||  
Db 531 KAVFFA 536

RESULT 21  
US-09-194-468A-30  
; Sequence 30, Application US/09194468A  
; Patent No. 6500924  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Chereah, David A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/09/194,468A  
; CURRENT FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 663  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-194-468A-30

Query Match 100.0%; Score 29; DB 2; Length 663;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||  
Db 534 KAVFFA 539

RESULT 22  
US-09-471-276-1595  
; Sequence 1595, Application US/09471276  
; Patent No. 6822072  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert A.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.025CPI  
; CURRENT APPLICATION NUMBER: US/09/471,276  
; CURRENT FILING DATE: 1999-12-21  
; EARLIER APPLICATION NUMBER: 09/057,719  
; EARLIER FILING DATE: 1998-04-09  
; EARLIER APPLICATION NUMBER: 09/069,047  
; EARLIER FILING DATE: 1998-04-28  
; EARLIER APPLICATION NUMBER: PCT/IB99/00712  
; EARLIER FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 1622  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1595  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-471-276-1595

Query Match 89.7%; Score 26; DB 2; Length 65;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||  
Db 54 KAVFFS 59

RESULT 23  
US-09-540-236-2808  
; Sequence 2808, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS  
; FILE REFERENCE: 2709,2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 2808  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: M.catarrhalis  
US-09-540-236-2808

```
Query Match      89.7%; Score 26; DB 2; Length 128;
Best Local Similarity 83.3%; Pred. NO. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      55 KAVFYA 60

RESULT 24
US-09-248-796A-18333
; Sequence 18333, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18333
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18333

Query Match      89.7%; Score 26; DB 2; Length 295;
Best Local Similarity 83.3%; Pred. NO. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      31 KAVFYA 36

RESULT 25
US-09-205-258-348
; Sequence 348, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P200721
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
```

```
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 348
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (288)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (334)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-348
```



Query Match 89.7%; Score 26; DB 2; Length 334;  
Best Local Similarity 83.3%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6  
|||:|  
Db 273 KAVFYA 278

RESULT 26  
US-10-004-860-348  
; Sequence 348, Application US/10004860  
; Patent No. 6914047  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/10/004,860  
; CURRENT FILING DATE: 2001-12-07  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 1227  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 348  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (288)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (334)  
; OTHER INFORMATION: Xaa equals stop translation  
US-10-004-860-348

Query Match 89.7%; Score 26; DB 2; Length 334;  
Best Local Similarity 83.3%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6  
|||:|  
Db 273 KAVFYA 278

RESULT 27  
US-09-328-352-7729  
; Sequence 7729, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7729  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-7729

Query Match 89.7%; Score 26; DB 2; Length 494;  
Best Local Similarity 83.3%; Pred. No. 6.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6  
|||:|  
Db 79 KSVFFA 84

RESULT 28

US-09-902-540-10002  
; Sequence 10002, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 10002  
; LENGTH: 535  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-10002

Query Match 89.7%; Score 26; DB 2; Length 535;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6  
|||:|  
Db 131 KALFFA 136

RESULT 29  
US-08-929-329-5  
; Sequence 5, Application US/08929329  
; Patent No. 6120770  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John H  
; APPLICANT: Dalton, John P  
; APPLICANT: Kappe, Stefan  
; TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing  
; TITLE OF INVENTION: Vaccine Compositions  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnes & Thornburg  
; STREET: 11 S Meridian  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: USA  
; ZIP: 46204  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/929,329  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Breen, John P  
; REGISTRATION NUMBER: 38,833  
; REFERENCE/DOCKET NUMBER: 835910-28685  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 231-7745  
; TELEFAX: (317) 231-7433  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1507 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

; ORIGINAL SOURCE:  
; ORGANISM: Plasmodium yoelii  
US-08-929-329-5

Query Match 89.7%; Score 26; DB 2; Length 1507;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
| | | | |  
Db 1454 KAVTFA 1459

RESULT 30  
US-09-095-106A-40  
; Sequence 40, Application US/09095106A  
; Patent No. 6331440  
; GENERAL INFORMATION:  
; APPLICANT: NORDSTEDT, Christer  
; APPLICANT: NASLUND, Jan  
; APPLICANT: THYBERG, Johan  
; APPLICANT: TJERNBERG, Lars O.  
; APPLICANT: TERENIUS, Lars  
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVPF-SEQUENCE OF AMYLOID-BETA  
; FILE REFERENCE: 000500-124  
; CURRENT APPLICATION NUMBER: US/09/095,106A  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: US 60/009,386  
; PRIOR FILING DATE: 1995-12-29  
; PRIOR APPLICATION NUMBER: PCT/SB96/01621  
; PRIOR FILING DATE: 1996-12-09  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Amyloidosis  
US-09-095-106A-40

Query Match 86.2%; Score 25; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
| | | | |  
Db 1 KAVPF 5

RESULT 31  
US-09-747-408-9  
; Sequence 9, Application US/09747408  
; Patent No. 6670399  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-408-9

Query Match 86.2%; Score 25; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
| | | | |  
Db 1 KVVFFA 6

RESULT 32  
US-09-747-408-17  
; Sequence 17, Application US/09747408  
; Patent No. 6670399  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-408-17

Query Match 86.2%; Score 25; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
| | | | |  
Db 1 KVVFFA 6

RESULT 33  
US-08-461-216-4  
; Sequence 4, Application US/08461216  
; Patent No. 5958883  
; GENERAL INFORMATION:  
; APPLICANT: Snow, A.D.  
; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness  
; STREET: 1420 Fifth Avenue, Suite 2800  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101-2347  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Dikette-5.25 inch, 1.2Mb storage  
; COMPUTER: IBM PC/386 Compatible  
; OPERATING SYSTEM: MS-DOS 4.01  
; SOFTWARE: Word for Windows-t  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,216  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,734  
; FILING DATE: October 23, 1992  
; APPLICATION NUMBER: 07/950,417  
; FILING DATE: September 23, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Broderick, Thomas F.  
; REGISTRATION NUMBER: 31,332  
; REFERENCE/DOCKET NUMBER: UOFW-1-6707  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)  
; TELEFAX: 1-206-224-0779



; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43456  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-43456

Query Match 86.2%; Score 25; DB 2; Length 261;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
Db 184 KAVFF 188

## RESULT 39

US-09-252-991A-29199  
; Sequence 29199, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29199  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29199

Query Match 86.2%; Score 25; DB 2; Length 281;  
Best Local Similarity 83.3%; Pred. No. 6.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 6  
Db 257 KAVFF 262

## RESULT 40

US-09-845-713A-2  
; Sequence 2, Application US/09845713A  
; Patent No. 6660476  
; GENERAL INFORMATION:  
; APPLICANT: MacMurray, James P.  
; TITLE OF INVENTION: Polymorphisms in the PMT Gene  
; FILE REFERENCE: 1954-327-II  
; CURRENT APPLICATION NUMBER: US/09/845,713A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,310  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 282  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-845-713A-2

Query Match 86.2%; Score 25; DB 2; Length 282;  
Best Local Similarity 83.3%; Pred. No. 6.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 6  
Db 270 KAVFF 275

## RESULT 41

US-09-303-518D-676  
; Sequence 676, Application US/09303518D  
; Patent No. 6914131  
; GENERAL INFORMATION:  
; APPLICANT: Scarlato, Vincenzo  
; APPLICANT: Massignani, Vega  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizza, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Neisserial Antigens  
; FILE REFERENCE: CHIR0160  
; CURRENT APPLICATION NUMBER: US/09/303,518D  
; CURRENT FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 1098  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 676  
; LENGTH: 306  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-303-518D-676

Query Match 86.2%; Score 25; DB 2; Length 306;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
Db 155 KAVFF 159

## RESULT 42

US-09-303-518D-678  
; Sequence 678, Application US/09303518D  
; Patent No. 6914131  
; GENERAL INFORMATION:  
; APPLICANT: Scarlato, Vincenzo  
; APPLICANT: Massignani, Vega  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizza, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Neisserial Antigens  
; FILE REFERENCE: CHIR0160  
; CURRENT APPLICATION NUMBER: US/09/303,518D  
; CURRENT FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 1098  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 678  
; LENGTH: 306  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (37)..(37)  
; OTHER INFORMATION: Xaa= any amino acid  
; NAME/KEY: misc\_feature  
; LOCATION: (67)..(67)  
; OTHER INFORMATION: Xaa= any amino acid  
; NAME/KEY: misc\_feature  
; LOCATION: (203)..(203)  
; OTHER INFORMATION: Xaa= any amino acid  
; NAME/KEY: misc\_feature  
; LOCATION: (208)..(208)  
; OTHER INFORMATION: Xaa= any amino acid

; NAME/KEY: misc feature  
; LOCATION: (227)..(227)  
; OTHER INFORMATION: Xaa= any amino acid  
; NAME/KEY: misc feature  
; LOCATION: (269)..(269)  
; OTHER INFORMATION: Xaa= any amino acid  
US-09-303-518D-678

Query Match 86.2%; Score 25; DB 2; Length 306;  
Best Local Similarity 100.0%; Pred. No. 7e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
|||  
Db 155 KAVFF 159

RESULT 43  
US-09-303-518D-680  
; Sequence 680, Application US/09303518D  
; Patent No. 6914131  
; GENERAL INFORMATION:  
; APPLICANT: Scarlato, Vincenzo  
; APPLICANT: Massignani, Vega  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizza, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Neisserial Antigens  
; FILE REFERENCE: CHIRO160  
; CURRENT APPLICATION NUMBER: US/09/303,518D  
; CURRENT FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 1098  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 680  
; LENGTH: 307  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-09-303-518D-680

Query Match 86.2%; Score 25; DB 2; Length 307;  
Best Local Similarity 100.0%; Pred. No. 7e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
|||  
Db 155 KAVFF 159

RESULT 44  
US-09-495-406-34  
; Sequence 34, Application US/09495406  
; Patent No. 6503744  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Michel  
; APPLICANT: Wakarchuk, Warren W.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics  
; FILE REFERENCE: 019633-000110US  
; CURRENT APPLICATION NUMBER: US/09/495,406  
; CURRENT FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: US 60/118,213  
; PRIOR FILING DATE: 1999-02-01  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
; FEATURE:  
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (cstI)  
; OTHER INFORMATION: from C. jejuni OH4384  
US-09-495-406-34

Query Match 86.2%; Score 25; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
|||  
Db 61 KAVFF 65

RESULT 45  
US-09-816-028A-48  
; Sequence 48, Application US/09816028A  
; Patent No. 6699705  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Michel  
; APPLICANT: Wakarchuk, Warren W.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics  
; FILE REFERENCE: 019633-000111US  
; CURRENT APPLICATION NUMBER: US/09/816,028A  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/118,213  
; PRIOR FILING DATE: 1999-02-01  
; PRIOR APPLICATION NUMBER: US 09/495,406  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 48  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
; FEATURE:  
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)  
; OTHER INFORMATION: from C. jejuni OH4384  
US-09-816-028A-48

Query Match 86.2%; Score 25; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
|||  
Db 61 KAVFF 65

RESULT 46  
US-10-303-162-48  
; Sequence 48, Application US/10303162  
; Patent No. 6723545  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Michel  
; APPLICANT: Wakarchuk, Warren W.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics  
; FILE REFERENCE: 019633-000111US  
; CURRENT APPLICATION NUMBER: US/10/303,162  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US/09/816,028  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/118,213  
; PRIOR FILING DATE: 1999-02-01  
; PRIOR APPLICATION NUMBER: US 09/495,406  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 48  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
; FEATURE:  
; OTHER INFORMATION: from C. jejuni OH4384  
US-10-303-162-48

```
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-162-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5
Db 61 KAVFP 65

RESULT 47
US-10-303-134-48
; Sequence 48, Application US/10303134
; Patent No. 6825019
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,134
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-134-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5
Db 61 KAVFP 65

RESULT 48
US-10-303-118-48
; Sequence 48, Application US/10303118
; Patent No. 6905867
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,118
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-118-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5
Db 61 KAVFP 65

RESULT 49
US-10-303-128-48
; Sequence 48, Application US/10303128
; Patent No. 6911337
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,128
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-128-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5
Db 61 KAVFP 65

RESULT 50
US-09-270-767-43522
; Sequence 43522, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43522
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
```

US-09-270-767-43522

Query Match 86.2%; Score 25; DB 2; Length 334;  
Best Local Similarity 66.7%; Pred. No. 7.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|:|:|:  
Db 282 KSIFFA 287

RESULT 51

US-09-438-185A-960  
; Sequence 960, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; PRIOR FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 960  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: Cpn0958  
US-09-438-185A-960

Query Match 86.2%; Score 25; DB 2; Length 337;  
Best Local Similarity 66.7%; Pred. No. 7.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|:|:|:  
Db 284 RAIFFA 289

RESULT 52

US-08-749-816-3  
; Sequence 3, Application US/08749816  
; Patent No. 6013470  
; GENERAL INFORMATION:  
; APPLICANT: Lesage, Florian  
; APPLICANT: Guillemaire, Eric  
; APPLICANT: Fink, Michel  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lazdunski, Michel  
; APPLICANT: Romey, Georges  
; APPLICANT: Bathelin, Jacques  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
; TITLE OF INVENTION: OF DRUGS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WEISER & ASSOCIATES  
; STREET: 230 South Fifteenth Street, Suite 500  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/749,816  
; FILING DATE: 15-NOV-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weiser, Gerard J.  
; REGISTRATION NUMBER: 19,763  
; REFERENCE/DOCKET NUMBER: 989.6351P  
; TELEPHONE: 215-875-8383  
; TELEFAX: 215-875-8394  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 347 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-749-816-3

Query Match 86.2%; Score 25; DB 2; Length 347;  
Best Local Similarity 66.7%; Pred. No. 7.9e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|:|:|:  
Db 111 KAIFFS 116

RESULT 53

US-09-144-914-6  
; Sequence 6, Application US/09144914  
; Patent No. 6309855  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lesage, Florian  
; APPLICANT: Fink, Michel  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
; FILE REFERENCE: 989.6705CIP  
; CURRENT APPLICATION NUMBER: US/09/144,914  
; CURRENT FILING DATE: 1998-09-01  
; EARLIER APPLICATION NUMBER: 08/749,816  
; EARLIER FILING DATE: 1996-11-15  
; EARLIER APPLICATION NUMBER: 60/095,234  
; EARLIER FILING DATE: 1998-08-04  
; EARLIER APPLICATION NUMBER: FR 96/01565  
; EARLIER FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 347  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog  
US-09-144-914-6

Query Match 86.2%; Score 25; DB 2; Length 347;  
Best Local Similarity 66.7%; Pred. No. 7.9e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|:|:|:  
Db 111 KAIFFS 116

RESULT 54

US-09-489-039A-11261

; Sequence 11261, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 11261  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-11261

Query Match 86.2%; Score 25; DB 2; Length 375;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
Db 19 KAVPF 23

RESULT 55  
US-09-543-681A-5731  
; Sequence 5731, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 5731  
; LENGTH: 421  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-5731

Query Match 86.2%; Score 25; DB 2; Length 421;  
Best Local Similarity 66.7%; Pred. No. 9.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPFA 6  
Db 334 RAIPFA 339

RESULT 56  
US-09-272-960-2  
; Sequence 2, Application US/09272960  
; Patent No. 6689604  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Michel  
; APPLICANT: Wakarchuk, Warren W.  
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of  
; TITLE OF INVENTION: Campylobacter jejuni and its Uses  
; FILE REFERENCE: 014137-013210US  
; CURRENT APPLICATION NUMBER: US/09/272,960  
; CURRENT FILING DATE: 1999-03-18  
; EARLIER APPLICATION NUMBER: US 60/078,891  
; EARLIER FILING DATE: 1998-03-20  
; EARLIER APPLICATION NUMBER: US 09/272,960  
; EARLIER FILING DATE: 1999-03-18

; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 430  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
US-09-272-960-2

Query Match 86.2%; Score 25; DB 2; Length 430;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
Db 61 KAVPF 65

RESULT 57  
US-10-058-636-2  
; Sequence 2, Application US/10058636  
; Patent No. 6709834  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Michel  
; APPLICANT: Wakarchuk, Warren W.  
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of  
; TITLE OF INVENTION: Campylobacter jejuni and its Uses  
; FILE REFERENCE: 014137-013210US  
; CURRENT APPLICATION NUMBER: US/10/058,636  
; CURRENT FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: US/09/272,960  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: US 60/078,891  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: US 09/272,960  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 430  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
US-10-058-636-2

Query Match 86.2%; Score 25; DB 2; Length 430;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
Db 61 KAVPF 65

RESULT 58  
US-09-583-110-3587  
; Sequence 3587, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lytton Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 3587  
; LENGTH: 462



;  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-3587

Query Match 86.2%; Score 25; DB 2; Length 462;  
Best Local Similarity 100.0%; Pred. No. 1.e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
Db 4 KAVFF 8

## RESULT 59

US-09-107-433-3273  
; Sequence 3273, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 5206  
CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: <Unknown>  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433  
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131  
FILING DATE: May 12, 1998  
APPLICATION NUMBER: 60/051553  
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-011

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3273:

SEQUENCE CHARACTERISTICS:

LENGTH: 473 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...473

SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

US-09-107-433-3273

Query Match 86.2%; Score 25; DB 2; Length 473;  
Best Local Similarity 100.0%; Pred. No. 1.e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
Db 15 KAVFF 19

## RESULT 60

US-09-489-039A-13140  
; Sequence 13140, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709,2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13140

LENGTH: 474

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-13140

Query Match 86.2%; Score 25; DB 2; Length 474;

Best Local Similarity 100.0%; Pred. No. 1.e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

Db 362 KAVFF 366

## RESULT 61

US-08-288-405A-10

; Sequence 10, Application US/08288405A

; Patent No. 5559009

; GENERAL INFORMATION:

APPLICANT: Chandy, Kanianthara G.

APPLICANT: Kalman, Katalin

APPLICANT: Chandy, Grischa

APPLICANT: Gutman, George A.

TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel

TITLE OF INVENTION: Gene

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert,

ATTN: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/288,405A

FILING DATE: 10-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/207,431

FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-59844-1/WHd

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 532 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-288-405A-10

Query Match 86.2%; Score 25; DB 1; Length 532;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
Db 310 KAVPF 314

## RESULT 62

US-10-162-012-13  
; Sequence 13, Application US/10162012  
; Patent No. 6682597  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS  
; FILE REFERENCE: 10448-190001  
; CURRENT APPLICATION NUMBER: US/10/162,012  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,845  
; PRIOR FILING DATE: 2000-06-06  
; PRIOR APPLICATION NUMBER: US 09/875,321  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: PCT/US01/18340  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/209,257  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: US 09/875,423  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: PCT/US01/18398  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/209,238  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: US 09/875,363  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: PCT/US01/18247  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/227,068  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: US 09/928,530  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: PCT/US01/25475  
; PRIOR FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: US 60/226,770  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: US 09/934,421  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: PCT/US01/26096  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: US 60/279,281  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 10/109,029  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: PCT/US02/09728  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 60/290,288  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US (not assigned)  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 532  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-162-012-13

Query Match 86.2%; Score 25; DB 2; Length 532;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
Db 310 KAVPF 314

## RESULT 63

US-09-605-703B-2398  
; Sequence 2398, Application US/09605703B  
; Patent No. 6962989  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Habethauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: BGI-129CP  
; CURRENT APPLICATION NUMBER: US/09/605,703B  
; CURRENT FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: 60/142,764  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: 60/152,318  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 2934  
; SEQ ID NO 2398  
; LENGTH: 547  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-605-703B-2398

Query Match 86.2%; Score 25; DB 2; Length 547;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
Db 454 KAVPF 458

## RESULT 64

US-08-594-031-90  
; Sequence 90, Application US/08594031  
; Patent No. 5783182  
; GENERAL INFORMATION:  
; APPLICANT: THOMPSON, Timothy C.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
; NUMBER OF SEQUENCES: 175  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BAKER & BOTTS, L.L.P.  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004-2400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,031  
; FILING DATE: 30-JAN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/006,838  
; FILING DATE: 16-NOV-1995  
; ATTORNEY/AGENT INFORMATION:

; NAME: Remenick, James  
; REGISTRATION NUMBER: 36,902  
; REFERENCE/DOCKET NUMBER: 0A146-0110  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-639-7700  
; TELEFAX: 202-639-7890  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 90:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 560 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
US-08-594-031-90

Query Match 86.2%; Score 25; DB 1; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
Db 537 KAVFF 541

RESULT 65  
US-09-643-597-225  
; Sequence 225, Application US/09643597  
; Patent No. 6426072  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C11  
; CURRENT FILING DATE: US/09/643,597  
; CURRENT FILING DATE: 2000-08-21  
; NUMBER OF SEQ ID NOS: 369  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 225  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-643-597-225

Query Match 86.2%; Score 25; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
Db 537 KAVFF 541

RESULT 66  
US-09-480-884A-225  
; Sequence 225, Application US/09480884A  
; Patent No. 6482597  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C6  
; CURRENT APPLICATION NUMBER: US/09/480,884A  
; CURRENT FILING DATE: 2001-08-27  
; NUMBER OF SEQ ID NOS: 330  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 225  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-480-884A-225

Query Match 86.2%; Score 25; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
Db 537 KAVFF 541

RESULT 67  
US-09-542-615A-225  
; Sequence 225, Application US/09542615A  
; Patent No. 6518256  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C8  
; CURRENT APPLICATION NUMBER: US/09/542,615A  
; CURRENT FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 225  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-542-615A-225

Query Match 86.2%; Score 25; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
Db 537 KAVFF 541

RESULT 68  
US-09-606-421B-225  
; Sequence 225, Application US/09606421B  
; Patent No. 6531315  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C9  
; CURRENT APPLICATION NUMBER: US/09/606.421B  
; CURRENT FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 225  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-606-421B-225

Query Match 86.2%; Score 25; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5  
Db 537 KAVFP 541

## RESULT 69

US-09-476-496A-225  
; Sequence 225, Application US/09476496A  
; Patent No. 6706262

## ; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF  
; TITLE OF INVENTION: LUNG CANCER  
; FILE REFERENCE: 210121.455C5  
; CURRENT APPLICATION NUMBER: US/09/476.496A  
; CURRENT FILING DATE: 1999-12-30  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 225  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-476-496A-225

Query Match 86.2%; Score 25; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5  
Db 537 KAVFP 541

## RESULT 70

US-09-630-940B-225  
; Sequence 225, Application US/09630940B  
; Patent No. 6737514

## ; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skelky, Yahir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C10  
; CURRENT APPLICATION NUMBER: US/09/630.940B

; CURRENT FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 367  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 225  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-630-940B-225

Query Match 86.2%; Score 25; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5  
Db 537 KAVFP 541

## RESULT 71

US-09-943-075A-6  
; Sequence 6, Application US/09943075A  
; Patent No. 6812002

## ; GENERAL INFORMATION:

; APPLICANT: Popoff, Steven N.  
; APPLICANT: Safado, Favez F.  
; APPLICANT: Owen, Thomas A.  
; APPLICANT: Smock, Steven L.  
; TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,  
; TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation  
; FILE REFERENCE: 71369.262  
; CURRENT APPLICATION NUMBER: US/09/943.075A  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/229,006  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Human  
US-09-943-075A-6

Query Match 86.2%; Score 25; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5  
Db 537 KAVFP 541

## RESULT 72

US-10-039-272A-2  
; Sequence 2, Application US/10039272A  
; Patent No. 6939955

## ; GENERAL INFORMATION:

; APPLICANT: RAMESHWAR, Pranela  
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-TYPE  
; FILE REFERENCE: 267/033 (UMD-0055)  
; CURRENT APPLICATION NUMBER: US/10/039.272A  
; CURRENT FILING DATE: 2001-10-20  
; PRIOR APPLICATION NUMBER: US 60/241,881  
; PRIOR FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-039-272A-2

Query Match 86.2%; Score 25; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

Db 537 KAVFF 541

#### RESULT 73

US-10-007-700-225

; Sequence 225; Application US/10007700

; Patent No. 6960570

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Li, Samuel X.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Fanger, Neil

; APPLICANT: Retter, Marc W.

; APPLICANT: Durham, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Peckman, David W.

; APPLICANT: Cai, Feng

; APPLICANT: Foy, Teresa M.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C17

; CURRENT APPLICATION NUMBER: US/10/007,700

; CURRENT FILING DATE: 2001-11-30

; NUMBER OF SEQ ID NOS: 469

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 225

; LENGTH: 560

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-007-700-225

Query Match

Best Local Similarity 86.2%; Score 25; DB 2; Length 560;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

Db 537 KAVFF 541

#### RESULT 74

US-09-985-799-90

; Sequence 90; Application US/09985799

; Patent No. RE38392

; GENERAL INFORMATION:

; APPLICANT: THOMPSON, Timothy C.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BAKER & BOTTS, L.L.P.

STREET: 1299 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004-2400

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/985,799

; FILING DATE: 06-NO. RE38392-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/594,031

; FILING DATE: 30-JAN-1996

; APPLICATION NUMBER: 60/006,838

; FILING DATE: 16-NOV-1995

; ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James

REGISTRATION NUMBER: 36,902

REFERENCE/DOCKET NUMBER: 0A146-0110

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700

TELEFAX: 202-639-7890

TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 90:

SEQUENCE CHARACTERISTICS:

LENGTH: 560 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

; SEQUENCE DESCRIPTION: SEQ ID NO: 90:

US-09-985-799-90

Query Match

Best Local Similarity 86.2%; Score 25; DB 5; Length 560;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

Db 537 KAVFF 541

#### RESULT 75

US-09-977-371-90

; Sequence 90; Application US/09977371

; Patent No. RE38490

; GENERAL INFORMATION:

; APPLICANT: THOMPSON, Timothy C.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BAKER & BOTTS, L.L.P.

STREET: 1299 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004-2400

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/977,371

FILING DATE: 16-Oct-2001

CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/594,031

FILING DATE: 30-JAN-1996

APPLICATION NUMBER: 60/006,838

FILING DATE: 16-NOV-1995

; ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James

REGISTRATION NUMBER: 36,902

REFERENCE/DOCKET NUMBER: 0A146-0110

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700

```

;
; TELEFAX: 202-639-7890
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 560 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-09-977-371-90

```

```

Query Match      86.2%; Score 25; DB 5; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVFP 5
Db      537 KAVFP 541

```

Search completed: December 29, 2005, 17:52:35  
Job time : 21.1323 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds  
(without alignments)  
32.238 Million cell updates/sec

Title: US-10-009-122-7

Perfect score: 29

Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4	AAB48480
2	29	100.0	6	4	AAB48488
3	29	100.0	6	4	AAB82636
4	29	100.0	6	4	AAB82628
5	29	100.0	6	5	AAB98824
6	29	100.0	6	5	AAU96816
7	29	100.0	6	5	AAU11662
8	29	100.0	6	5	AAU11654
9	29	100.0	6	6	AAE35450
10	29	100.0	6	6	AAE35443
11	29	100.0	6	8	AQ37275
12	29	100.0	6	8	AQ37267
13	29	100.0	6	8	AQ37319
14	29	100.0	6	8	AQ37327
15	29	100.0	6	9	ADY37934
16	29	100.0	6	9	ADY37926
17	29	100.0	37	3	AB05509
18	29	100.0	37	8	ADK34079
19	29	100.0	42	8	ADL70726
20	29	100.0	42	8	ADG17617
21	29	100.0	42	8	ADG17612
22	29	100.0	74	2	AAW41091
23	29	100.0	74	2	AAW41085
24	29	100.0	74	2	AAW41230

25	29	100.0	74	8	ADT05998	Modified
26	29	100.0	74	8	ADT05965	Human mat
27	29	100.0	74	8	ADT05971	Chicken m
28	29	100.0	108	2	AAW41086	Human mat
29	29	100.0	108	2	AAW41092	Chicken m
30	29	100.0	108	2	AAW41231	Alpha-v-b
31	29	100.0	108	2	AAW41237	Alpha-v-b
32	29	100.0	108	8	ADT05972	Chicken m
33	29	100.0	108	8	ADT05966	Human mat
34	29	100.0	108	8	ADT05999	Modified
35	29	100.0	122	2	AAW41238	Alpha-v-b
36	29	100.0	152	2	AAW41232	Alpha-v-b
37	29	100.0	193	2	AAW41090	Chicken m
38	29	100.0	193	2	AAW41084	Human mat
39	29	100.0	193	2	AAW41229	Alpha-v-b
40	29	100.0	193	2	AAW41235	Alpha-v-b
41	29	100.0	193	8	ADT05964	Human mat
42	29	100.0	193	8	ADT05970	Chicken m
43	29	100.0	222	2	AAW41083	Human mat
44	29	100.0	222	2	AAW41228	Alpha-v-b
45	29	100.0	222	8	ADT05963	Human mat
46	29	100.0	228	2	AAW41089	Chicken m
47	29	100.0	228	2	AAW41234	Alpha-v-b
48	29	100.0	228	8	ADT05969	Chicken m
49	29	100.0	261	8	ADT05661	Haemophil
50	29	100.0	429	2	AAW41112	Human mat
51	29	100.0	429	8	ADT05991	Human mat
52	29	100.0	468	4	ABG24001	Novel hum
53	29	100.0	623	8	ABM84057	Human dia
54	29	100.0	626	8	ADG17622	Modified
55	29	100.0	626	8	ADG17627	Modified
56	29	100.0	631	1	AAW41143	Sequence
57	29	100.0	631	1	AAW41139	Human typ
58	29	100.0	631	2	AAW41139	Complete
59	29	100.0	631	2	AAW41139	Human typ
60	29	100.0	631	7	ADM48668	Human mat
61	29	100.0	631	8	ADT05996	Human mat
62	29	100.0	633	8	ADT05997	Mouse mat
63	29	100.0	644	4	AAW41240	Human mat
64	29	100.0	660	2	AAW41240	Type IV c
65	29	100.0	660	4	AAW41240	Amino aci
66	29	100.0	660	4	AAW41240	Human mat
67	29	100.0	660	4	AAW41240	Human mat
68	29	100.0	660	5	ABW79413	Human mat
69	29	100.0	660	5	ABW79413	Human mat
70	29	100.0	660	5	AAW41240	Protein M
71	29	100.0	660	6	ABW4445	Human mat
72	29	100.0	660	6	ABW79136	Human mat
73	29	100.0	660	6	AAW41240	Human mat
74	29	100.0	660	6	ABW79136	Human mat
75	29	100.0	660	7	ADW18578	Human dis
76	29	100.0	660	7	ADW18578	Human mat
77	29	100.0	660	8	ADW17697	Human mat
78	29	100.0	660	8	ADW17697	Human mat
79	29	100.0	660	9	ADW30301	Protease-
80	29	100.0	660	9	ADW30301	Human mat
81	29	100.0	662	7	ADW68478	Rat Prote
82	29	100.0	662	7	ADW68478	Rat Prote
83	29	100.0	663	2	AAW41111	Chicken m
84	29	100.0	663	2	AAW41111	Chicken m
85	29	100.0	663	8	ADT05976	Chicken m
86	29	100.0	663	8	ADT05995	Chicken m
87	29	100.0	708	9	ADW60554	Human con
88	29	100.0	708	9	ADW60554	Novel hum
89	29	100.0	718	8	ADN22220	Bacterial
90	29	100.0	737	8	ADN22220	Bacterial
91	29	100.0	1147	2	AAW41227	Rat induc
92	29	100.0	1330	4	ABW23999	Novel hum
93	28	96.6	383	8	ADN25046	Bacterial
94	28	96.6	383	8	ADN22288	Bacterial
95	26	89.7	65	3	AAW41091	Human 5'
96	26	89.7	65	8	ADU72998	Non-aligna
97	26	89.7	65	9	ADZ73989	Human Com



98	26	89.7	128	8	ADL05122	Adl05122 M. catarr	171	25	86.2	117	4	AAM17468	Aam17468 Peptide #
99	26	89.7	138	4	ABG09090	Abg09090 Novel hum	172	25	86.2	117	4	ABE36488	Abb36488 Peptide #
100	26	89.7	149	9	AEb41486	Aeb41486 L. pneumo	173	25	86.2	117	4	AAM29987	Aam29987 Peptide #
101	26	89.7	166	9	ABb38197	Abb38197 L. pneumo	174	25	86.2	117	4	ABB31282	Abb31282 Peptide #
102	26	89.7	208	4	ABG09092	Abg09092 Novel hum	175	25	86.2	117	4	ABB21830	Abb21830 Protein #
103	26	89.7	210	6	ABU33715	Abu33715 Protein e	176	25	86.2	117	4	AAM69653	Aam69653 Human bon
104	26	89.7	238	4	AAM31660	Aam31660 Novel hum	177	25	86.2	117	4	AAM57251	Aam57251 Human bra
105	26	89.7	292	4	AAM42075	Aam42075 Human pol	178	25	86.2	117	4	ABG51335	Abg51335 Human liv
106	26	89.7	296	3	AAB43372	Aab43372 Human ORF	179	25	86.2	117	4	AAM05146	Aam05146 Peptide #
107	26	89.7	320	8	ADY08844	Ady08844 Plant ful	180	25	86.2	117	5	ABG39273	Abg39273 Human pep
108	26	89.7	320	8	ADY73944	Ady73944 Plant ful	181	25	86.2	117	5	ABG55307	Abg55307 Human gen
109	26	89.7	322	5	ABBO6658	Abbo6658 G protein	182	25	86.2	132	8	ABO56701	Abos56701 Carassius
110	26	89.7	329	4	AAM40289	Aam40289 Human pol	183	25	86.2	141	7	AAW20912	Aaw20912 H. pylori
111	26	89.7	334	2	AAM88633	Aam88633 Secreted	184	25	86.2	150	2	AAU60292	Aau60292 Propionib
112	26	89.7	334	4	ABBS0400	Abbs0400 Human sec	185	25	86.2	160	4	ABM56811	Abms56811 Propionib
113	26	89.7	334	6	ABO44657	Abos44657 Novel hum	186	25	86.2	160	6	ABM56811	Abms56811 Propionib
114	26	89.7	334	7	ABO26137	Abos26137 Human pro	187	25	86.2	174	3	AGC233502	Agc233502 Arabidops
115	26	89.7	352	8	ADP29738	Adp29738 Human sec	188	25	86.2	174	3	AGC39522	Agc39522 Arabidops
116	26	89.7	358	8	ADQ96208	Adq96208 T cell ac	189	25	86.2	175	4	AAO11219	Aao11219 Human pol
117	26	89.7	358	8	ADQ96210	Adq96210 T cell ac	190	25	86.2	186	7	ADC07962	Adc07962 Rice prot
118	26	89.7	421	4	AGG98352	Agg98352 Escherich	191	25	86.2	186	7	ADC07948	Adc07948 Rice prot
119	26	89.7	421	6	ABU14827	Abu14827 Protein e	192	25	86.2	190	4	AAM83792	Aam83792 Human imm
120	26	89.7	441	3	AY53014	Aay53014 Human sec	193	25	86.2	200	7	ABM89622	Abm89622 Rice abio
121	26	89.7	494	6	ADA36442	Ada36442 Acinetoba	194	25	86.2	201	8	ADY12035	Ady12035 Plant ful
122	26	89.7	535	9	ABM90803	Abm90803 M. xanthu	195	25	86.2	202	8	ADU05630	Adu05630 H. pylori
123	26	89.7	555	4	AAM93388	Aam93388 Human pol	196	25	86.2	206	3	AGC39521	Agc39521 Arabidops
124	26	89.7	555	4	AGG66415	Agg66415 Human maj	197	25	86.2	207	3	AGC233501	Agc233501 Arabidops
125	26	89.7	555	8	ADL30943	Adl30943 Human pro	198	25	86.2	210	6	ABP79894	Abp79894 N. gonorr
126	26	89.7	555	8	ADQ96132	Adq96132 T cell ac	199	25	86.2	210	6	ABU37523	Abu37523 Protein e
127	26	89.7	555	9	ADY07709	Ady07709 Cyclin-de	200	25	86.2	210	6	ABU38175	Abu38175 Protein e
128	26	89.7	556	3	AY87342	Aay87342 Human sig	201	25	86.2	213	3	AGS51077	Aggs51077 Arabidops
129	26	89.7	564	4	AAH88362	Aah88362 Human mem	202	25	86.2	239	8	ADN46479	Adn46479 Thermoco
130	26	89.7	564	8	ADQ96212	Adq96212 T cell ac	203	25	86.2	242	3	AGC12759	Agc12759 Arabidops
131	26	89.7	564	9	ADY63089	Ady63089 Human clo	204	25	86.2	243	3	AGC12759	Agc12759 Arabidops
132	26	89.7	715	6	ABU47623	Abu47623 Protein e	205	25	86.2	246	3	AGS51075	Aggs51075 Arabidops
133	26	89.7	1042	6	ABU33994	Abu33994 Protein e	206	25	86.2	246	4	ABM58652	Abms58652 Drosophi
134	26	89.7	1172	4	ABG06613	Abg06613 Novel hum	207	25	86.2	247	2	AAW20248	Aaw20248 H. pylori
135	26	89.7	1507	3	ABZ41128	Aab41128 Plasmodiu	208	25	86.2	249	8	ADS21551	Ads21551 Bacterial
136	25	86.2	5	2	AAW45963	Aaw45963 Peptide d	209	25	86.2	254	8	ADS27681	Ads27681 Bacterial
137	25	86.2	6	4	AAW48482	Aab48482 Antifibri	210	25	86.2	255	4	ABM67621	Abm67621 Drosophi
138	25	86.2	6	4	AAW48490	Aab48490 Antifibri	211	25	86.2	255	6	ABM68528	Abm68528 Phototab
139	25	86.2	6	4	AAW82630	Aab82630 All-D pep	212	25	86.2	256	8	ADS41641	Ads41641 Bacterial
140	25	86.2	6	4	AAW82638	Aab82638 All-D pep	213	25	86.2	268	8	ADS41641	Ads41641 Bacterial
141	25	86.2	6	5	AAU96818	Aau96818 Amyloid t	214	25	86.2	272	3	AGI12758	Aggi12758 Arabidops
142	25	86.2	6	5	AAU96818	Aau96818 Amyloid t	215	25	86.2	276	3	AGI12758	Aggi12758 Arabidops
143	25	86.2	6	5	AAU11664	Aau11664 Peptide #	216	25	86.2	281	1	ABO80453	Abos80453 Pseudomon
144	25	86.2	6	5	AAU11656	Aau11656 Peptide #	217	25	86.2	282	1	ABP90422	Abp90422 Human phe
145	25	86.2	6	6	AAU11656	Aau11656 Peptide #	218	25	86.2	282	8	ADH13186	Adh13186 Human mal
146	25	86.2	6	6	AAU35452	Aau35452 Abeta pep	219	25	86.2	282	8	ADH13186	Adh13186 Human mal
147	25	86.2	6	8	ADQ37277	Adq37277 Vaccine a	220	25	86.2	282	9	AEA15073	Aea15073 Human pol
148	25	86.2	6	8	ADQ37321	Adq37321 Antifibri	221	25	86.2	282	9	AEA08357	Aea08357 Human phe
149	25	86.2	6	9	ADY37928	Ady37928 Amyloid-t	222	25	86.2	285	4	AAM39174	Aam39174 Human pol
150	25	86.2	6	9	ADY37936	Ady37936 Amyloid-t	223	25	86.2	297	8	ADY25262	Ady25262 Plant ful
151	25	86.2	22	8	ADQ09761	Adq09761 Rice 26kD	224	25	86.2	303	6	ABR40195	Abra40195 alpha-2.3
152	25	86.2	23	8	ADY33984	Ady33984 Rice 26 k	225	25	86.2	306	2	AAU38837	Aau38837 Neisseria
153	25	86.2	25	4	ABBO3313	Abbo3313 Human mus	226	25	86.2	306	2	AAU38836	Aau38836 Neisseria
154	25	86.2	25	6	ABU12607	Abu12607 Novel hum	227	25	86.2	306	9	ABE49486	Aeb49486 N. mening
155	25	86.2	25	8	ADY328633	Ady328633 Human mus	228	25	86.2	306	9	ABE49484	Aeb49484 N. mening
156	25	86.2	28	2	ADY328633	Ady328633 Human mus	229	25	86.2	307	9	AAU38838	Aau38838 Neisseria
157	25	86.2	34	7	ADY24404	Ady24404 Human end	230	25	86.2	307	9	ABE49488	Aeb49488 N. gonorr
158	25	86.2	37	3	AAW05910	Aaw05910 Mouse ind	231	25	86.2	309	5	ABO66559	Abos66559 G protein
159	25	86.2	37	8	ADK34080	Adk34080 Human rNO	232	25	86.2	314	5	AAU833579	Aau833579 Human nov
160	25	86.2	37	8	ADL70727	Adl70727 Mouse iNO	233	25	86.2	314	7	ADM29640	Adm29640 Novel hum
161	25	86.2	42	3	AAW04347	Aaw04347 Arabidops	234	25	86.2	319	7	ABM87620	Abm87620 Rice abio
162	25	86.2	50	3	AAW04346	Aaw04346 Arabidops	235	25	86.2	322	5	AAU24642	Aau24642 Human Olf
163	25	86.2	65	3	ABO55025	Abos55025 Human gen	236	25	86.2	322	5	ABO6657	Abos6657 G protein
164	25	86.2	69	3	AAW24897	Aaw24897 Arabidops	237	25	86.2	322	5	ABP95886	Abp95886 Human GPC
165	25	86.2	77	3	AAW02840	Aaw02840 Human sec	238	25	86.2	322	5	AAU95597	Aau95597 Human Olf
166	25	86.2	80	6	ABO00562	Abos00562 Novel hum	239	25	86.2	322	6	AAU85262	Aau85262 G-coupled
167	25	86.2	83	4	AAW92860	Aaw92860 Human dig	240	25	86.2	322	7	ADH11149	Adh11149 Human G-p
168	25	86.2	90	4	AAU47327	Aau47327 Propionib	241	25	86.2	322	7	ADH85681	Adh85681 Human GPC
169	25	86.2	90	6	ABM43846	Abm43846 Propionib	242	25	86.2	322	8	ADG83362	Adg83362 Human Olf
170	25	86.2	105	4	AAO00117	Aao00117 Human pol	243	25	86.2	332	8	ADS44454	Ads44454 Bacterial

244	25	86.2	332	8	ADS22134
245	25	86.2	347	3	AAY79676
246	25	86.2	354	4	ABB59799
247	25	86.2	371	3	AAG31391
248	25	86.2	372	3	AAB10940
249	25	86.2	372	3	AAB10944
250	25	86.2	372	3	AAB10939
251	25	86.2	372	3	AAB10938
252	25	86.2	372	3	AAB10943
253	25	86.2	372	3	AAB10941
254	25	86.2	372	3	AAB10937
255	25	86.2	372	3	AAB10942
256	25	86.2	372	3	AAG31390
257	25	86.2	375	7	ABO64744
258	25	86.2	380	8	ADN25333
259	25	86.2	382	8	ADS22130
260	25	86.2	411	3	AAG13578
261	25	86.2	411	6	ABU49877
262	25	86.2	412	3	AAG13577
263	25	86.2	415	6	ABU40846
264	25	86.2	420	3	AAG31389
265	25	86.2	421	7	ADF05446
266	25	86.2	430	2	AAV45221
267	25	86.2	454	5	ABG31335
268	25	86.2	460	3	AAG13576
269	25	86.2	460	5	ABP27238
270	25	86.2	460	8	ADV89577
271	25	86.2	460	8	ADV82984
272	25	86.2	460	8	ADV80830
273	25	86.2	462	5	ABP27239
274	25	86.2	462	5	ABB54050
275	25	86.2	462	8	ADK47072
276	25	86.2	466	5	ABP26930
277	25	86.2	466	8	ADV81295
278	25	86.2	472	8	ABU02501
279	25	86.2	473	8	ADR94638
280	25	86.2	473	9	ASA58508
281	25	86.2	474	9	ABO66623
282	25	86.2	475	3	ABAB01368
283	25	86.2	481	4	ABB58790
284	25	86.2	507	6	ABG76432
285	25	86.2	512	8	ADO26827
286	25	86.2	532	2	AAR82937
287	25	86.2	532	6	ABP98780
288	25	86.2	539	6	ABU20239
289	25	86.2	544	2	AAR82213
290	25	86.2	552	6	ABU21210
291	25	86.2	558	6	ABU22708
292	25	86.2	560	2	AAW35382
293	25	86.2	560	3	ABU11329
294	25	86.2	560	4	AAG91711
295	25	86.2	560	5	ABB78200
296	25	86.2	560	5	ABB74961
297	25	86.2	560	5	ABP61881
298	25	86.2	560	5	ABU56592
299	25	86.2	560	6	ABG72962
300	25	86.2	560	6	ABU70852

ALIGNMENTS

RESULT 1  
 AAB48480  
 ID AAB48480 standard; peptide; 6 AA.  
 XX  
 AC AAB48480;  
 XX  
 XX 02-MAR-2001 (first entry)  
 XX  
 DE Antifibrillogenic peptide #7.  
 XX  
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;

ADs22134 Bacterial  
 Aay79676 Caenorhab  
 ABB59799 Drosophil  
 Aag31391 Arabidops  
 Aab10940 L. donova  
 Aab10944 L. major  
 Aab10939 L. infant  
 Aab10938 L. amazon  
 Aab10943 L. tropic  
 Aab10941 L. chagas  
 Aab10937 L. mexica  
 Aab10942 L. aethio  
 Aag31390 Arabidops  
 Abo64744 Klebsiell  
 Adn25333 Bacterial  
 Ads22130 Bacterial  
 Aag13578 Arabidops  
 Abu49877 Protein e  
 Aag13577 Arabidops  
 Abu40846 Protein e  
 Aag31389 Arabidops  
 Adf05446 Bacterial  
 Aay45221 Campyloba  
 Abg31335 Murine KC  
 Aag13576 Arabidops  
 Abp27238 Streptoco  
 Adv89577 Streptoco  
 Adv82984 Streptoco  
 Adv80830 Streptoco  
 Abp27239 Streptoco  
 Abb54050 Lactococc  
 Adk47072 Streptoco  
 Abp26930 Streptoco  
 Adv81295 Streptoco  
 Abu02501 S. pneumo  
 ADR94638 Novel S.  
 Aea58508 Streptoco  
 Abo66623 Klebsiell  
 Aab01368 1-deoxy-D  
 Abb58790 Drosophil  
 Abg76432 Sindbis p  
 Abo26827 Human rec  
 Aar82937 Mouse Kv1  
 App98780 Mouse Kv1  
 Abu20239 Protein e  
 Aar82213 Talaromyc  
 Abu21210 Protein e  
 Abu22708 Protein e  
 Aaw35382 Murine me  
 Aab11329 Human lun  
 Aag91711 C glutami  
 Abb78200 Amino aci  
 Abb74961 Human lun  
 Abp61881 Human lun  
 Abu56592 Lung canc  
 Abg72962 Human oet  
 Abu70852 Human adi

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 XX Homo sapiens.  
 OS  
 PN WO200068263-A2.  
 XX  
 PD 16-NOV-2000.  
 XX  
 XX 04-MAY-2000; 2000WO-CA000515.  
 PF  
 XX 05-MAY-1999; 99US-0132592P.  
 PR  
 XX (NEUR-) NEUROCHEM INC.  
 PA  
 XX Chalfour R, Gervais F, Gupta A;  
 PI  
 XX WPI; 2001-031852/04.  
 DR  
 XX  
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.  
 PS  
 XX Claim 7; Page 25; 46pp; English.  
 CC  
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycoaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein  
 CC  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||  
 Db 1 KAVFFA 6

RESULT 2  
 AAB48480  
 ID AAB48480 standard; peptide; 6 AA.  
 XX  
 AC AAB48480;  
 XX  
 XX 02-MAR-2001 (first entry)  
 DT  
 XX Antifibrillogenic peptide #15.  
 DE  
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 6  
 FT /note= "C-terminal amide"  
 XX  
 PN WO200068263-A2.  
 XX  
 PD 16-NOV-2000.  
 XX  
 XX 04-MAY-2000; 2000WO-CA000515.  
 PF  
 XX 05-MAY-1999; 99US-0132592P.  
 PR  
 XX (NEUR-) NEUROCHEM INC.  
 PA

XX Chalifour R, Gervais F, Gupta A;  
 XX WPI; 2001-031852/04.  
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 XX cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 XX its isomer or peptidomimetic.  
 XX Claim 7; Page 25; 46pp; English.  
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 XX for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 XX AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 XX useful for treating amyloidosis disorders such as Alzheimer's disease.  
 XX Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 XX binding region and the prot-prot interaction region of the human amyloid  
 XX protein.  
 XX Sequence 6 AA;  
 SQ Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 Db 1 KAVFFA 6  
 RESULT 3  
 AAB82636  
 ID AAB82636 standard; peptide; 6 AA.  
 AC AAB82636;  
 XX 02-OCT-2001 (first entry)  
 XX All-D peptide used in Alzheimer's disease vaccine.  
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 FH Misc-difference 1..6 /note= "all D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"  
 FT  
 XX WO200139796-A2.  
 PN 07-JUN-2001.  
 XX 29-NOV-2000; 2000WO-CA001413.  
 XX 29-NOV-1999; 99US-0168594P.  
 PR 28-NOV-2000; 2000US-00724842.  
 XX (NEUR-) NEUROCHEM INC.  
 PA Chalifour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 XX which elicits production of antibodies to prevent fibrillogenesis and  
 XX associated cellular toxicity.  
 XX Disclosure; Page 11; 31pp; English.

CC The present sequence is that of an all-D peptide suitable for use in  
 CC preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients  
 XX Sequence 6 AA;  
 SQ Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 Db 1 KAVFFA 6  
 RESULT 4  
 AAB82628  
 ID AAB82628 standard; peptide; 6 AA.  
 AC AAB82628;  
 XX 02-OCT-2001 (first entry)  
 XX All-D peptide used in Alzheimer's disease vaccine.  
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 FH Misc-difference 1..6 /note= "all D-form residues"  
 FT  
 XX WO200139796-A2.  
 PN 07-JUN-2001.  
 XX 29-NOV-2000; 2000WO-CA001413.  
 XX 29-NOV-1999; 99US-0168594P.  
 PR 28-NOV-2000; 2000US-00724842.  
 XX (NEUR-) NEUROCHEM INC.  
 PA Chalifour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and  
 FT associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for  
 CC preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see A4882622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in A4882623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||  
 Db 1 KAVFFA 6

RESULT 5

AAU96824  
 ID AAU96824 standard; peptide; 6 AA.

AC AAU96824;

DT 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #14.

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1, 6

FT /note= "Preferably D-form residue"

FT Modified-site 6

FT /note= "Ala is amidated"

XX WO200207781-A2.

XX 31-JAN-2002.

XX

PF 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

PA

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX

DR New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX

XX The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A t-(A 1 n k) z-A 1 a b (I) where z = 0 - 1;  
 CC A t = an amyloid targeting moiety; A 1 n k = a linker moiety; and A 1 a b  
 CC = a labelling moiety. Also included are imaging amyloid deposition or  
 CC diagnosing an amyloid-related condition in a patient involving  
 CC administering (I) to the patient, and ultrasound imaging (I) in the  
 CC patient to determine the presence of amyloid or amyloid-related condition  
 CC , and a kit for preparing a radiopharmaceutical preparation comprising  
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and  
 CC instructions for the preparation and use of the radiopharmaceutical in  
 CC the imaging of amyloid or an amyloid-related condition. The agents are  
 CC used for imaging amyloid deposition and for diagnosing an amyloid related  
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible  
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||

Db 1 KAVFFA 6

RESULT 6

AAU96816

ID AAU96816 standard; peptide; 6 AA.

XX

AC AAU96816;

DT 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #6.

XX

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

OS Synthetic.

XX

FH Key Location/Qualifiers  
 FT Misc-difference 1..6  
 FT /note= "Preferably D-form residue"  
 XX WO200207781-A2.  
 PN 31-JAN-2002.  
 PD  
 XX 25-JUL-2001; 2001WO-CA001071.  
 XX 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.  
 XX (NEUR-) NEUROCHEM INC.  
 XX Gervais F, Kong X, Chalifour R, Migneault D;  
 XX WPI; 2002-371447/40.  
 DR  
 XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 FT plaques and/or for the treatment of amyloidosis disorders.  
 XX  
 XX Claim 49; Page 21; 57pp; English.

CC The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A<sub>1</sub>-L<sub>1</sub>-A<sub>2</sub> (where z = 0 - 1;  
 CC A<sub>1</sub> is an amyloid targeting moiety; L<sub>1</sub> is a linker moiety; and A<sub>2</sub> is a  
 CC labelling moiety. Also included are imaging amyloid deposition or  
 CC diagnosing an amyloid-related condition in a patient involving  
 CC administering (i) to the patient, and ultrasound imaging (i) in the  
 CC patient to determine the presence of amyloid or amyloid-related condition  
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising  
 CC (i), a reducing agent, a buffering agent, a transchelating agent, and  
 CC instructions for the preparation and use of the radiopharmaceutical in  
 CC the imaging of amyloid or an amyloid-related condition. The agents are  
 CC used for imaging amyloid deposition and for diagnosing an amyloid related  
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible  
 CC cerebral amyloidosis (transmissible virus dementias), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention

Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6  
 DB 1 KAVFFFA 6

RESULT 7

AAU11662  
 ID AAU11662 standard; peptide; 6 AA.

AC AAU11662;

DT 09-APR-2002 (first entry)

DE Peptide #15, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.

KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Modified-site 6  
 FT /note= "C-terminal amide"  
 XX WO200185093-A2.  
 XX 15-NOV-2001.  
 XX 22-DEC-2000; 2000WO-IB002078.  
 XX 23-DEC-1999; 99US-0171877P.  
 XX (NEUR-) NEUROCHEM INC.  
 XX Green AM, Gervais F;  
 XX WPI; 2002-075222/10.  
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
 FT disease comprises contacting blood vessel wall cell with amyloid-beta 40  
 FT inhibitor.

Disclosure; Page 10; 68pp; English.

CC The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting a  
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
 CC The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)

Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6  
 DB 1 KAVFFFA 6

RESULT 8

AAU11654  
 ID AAU11654 standard; peptide; 6 AA.

AC AAU11654;

DT 09-APR-2002 (first entry)

DE Peptide #7, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.

KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

OS Synthetic.

XX WO200185093-A2.

XX 15-NOV-2001.

XX 22-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.  
 XX Green AM, Gervais F;  
 XX WPI; 2002-075222/10.  
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40  
 PT inhibitor.  
 XX Disclosure; Page 10; 68pp; English.  
 XX The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting a  
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
 CC The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)  
 XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFFA 6  
 |||||  
 Db 1 KAVFFFA 6

RESULT 9  
 AAE35450  
 ID AAE35450 standard; peptide; 6 AA.

XX AAE35450;  
 AC AAE35450;  
 DT 17-JUN-2003 (first entry)  
 XX Abeta peptide #21.  
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.  
 XX Unidentified.

XX Key Location/Qualifiers  
 FH Misc-difference 1. .6 /note= "D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"  
 FT

XX WO200296937-A2.  
 XX 05-DEC-2002.  
 XX 29-MAY-2002; 2002WO-CA000763.  
 XX 29-MAY-2001; 2001US-00867847.  
 XX (NEUR-) NEUROCHEM INC.

FI Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.  
 XX Prevention and/or treatment of an amyloid-related disease e.g.  
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 XX Claim 1; Page 59; 44pp; English.

XX The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFFA 6  
 |||||  
 Db 1 KAVFFFA 6

RESULT 10  
 AAE35443  
 ID AAE35443 standard; peptide; 6 AA.

XX AAE35443;  
 AC AAE35443;  
 DT 17-JUN-2003 (first entry)  
 XX Abeta peptide #14.  
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.  
 XX Unidentified.

XX Key Location/Qualifiers  
 FH Misc-difference 1. .6 /note= "D-form residues"  
 FT

XX WO200296937-A2.  
 XX 05-DEC-2002.  
 XX 29-MAY-2002; 2002WO-CA000763.  
 XX 29-MAY-2001; 2001US-00867847.  
 XX (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;  
 XX WPI; 2003-201269/19.  
 XX Prevention and/or treatment of an amyloid-related disease e.g.  
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 XX  
 XX Claim 1; Page 59; 44pp; English.  
 XX  
 XX The invention relates to a method for prevention and/or treatment of an  
 XX amyloid-related disease which comprises administration of an all-D-  
 XX amyloid-beta peptide. The method is used for preventing and/or treating  
 XX Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 XX angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 XX favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 XX the mammal; and reducing or inhibiting the formation of plaques. It is  
 XX also used for treating AA (reactive) amyloid diseases including  
 XX inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 XX arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 XX Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 XX disease. AA deposits are also produced as a result of chronic microbial  
 XX infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 XX ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 XX Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 XX including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 XX and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 XX present sequence is an A-beta peptide used to illustrate the method of the  
 XX invention  
 XX  
 XX Sequence 6 AA;  
 XX  
 XX Query Match 100.0%; Score 29; DB 6; Length 6;  
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 KAVFFFA 6  
 Db |||||  
 1 KAVFFFA 6  
 RESULT 11  
 ADQ37275  
 ID ADQ37275 standard; peptide; 6 AA.  
 XX  
 AC ADQ37275;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Vaccine antigen amyloid-beta related amino acid sequence.  
 XX  
 KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antihypertoid; vasotropic; cardiovascular; tranquiliser; uteropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..6  
 FT /note= "D-form residues"  
 FT Modified-site 6  
 FT /note= "amidated"

XX WO2004058239-A1.  
 XX 15-JUL-2004.  
 XX 24-DEC-2003; 2003WO-CA002021.  
 XX 24-DEC-2002; 2002US-0436379P.  
 XX 23-JUN-2003; 2003US-0482214P.  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX Gervais F, Bellini F;  
 XX WPI; 2004-543342/52.  
 XX  
 XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 XX that prevents or treats amyloid-beta related disease and second agent  
 XX that is either a peptide or peptidomimetic or an immune system modulator.  
 XX  
 XX Disclosure; Page 67; 143pp; English.  
 XX  
 XX The present invention describes compositions (C) comprising: (a) a first  
 XX agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 XX a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 XX modulates amyloid-beta fibril formation or induces a prophylactic or  
 XX therapeutic immune response against amyloid-beta fibril formation; or  
 XX (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 XX fibril formation. Also described is a kit comprising (C). (C) have  
 XX neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 XX ophthalmological, antihypertoid, vasotropic, cardiovascular, tranquiliser,  
 XX uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 XX neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 XX and can be used as amyloid-beta fibril formation modulators, and as  
 XX immune system modulators. (C) can be used for preventing or treating an  
 XX amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 XX (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 XX mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 XX amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 XX Down's syndrome, inclusion body myositis, age-related macular  
 XX degeneration, or a condition associated with Alzheimer's disease  
 XX (including hypothyroidism, cerebrovascular disease, cardiovascular  
 XX disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 XX aggression, or incontinence), a neurological condition (e.g. Huntington's  
 XX disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 XX Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 XX with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 XX field deficits, incoordination, gait disturbance, transient ischaemic  
 XX attack or stroke, transient alertness, attention deficit, frequent falls,  
 XX haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 XX damage), or a psychological condition (e.g. depression, delusions,  
 XX illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 XX disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 XX ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 XX excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 XX amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 XX having amyloid-beta deposits. The present sequence represents a peptide  
 XX that can be used as a vaccine antigen in the exemplification of the  
 XX present invention.  
 XX  
 XX Sequence 6 AA;  
 XX  
 XX Query Match 100.0%; Score 29; DB 8; Length 6;  
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFFA 6  
 Db |||||  
 1 KAVFFFA 6  
 RESULT 12



ADQ37267  
 ID ADQ37267 standard; peptide; 6 AA.  
 AC ADQ37267;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Vaccine antigen amyloid-beta related amino acid sequence.  
 XX  
 KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..6 /note= "D-form residues"  
 FT  
 XX  
 PN WO2004058239-A1.  
 XX  
 XX 15-JUL-2004.  
 XX  
 XX 24-DEC-2003; 2003WO-CA002021.  
 XX  
 XX 24-DEC-2002; 2002US-0436379P.  
 XX  
 XX 23-JUN-2003; 2003US-0482214P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 PA  
 XX Gervais F, Bellini F;  
 XX  
 XX WPI; 2004-543342/52.  
 XX  
 XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.  
 XX  
 PS Disclosure; Page 67; 143pp; English.  
 XX  
 CC The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

aggression, or incontinence), a neurological condition (e.g. Huntington's  
 disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 field deficits, incoordination, gait disturbance, transient ischaemic  
 attack or stroke, transient alertness, attention deficit, frequent falls,  
 syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as a vaccine antigen in the exemplification of the  
 CC present invention.  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 100.0%; Score 29; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KAVFFA 6  
 Db 1 KAVFFA 6  
 |||||  
 RESULT 13  
 ADQ37319  
 ID ADQ37319 standard; peptide; 6 AA.  
 AC ADQ37319;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Antifibrillogenic amyloidosis inhibiting peptide.  
 XX  
 KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2004058239-A1.  
 XX  
 XX 15-JUL-2004.  
 XX  
 XX 24-DEC-2003; 2003WO-CA002021.  
 XX  
 XX 24-DEC-2002; 2002US-0436379P.  
 XX  
 XX 23-JUN-2003; 2003US-0482214P.  
 XX  
 XX (NEUR-) NEUROCHEM INT LTD.  
 PA  
 XX Gervais F, Bellini F;  
 XX  
 XX WPI; 2004-543342/52.  
 XX  
 XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.  
 XX  
 PS Disclosure; Page 67; 143pp; English.  
 XX  
 CC The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,



PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.  
 PS Disclosure; Page 69; 143pp; English.  
 XX  
 XX The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.  
 XX Sequence 6 AA;  
 SQ  
 Query Match 100.0%; Score 29; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFPA 6  
 Db 1 KAVFFPA 6  
 RESULT 14  
 ADQ37327  
 ID ADQ37327 standard; peptide; 6 AA.  
 XX  
 AC ADQ37327;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Antifibrillogenic amyloidosis inhibiting peptide.  
 XX  
 KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; nootropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 6 /note= "amidated"  
 FT WO2004058239-A1.  
 XX 15-JUL-2004.  
 XX 24-DEC-2003; 2003WO-CA002021.  
 XX 24-DEC-2002; 2002US-0436379P.  
 XX 23-JUN-2003; 2003US-0482214P.  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX Gervais F, Bellini F;  
 XX WPI; 2004-543342/52.  
 XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 XX that prevents or treats amyloid-beta related disease and second agent  
 XX that is either a peptide or peptidomimetic or an immune system modulator.  
 XX Disclosure; Page 70; 143pp; English.  
 XX The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,  
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.

XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAVFFA 6  
 |||||  
 Db 1 KAVFFA 6

RESULT 15  
 ADY37934  
 ID ADY37934 standard; peptide; 6 AA.  
 AC ADY37934;  
 DT 19-MAY-2005 (first entry)  
 XX Amyloid-targeting peptide, SEQ ID NO:14, for use in imaging agent.  
 DE  
 KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 KW transmissible spongiform encephalopathy; scrapie; BSE;  
 KW Alzheimers disease; neurological disease; amyloidosis;  
 KW non-insulin dependent diabetes; metabolic disorder.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 6 /note= "C-terminal amide"  
 FT  
 XX US2005048000-A1.  
 PN  
 XX 03-MAR-2005.  
 PD  
 XX 03-DEC-2003; 2003US-00728028.  
 PF  
 XX 25-JUL-2000; 2000US-0220808P.  
 PR  
 XX 24-JUL-2001; 2001US-00915092.  
 PR  
 XX 29-JAN-2003; 2003US-0443291P.  
 XX  
 PA (NEUR-) NEUROCHEM INT LTD.  
 XX  
 XX Gervais P, Kong X, Chalifour R, Migneault D;  
 PI  
 XX WPI; 2005-212201/22.  
 DR  
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform  
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.  
 XX  
 XX Disclosure; SEQ ID NO 14; 34pp; English.

The invention relates to an amyloid-targeting imaging agent. The imaging agent comprises an amyloid targeting moiety (such as a peptide) joined to a labeling moiety via a linking moiety, and is preferably able to cross the blood-brain barrier. The invention also relates to a kit for preparing a radiopharmaceutical preparation from the imaging agent of the invention, a method for imaging amyloid deposition in a patient and a method for diagnosing an amyloid-related condition in a patient. The amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-related conditions such as Creutzfeld-Jakob disease (CJD), Kuru, transmissible cerebral amyloidosis (also known as transmissible virus dementias), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a patient. The agent does not exhibit excessive toxicity or irritation, does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence prevention of the undesirable effects of such disorders. Sequences ADY37921-ADY37947 and ADY37949 represent peptides which may be used as the amyloid-targeting moiety in an imaging agent of the invention.

XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAVFFA 6  
 |||||  
 Db 1 KAVFFA 6

RESULT 16  
 ADY37926  
 ID ADY37926 standard; peptide; 6 AA.  
 AC ADY37926;  
 XX  
 XX 19-MAY-2005 (first entry)  
 DT  
 XX Amyloid-targeting peptide, SEQ ID NO:6, for use in imaging agent.  
 DE  
 KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 KW transmissible spongiform encephalopathy; scrapie; BSE;  
 KW Alzheimers disease; neurological disease; amyloidosis;  
 KW non-insulin dependent diabetes; metabolic disorder.  
 XX  
 OS Synthetic.  
 XX  
 XX US2005048000-A1.  
 PN  
 XX 03-MAR-2005.  
 PD  
 XX 03-DEC-2003; 2003US-00728028.  
 PF  
 XX 25-JUL-2000; 2000US-0220808P.  
 PR  
 XX 24-JUL-2001; 2001US-00915092.  
 PR  
 XX 29-JAN-2003; 2003US-0443291P.  
 XX  
 PA (NEUR-) NEUROCHEM INT LTD.  
 XX  
 XX Gervais P, Kong X, Chalifour R, Migneault D;  
 PI  
 XX WPI; 2005-212201/22.  
 DR  
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform  
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.  
 XX  
 XX Disclosure; SEQ ID NO 6; 34pp; English.

The invention relates to an amyloid-targeting imaging agent. The imaging agent comprises an amyloid targeting moiety (such as a peptide) joined to a labeling moiety via a linking moiety, and is preferably able to cross the blood-brain barrier. The invention also relates to a kit for preparing a radiopharmaceutical preparation from the imaging agent of the invention, a method for imaging amyloid deposition in a patient and a method for diagnosing an amyloid-related condition in a patient. The amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-related conditions such as Creutzfeld-Jakob disease (CJD), Kuru, transmissible cerebral amyloidosis (also known as transmissible virus dementias), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a patient. The agent does not exhibit excessive toxicity or irritation, does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.  
 XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0;

QY 1 KAVFFA 6  
 |||||  
 Db 1 KAVFFA 6

RESULT 17  
 AAB05909  
 ID AAB05909 standard; peptide; 37 AA.

XX AC

XX AAB05909;

XX 16-OCT-2000 (first entry)

XX DE Rat inducible nitric oxide synthase calmodulin-binding region.

XX KW Rat; inducible nitric oxide synthase; iNOS;  
 KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;  
 KW AMP-activated protein kinase; AMPK; calmodulin; CaM;  
 KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;  
 KW obstructive airways disease.

XX OS Rattus sp.

XX PN WO200028076-A1.

XX PD 18-MAY-2000.

XX PF 05-NOV-1999; 99WO-AU000968.

XX PR 06-NOV-1998; 98AU-00006976.

XX PA (SVIN-) ST VINCENTS INST MEDICAL RES.

XX PI Stapleton DI, Chen Z, Michell BJ, Kemp BE, Mitchellhill KI;

XX DR WPI; 2000-376583/32.

XX PT Identifying modulators of AMP-activated protein kinase-mediated  
 PT activation of a nitric oxide synthase (NOS), for use in ischemic heart  
 PT disease, comprises testing for the increase or decrease in  
 PT phosphorylation of NOS.

XX PS Example 4; Fig 5; 41pp; English.

XX CC The present sequence is the calmodulin (CaM)-binding region of rat  
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of  
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-  
 CC arginine. The sequence is provided for comparison with endothelial nitric  
 CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is  
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of  
 CC Ca2+-CaM. Phosphorylation results in inhibition of eNOS. In the presence  
 CC of Ca2+-CaM, phosphorylation by AMPK occurs predominantly at Ser-1177 and  
 CC eNOS is activated. Modulators which activate AMPK may be used in the  
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid  
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.  
 CC They may also be used for the treatment of pulmonary hypertension and  
 CC obstructive airways disease

XX SQ Sequence 37 AA;

Query Match 100.0%; Score 29; DB 3; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 43;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 |||||  
 Db 18 KAVFFA 23

RESULT 18  
 ADK34079  
 ID ADK34079 standard; peptide; 37 AA.

XX AC ADK34079;

XX DT 20-MAY-2004 (first entry)

XX DE Mouse iNOS calmodulin binding domain peptide seqid 6.

XX KW vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;  
 KW eNOS; endothelial nitric oxide synthase; angiogenesis;  
 KW microvascular dysfunction; mouse; calmodulin binding domain;  
 KW inducible nitric oxide; iNOS.

XX OS Mus musculus.

XX PN WO2004016761-A2.

XX PD 26-FEB-2004.

XX PF 15-AUG-2003; 2003WO-US025626.

XX PR 16-AUG-2002; 2002US-0403637P.

XX PA (SCHD ) SCHERING AG.

XX PI Dole WP, Kauser K, Qian HS, Rubanyi G;

XX DR WPI; 2004-203789/19.

XX PT Treating critical limb ischemia (CLI), or angiogenesis comprises  
 PT administering to a patient a polynucleotide encoding a mammalian  
 PT endothelial nitric oxide synthase (eNOS) polypeptide.

XX PS Example 1; SEQ ID NO 6; 82pp; English.

XX CC The invention describes a method of creating critical limb ischaemia  
 CC (CLI) comprising administering to a patient a polynucleotide encoding a  
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also  
 CC described are: a method for treating angiogenesis by administering to a  
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular  
 CC dysfunction by administering to the patient the polynucleotide encoding  
 CC the eNOS polypeptide. The method is useful for treating critical limb  
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.  
 CC This is the amino acid sequence of a mouse inducible nitric synthase  
 CC (iNOS) calmodulin binding domain peptide.

XX SQ Sequence 37 AA;

Query Match 100.0%; Score 29; DB 8; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||||  
 Db 18 KAVFFA 23

RESULT 19  
 ADL70726  
 ID ADL70726 standard; peptide; 37 AA.

XX AC ADL70726;

XX DT 20-MAY-2004 (first entry)

XX DE Rat iNOS calmodulin-binding site amino acid sequence SEQ ID NO:6.  
 XX KW rat; endothelial nitric oxide synthase; eNOS; enzyme; mutant;  
 XX KW calmodulin-binding domain; vasotropic; antiarteriosclerotic; hypotensive;  
 XX KW antidiabetic; vulnary; antilipaeic; anorectic;  
 XX KW reduced calcium dependence; ischaemia; atherosclerosis; hypertension;  
 XX KW diabetes; Raynaud's phenomenon; poor wound healing; hyperlipidaemia;  
 XX KW obesity; iNOS.  
 XX OS Rattus rattus.  
 XX KW WO2004016764-A2.  
 XX PD 26-FEB-2004.  
 XX XX 15-AUG-2003; 2003WO-US025745.  
 XX XX 16-AUG-2002; 2002US-0403638P.  
 XX XX (SCHD ) SCHERING AG.  
 XX PA Blasko E, Kauser K, Parkinson J;  
 XX PI WPI; 2004-203792/19.  
 XX XX New isolated endothelial nitric oxide synthase polypeptide mutant, useful  
 XX PT for diagnosing or treating ischemia, atherosclerosis, hypertension,  
 XX PT diabetes, Raynaud's phenomenon, poor wound healing, hyperlipidemia or  
 XX PT obesity.

## Example 1; SEQ ID NO 6; 57pp; English.

XX The present sequence represents the calmodulin-binding site of rat iNOS  
 XX amino acid sequence. The present invention describes endothelial nitric  
 XX oxide synthase (eNOS) mutants having one or more mutations in an amino  
 XX acid sequence corresponding to a functional domain of a mammalian eNOS.  
 XX At least one of the mutations is at a position corresponding to an amino  
 XX acid residue in a calmodulin-binding domain that is phosphorylated in  
 XX mammalian cells, and not an amino acid substitution to Ala or Asp. Also  
 XX described: (1) an isolated eNOS polypeptide mutant that is substantially  
 XX homologous, or has a 95-98% sequence identity to the amino acid sequence  
 XX of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide  
 XX encoding the polypeptide mutant; (3) a recombinant vector comprising the  
 XX polynucleotide operably linked to at least one regulatory sequence; (4) a  
 XX pharmaceutical composition comprising the polypeptide mutant or the  
 XX polynucleotide; (5) a binding partner of the polypeptide mutant; (6)  
 XX modulating eNOS activity in a cell by administering to the cell the  
 XX polypeptide mutant; (7) modulating eNOS activity in a cell by  
 XX administering the polypeptide mutant or the polynucleotide to the cell,  
 XX such that the polypeptide mutant is expressed in the cell; (8) diagnosing  
 XX a condition associated with aberrant eNOS activity by contacting a cell  
 XX of a patient with the polynucleotide, and detecting a level of eNOS  
 XX activity indicative of the medical condition; and (9) prophylactic and  
 XX therapeutic methods of treating a condition associated with aberrant eNOS  
 XX activity by administering the polypeptide mutant or polynucleotide to the  
 XX patient. The eNOS mutant has vasotropic, antiarteriosclerotic,  
 XX hypotensive, antidiabetic, vulnary, antilipaeic and anorectic  
 XX activities, and has reduced calcium dependence and increased activity.  
 XX The polypeptide mutant, polynucleotide and methods are useful for  
 XX diagnosing or treating a condition associated with aberrant eNOS  
 XX activity, e.g. ischaemia, atherosclerosis, hypertension, diabetes,  
 XX Raynaud's phenomenon, poor wound healing, hyperlipidaemia or obesity.

## Sequence 37 AA;

Query Match 100.0%; Score 29; DB 8; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPFA 6  
 |||||  
 Db 18 KAVPFA 23

RESULT 20  
 ADG17617  
 ID ADG17617 standard; protein; 42 AA.  
 XX AC ADG17617;  
 XX DT 26-FEB-2004 (first entry)  
 XX XX Modified amyloid beta precursor protein-related partial protein SeqID8.  
 XX KW amyloid beta precursor protein; APP; beta-selectase cleavage;  
 XX KW alpha-selectase cleavage; Alzheimer's disease; dementia.  
 XX OS Unidentified.  
 XX XX WO2003102177-A1.  
 XX XX 11-DEC-2003.  
 XX XX 21-MAY-2003; 2003WO-JP006319.  
 XX PF 31-MAY-2002; 2002JP-00159472.  
 XX PR (SAKA ) OTSUKA PHARM CO LTD.  
 XX PA Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;  
 XX PI WPI; 2004-053473/05.  
 XX DR Amyloid beta precursor protein cleaved by beta- but not alpha-selectase  
 XX PT for screening for treatments for Alzheimers disease.  
 XX PS Claim 14; SEQ ID NO 8; 89pp; Japanese.  
 XX CC This invention relates to a novel modified amyloid beta precursor protein  
 XX CC (APP) which contains a beta-selectase cleavage site and a modification  
 XX CC which prevents cleavage by alpha-selectase. The invention may be useful  
 XX CC for screening for, treating and preventing Alzheimer's disease and  
 XX CC dementia. The present sequence is that of a protein which is related to  
 XX CC the modified amyloid beta precursor proteins of the invention.  
 XX SQ Sequence 42 AA;  
 Query Match 100.0%; Score 29; DB 8; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KAVPFA 6  
 |||||  
 Db 18 KAVPFA 23  
 RESULT 21  
 ADG17612  
 ID ADG17612 standard; protein; 42 AA.  
 XX AC ADG17612;  
 XX DT 26-FEB-2004 (first entry)  
 XX XX Modified amyloid beta precursor protein-related partial protein SeqID3.  
 XX KW amyloid beta precursor protein; APP; beta-selectase cleavage;  
 XX KW alpha-selectase cleavage; Alzheimer's disease; dementia.  
 XX OS Unidentified.  
 XX XX WO2003102177-A1.  
 XX XX 11-DEC-2003.

PF 21-MAY-2003; 2003WO-JP006319.  
 XX  
 PR 31-MAY-2002; 2002JP-00159472.  
 XX  
 PA (SAKA ) OTSUKA PHARM CO LTD.  
 XX  
 PI Shinabuku A, Ogino K, Taki T, Shin R, Kitamoto T;  
 XX  
 DR WPI; 2004-053473/05.  
 XX  
 XX Amyloid beta precursor protein cleaved by beta- but not alpha-selectase  
 PT for screening for treatments for Alzheimers disease.  
 PT  
 XX Claim 13; SEQ ID NO 3; 89pp; Japanese.  
 XX  
 XX This invention relates to a novel modified amyloid beta precursor protein  
 CC (APP) which contains a beta-selectase cleavage site and a modification  
 CC which prevents cleavage by alpha-selectase. The invention may be useful  
 CC for screening for, treating and preventing Alzheimer's disease and  
 CC dementia. The present sequence is that of a protein which is related to  
 CC the modified amyloid beta precursor proteins of the invention.  
 XX  
 XX Sequence 42 AA;  
 SQ  
 Query Match 100.0%; Score 29; DB 8; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 18 KAVFFA 23  
 |||||  
 RESULT 22  
 AAW41091  
 ID AAW41091 standard; protein; 74 AA.  
 XX  
 AC AAW41091;  
 XX  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Chicken matrix metalloproteinase chMMP-2 (aa445-518).  
 XX  
 KW Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;  
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.  
 XX  
 OS Gallus sp.  
 XX  
 PN WO9745137-A1.  
 XX  
 PD 04-DEC-1997.  
 XX  
 PF 30-MAY-1997; 97WO-US009158.  
 XX  
 PR 31-MAY-1996; 96US-0015869P.  
 XX  
 PR 31-MAY-1996; 96US-0018733P.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheres DA;  
 XX  
 DR WPI; 1998-032334/03.  
 XX  
 XX Packaging material containing polypeptide antagonist of alphav, beta3  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.  
 PT  
 XX Claim 2; Page 159-160; 234pp; English.  
 PS  
 XX This polypeptide comprises amino acid residues 445-518 of chicken mature  
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by

CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2  
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for  
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.  
 CC The invention relates to the discovery that angiogenesis is mediated by  
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of  
 CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of  
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human  
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see  
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or  
 CC organic mimetic compound. The antagonists are used to inhibit  
 CC angiogenesis in: inflamed tissue for treatment of arthritis or  
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce  
 CC tumour regression or inhibit growth of tumours; and in ocular disorders  
 CC such as diabetic retinopathy or macular degeneration (all claimed). They  
 CC can also be used to treat restenosis caused by migration of smooth muscle  
 CC cells following angioplasty and to reduce blood supply to selected  
 CC tissues (claimed). The new antagonists are highly selective for  
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature  
 CC vessels are unaffected, and the antagonists should be of low toxicity  
 XX  
 XX Sequence 74 AA;  
 SQ

Query Match 100.0%; Score 29; DB 2; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 64 KAVFFA 69  
 |||||

RESULT 23  
 AAW41085  
 ID AAW41085 standard; protein; 74 AA.  
 XX  
 AC AAW41085;  
 XX  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Human matrix metalloproteinase huMMP-2 (aa439-512).  
 XX  
 KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;  
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;  
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;  
 KW macular degeneration; restenosis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9745137-A1.  
 XX  
 PD 04-DEC-1997.  
 XX  
 PF 30-MAY-1997; 97WO-US009158.  
 XX  
 PR 31-MAY-1996; 96US-0015869P.  
 XX  
 PR 31-MAY-1996; 96US-0018733P.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheres DA;  
 XX  
 DR WPI; 1998-032334/03.  
 XX  
 XX Packaging material containing polypeptide antagonist of alphav, beta3  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.  
 PT  
 XX Claim 2; Page 153; 234pp; English.  
 PS  
 XX This polypeptide comprises amino acid residues 439-512 of human mature  
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant  
 CC methods such as PCR amplification of huMMP-2 coding sequence and cloning  
 CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein

CC with glutathione-S-transferase. The invention relates to the discovery  
 CC that angiogenesis is mediated by the specific vitronectin receptor alpha-  
 CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits  
 CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal  
 CC fragments (see AAW41083-94) of human or chicken MMP-2, fusion  
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),  
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic  
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed  
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours  
 CC or metastases, particularly to induce regression or to inhibit growth of  
 CC tumours; and in ocular disorders such as diabetic retinopathy or macular  
 CC degeneration (all claimed). They can also be used to treat restenosis  
 CC caused by migration of smooth muscle cells following angioplasty and to  
 CC reduce blood supply to selected tissues (claimed). The new antagonists  
 CC are highly selective for angiogenesis. Only new blood vessels express  
 CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists  
 CC should be of low toxicity

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 2; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||||  
 DB 64 KAVFFA 69

RESULT 24

AAW41230  
 ID AAW41230 standard; protein; 74 AA.

AC AAW41230;

DT 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

DE Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;  
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;  
 KW restenosis; neovascularisation.

XX Synthetic.

OS Homo sapiens.

XX WO9745447-A1.

PN 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI ) SCRIPPS RES INST.

XX Brooks P, Cheresch DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, betas  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix  
 CC metalloprotease-2 (MMP-2) (AAW41226). The present peptide is derived from  
 CC amino acids 439-512. The peptides are able to act as alpha-v-beta-5  
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of  
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a  
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an

CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-  
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The  
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid  
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.  
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal  
 CC transplants). They are particularly used to induce regression or to  
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be  
 CC used to treat restenosis caused by migration of smooth muscle cells  
 CC following angioplasty and to reduce blood supply to selected tissues. The  
 CC antagonists particularly inhibit neovascularisation where this is induced  
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth  
 CC factor or especially vascular endothelial growth factor. note: this  
 CC sequence does not appear in the specification; it was created using  
 CC information provided

XX Sequence 74 AA;

Query Match 100.0%; Score 29; DB 2; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||||  
 DB 64 KAVFFA 69

RESULT 25

ADT05998

ID ADT05998 standard; protein; 74 AA.

XX ADT05998;

DT 30-DEC-2004 (first entry)

XX Modified chicken MMP-2 Y517C, residues 445-518.

XX Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;  
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;  
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;  
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;  
 KW cytotatic; antiinflammatory; antiarthritic; antirheumatic;  
 KW ophthalmologic; antidiabetic; vasotropic; muscular-gen.;  
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;  
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken;  
 KW mutant; mutein; cyclic.

XX Gallus gallus.

OS Synthetic.

XX Key Location/Qualifiers

FH Disulfide-bond 2..73

FT Misc-difference 73

FT /note= "Cys replaces wild-type Tyr. This residue  
 corresponds to residue 517 of the mature MMP-2 protein"

XX WO2004087057-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009321.

XX 28-MAR-2003; 2003US-00402212.

XX (SCRI ) SCRIPPS RES INST.

XX Brooks PC, Cheresch DA;

XX WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v  
 CC beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue  
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX

```

PS Example 2; Page; 184pp; English.
XX
CC The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADR05998-ADR06001 represent C-terminal (hemopexin
CC domain) fragments of chicken matrix metalloprotease 2 (MMP-2, gelatinase)
CC containing the amino acid substitutions Y517C and/or W551C which are
CC components of glutathione-S-transferase (GST)/MMP-2 fusion proteins used
CC in an example of the invention. Note: The present sequence is not shown
CC in the specification, but was derived from the wild-type chicken MMP-2 C-
CC terminal fragment ADR05971 and the information given on page 49.
XX
SQ Sequence 74 AA;

Query Match      100.0%; Score 29; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 64 KAVFFA 69
|||||

RESULT 26
ADR05965
ID ADR05965 standard; protein; 74 AA.
XX
AC ADR05965;
XX
DT 30-DEC-2004 (first entry)
XX
DE Human matrix metalloprotease (MMP-2) residues 439-512, SEQ ID NO:19.
XX
KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cytotstatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; human.
XX
OS Homo sapiens.
XX
PN WO2004087057-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-US009321.
XX
PR 28-MAR-2003; 2003US-00402212.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Brooks PC, Chereah DA;
XX
DR WPI; 2004-737508/72.
XX
PT Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX
PS Example 1A; SEQ ID NO 19; 184pp; English.
XX
CC The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADR05963-ADR05974 represent C-terminal (hemopexin
CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
CC gelatinase) used in an example of the invention in assays of inhibition
CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-
CC receptor binding.
XX
SQ Sequence 74 AA;

Query Match      100.0%; Score 29; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 64 KAVFFA 69
|||||

RESULT 27
ADR05971
ID ADR05971 standard; protein; 74 AA.
XX
AC ADR05971;
XX
DT 30-DEC-2004 (first entry)
XX
DE Chicken matrix metalloprotease (MMP-2) residues 445-518, SEQ ID NO:25.
XX
KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cytotstatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.
XX
OS Gallus gallus.
XX
PN WO2004087057-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-US009321.
XX
PR 28-MAR-2003; 2003US-00402212.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Brooks PC, Chereah DA;
XX
DR WPI; 2004-737508/72.
XX
PT Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX
PS Example 1A; SEQ ID NO 25; 184pp; English.
XX

```



CC The invention relates to a method of inhibiting angiogenesis in a tissue  
 CC by the administration of a composition comprising an organic  
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin  
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions  
 CC containing it are useful for inhibiting angiogenesis in a variety of  
 CC medical conditions. The antagonist may be used to induce the regression  
 CC of solid tumours or solid tumour metastases; to inhibit the growth of  
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in  
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to  
 CC treat neovascularisation in retinal tissue (e.g., in diabetic  
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle  
 CC cell migration (such as that which occurs following angioplasty); and to  
 CC reduce the blood supply to a tissue required to support new growth of the  
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin  
 CC domain) fragments of human and chicken matrix metalloproteinase 2 (MMP-2,  
 CC gelatinase) used in an example of the invention in assays of inhibition  
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-  
 CC receptor binding.

XX SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 8; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6  
 |||||  
 Db 64 KAVFFPA 69

RESULT 28

AAW41086  
 ID AAW41086 standard; protein; 108 AA.

AC AAW41086;

XX 08-JUN-1998 (first entry)

DE Human matrix metalloproteinase huMMP-2 (aa439-546).

XX Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;  
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;  
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;  
 KW macular degeneration; restenosis; therapy.

OS Homo sapiens.

PN WO9745137-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009158.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI ) SCRIPPS RES INST.

XX Brooks P, Cheresh DA;

PI WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, beta3  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.

XX Claim 2; Page 154; 234pp; English.

XX This polypeptide comprises amino acid residues 439-546 of human mature  
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant  
 CC methods such as PCR amplification of huMMP-2 coding sequence and cloning  
 CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein  
 CC with glutathione-S-transferase. The invention relates to the discovery

CC that angiogenesis is mediated by the specific vitronectin receptor alpha-  
 CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits  
 CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal  
 CC fragments (see AAW41083-94) of human or chicken MMP-2, fusion  
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),  
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic  
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed  
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours  
 CC or metastases, particularly to induce regression or to inhibit growth of  
 CC tumours; and in ocular disorders such as diabetic retinopathy or macular  
 CC degeneration (all claimed). They can also be used to treat restenosis  
 CC caused by migration of smooth muscle cells following angioplasty and to  
 CC reduce blood supply to selected tissues (claimed). The new antagonists  
 CC are highly selective for angiogenesis. Only new blood vessels express  
 CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists  
 CC should be of low toxicity

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6  
 |||||  
 Db 64 KAVFFPA 69

RESULT 29

AAW41092  
 ID AAW41092 standard; protein; 108 AA.

XX AAW41092;

XX 08-JUN-1998 (first entry)

DE Chicken matrix metalloproteinase chMMP-2 (aa445-552).

XX Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;  
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.

OS Gallus sp.

PN WO9745137-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009158.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI ) SCRIPPS RES INST.

XX Brooks P, Cheresh DA;

PI WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, beta3  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.

XX Claim 2; Page 160; 234pp; English.

XX This polypeptide comprises amino acid residues 445-552 of chicken mature  
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by  
 CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2  
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for  
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.  
 CC The invention relates to the discovery that angiogenesis is mediated by  
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of



CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of  
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human  
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see  
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or  
 CC organic mimetic compound. The antagonists are used to inhibit  
 CC angiogenesis in: inflamed tissue for treatment of arthritis or  
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce  
 CC tumour regression or inhibit growth of tumours; and in ocular disorders  
 CC such as diabetic retinopathy or macular degeneration (all claimed). They  
 CC can also be used to treat restenosis caused by migration of smooth muscle  
 CC cells following angioplasty and to reduce blood supply to selected  
 CC tissues (claimed). The new antagonists are highly selective for  
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature  
 CC vessels are unaffected, and the antagonists should be of low toxicity  
 XX

XX Sequence 108 AA;  
 Query Match 100.0%; Score 29; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||||  
 Db 64 KAVFFA 69

RESULT 30  
 AAW41231  
 ID AAW41231 standard; protein; 108 AA.

XX AC AAW41231;

XX DT 09-JUN-1998 (first entry)

XX DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

XX KW Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;  
 XX vitronectin receptor; inhibition; angiogenesis; tumour growth;  
 XX restenosis; neovascularisation.

XX OS Synthetic.  
 XX OS Homo sapiens.

XX PN WO9745447-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009099.

XX PR 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA, Friedlander M;

XX DR WPI; 1998-041758/04.

XX PT Packaging material containing polypeptide antagonist of alphav, beta5  
 XX integrin - used for inhibition of angiogenesis, and for treating tumours,  
 XX inflammation, eye diseases etc.

XX PS Claim 2; Page; 117pp; English.

XX CC Peptides AAW41228-33 are derived from the mature protein of human matrix  
 CC metalloprotease-2 (MMP-2) (AAW41226). The present peptide is derived from  
 CC amino acids 439-546. The peptides are able to act as alpha-v-beta-5  
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of  
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a  
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an  
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-  
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The  
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

CC tumours or metastases, and in a wide range of ocular disorders (e.g.  
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal  
 CC transplants). They are particularly used to induce regression or to  
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be  
 CC used to treat restenosis caused by migration of smooth muscle cells  
 CC following angioplasty and to reduce blood supply to selected tissues. The  
 CC antagonists particularly inhibit neovascularisation where this is induced  
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth  
 CC factor or especially vascular endothelial growth factor. note: this  
 CC sequence does not appear in the specification; it was created using  
 CC information provided

XX Sequence 108 AA;

XX Query Match 100.0%; Score 29; DB 2; Length 108;  
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||||  
 Db 64 KAVFFA 69

RESULT 31  
 AAW41237  
 ID AAW41237 standard; protein; 108 AA.

XX AC AAW41237;

XX DT 09-JUN-1998 (first entry)

XX DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX KW Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;  
 XX vitronectin receptor; inhibition; angiogenesis; tumour growth;  
 XX restenosis; neovascularisation.

XX OS Synthetic.  
 XX OS Gallus sp.

XX PN WO9745447-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009099.

XX PR 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA, Friedlander M;

XX DR WPI; 1998-041758/04.

XX PT Packaging material containing polypeptide antagonist of alphav, beta5  
 XX integrin - used for inhibition of angiogenesis, and for treating tumours,  
 XX inflammation, eye diseases etc.

XX PS Claim 2; Page; 117pp; English.

XX CC Peptides AAW41234-39 are derived from the chicken matrix metalloprotease-  
 CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino  
 CC acids 445-552. The peptides are able to act as alpha-v-beta-5  
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of  
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a  
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an  
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-  
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The  
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid  
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.  
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal  
 CC transplants). They are particularly used to induce regression or to

CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be  
 CC used to treat restenosis caused by migration of smooth muscle cells  
 CC following angioplasty and to reduce blood supply to selected tissues. The  
 CC antagonists particularly inhibit neovascularisation where this is induced  
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth  
 CC factor or especially vascular endothelial growth factor. note: this  
 CC sequence does not appear in the specification; it was created using  
 CC information provided

XX SQ Sequence 108 AA;  
 Query Match 100.0%; Score 29; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||||  
 Db 90 KAVFFA 95

## RESULT 32

ADT05972  
 ID ADT05972 standard; protein; 108 AA.

XX AC ADT05972;

XX DT 30-DEC-2004 (first entry)

XX DE Chicken matrix metalloprotease (MMP-2) residues 445-552, SEQ ID NO:26.

XX KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;  
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;  
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;  
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;  
 KW cytosolic; antiinflammatory; antiarthritic; antirheumatic;  
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;  
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;  
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.

XX OS Gallus gallus.

XX PN WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v  
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue  
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX PS Example 1A; SEQ ID NO 26; 184pp; English.

XX CC The invention relates to a method of inhibiting angiogenesis in a tissue  
 CC by the administration of a composition comprising an organic  
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin  
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions  
 CC containing it are useful for inhibiting angiogenesis in a variety of  
 CC medical conditions. The antagonist may be used to induce the regression  
 CC of solid tumours or solid tumour metastases; to inhibit the growth of  
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in  
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to  
 CC treat restenosis in retinal tissue (e.g., in diabetic  
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle  
 CC cell migration (such as that which occurs following angioplasty); and to

CC reduce the blood supply to a tissue required to support new growth of the  
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin  
 CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,  
 CC gelatinase) used in an example of the invention in assays of inhibition  
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-  
 CC receptor binding.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||||  
 Db 64 KAVFFA 69

## RESULT 33

ADT05966  
 ID ADT05966 standard; protein; 108 AA.

XX AC ADT05966;

XX DT 30-DEC-2004 (first entry)

XX DE Human matrix metalloprotease (MMP-2) residues 439-546, SEQ ID NO:20.

XX KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;  
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;  
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;  
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;  
 KW cytosolic; antiinflammatory; antiarthritic; antirheumatic;  
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;  
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;  
 KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX OS Homo sapiens.

XX PN WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v  
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue  
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.  
 XX PS Example 1A; SEQ ID NO 20; 184pp; English.

XX CC The invention relates to a method of inhibiting angiogenesis in a tissue  
 CC by the administration of a composition comprising an organic  
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin  
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions  
 CC containing it are useful for inhibiting angiogenesis in a variety of  
 CC medical conditions. The antagonist may be used to induce the regression  
 CC of solid tumours or solid tumour metastases; to inhibit the growth of  
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in  
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to  
 CC treat restenosis in retinal tissue (e.g., in diabetic  
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle  
 CC cell migration (such as that which occurs following angioplasty); and to  
 CC reduce the blood supply to a tissue required to support new growth of the  
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin

CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,  
 CC gelatinase) used in an example of the invention in assays of inhibition  
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-  
 CC receptor binding.

XX Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 64 KAVFFA 69

RESULT 34

ADT05999  
 ID ADT05999 standard; protein; 108 AA.

XX AC

ADT05999;

XX DT 30-DEC-2004 (first entry)

XX DE Modified chicken MMP-2 Y517C/W551C, residues 445-552.

XX Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;  
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;  
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;  
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;  
 KW cytosolic; antiinflammatory; antiarthritic; antirheumatic;  
 KW ophthalmologic; antidiabetic; vasotropic; muscular-gen.;  
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;  
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken;  
 KW mutant; mutein.

XX OS Gallus gallus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 73

XX FT /note= "Cys replaces wild-type Tyr. This residue  
 corresponds to residue 517 of the mature MMP-2 protein"

XX FT Misc-difference 107

XX FT /note= "Cys replaces wild-type Trp. This residue  
 corresponds to residue 551 of the mature MMP-2 protein"

XX PN WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Brooks PC, Cheresch DA;

XX DR WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v  
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue  
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX Example 2; Page; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue  
 CC by the administration of a composition comprising an organic  
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin  
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions  
 CC containing it are useful for inhibiting angiogenesis in a variety of  
 CC medical conditions. The antagonist may be used to induce the regression

CC of solid tumours or solid tumour metastases; to inhibit the growth of  
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in  
 CC which neovascularisation is occurring (e.g. in rheumatoid arthritis); to  
 CC treat neovascularisation in retinal tissue (e.g., in diabetic  
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle  
 CC cell migration (such as that which occurs following angioplasty); and to  
 CC reduce the blood supply to a tissue required to support new growth of the  
 CC tissue. Sequences ADT05998-ADT06001 represent C-terminal (hemopexin  
 CC domain) fragments of chicken matrix metalloprotease 2 (MMP-2, gelatinase)  
 CC containing the amino acid substitutions Y517C and/or W551C which are  
 CC components of glutathione-S-transferase (GST)/MMP-2 fusion proteins used  
 CC in an example of the invention. Note: The present sequence is not shown  
 CC in the specification, but was derived from the wild-type chicken MMP-2 C-  
 CC terminal fragment ADT05971 and the information given on page 49.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 64 KAVFFA 69

RESULT 35

AAW41238  
 ID AAW41238 standard; protein; 122 AA.

XX AC AAW41238;

XX DT 09-JUN-1998 (first entry)

XX DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;  
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;  
 KW restenosis; neovascularisation.

XX OS Synthetic.

XX OS Gallus sp.

XX PN WO9745447-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009099.

XX PR 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Brooks P, Cheresch DA, Friedlander M;

XX DR WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.

XX PS Claim 2; Page; 117pp; English.

XX Peptides AAW41234-39 are derived from the chicken matrix metalloprotease-  
 CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino  
 CC acids 516-637. The peptides are able to act as alpha-v-beta-5  
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of  
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a  
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an  
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-  
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The  
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

CC tumours or metastases, and in a wide range of ocular disorders (e.g.  
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal  
 CC transplants). They are particularly used to induce regression or to  
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be  
 CC used to treat restenosis caused by migration of smooth muscle cells  
 CC following angioplasty and to reduce blood supply to selected tissues. The  
 CC antagonists particularly inhibit neovascularisation where this is induced  
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth  
 CC factor or especially vascular endothelial growth factor. note: this  
 CC sequence does not appear in the specification; it was created using  
 CC information provided

XX  
 SQ Sequence 122 AA;

Query Match 100.0%; Score 29; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||  
 Db 19 KAVFFA 24

## RESULT 36

AAW41232  
 ID AAW41232 standard; protein; 152 AA.

AC AAW41232;

XX 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

DE Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;  
 XX vitronectin receptor; inhibition; angiogenesis; tumour growth;  
 KW restenosis; neovascularisation.

XX Synthetic.

OS Homo sapiens.

XX WO9745447-A1.

PD 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI ) SCRIPPS RES INST.

XX Brooks P, Cheres DA, Friedlander M;

PI WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, betas  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix  
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from  
 CC amino acids 510-631. The peptides are able to act as alpha-v-beta-5  
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of  
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a  
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an  
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-  
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The  
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid  
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.  
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal  
 CC transplants). They are particularly used to induce regression or to

CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be  
 CC used to treat restenosis caused by migration of smooth muscle cells  
 CC following angioplasty and to reduce blood supply to selected tissues. The  
 CC antagonists particularly inhibit neovascularisation where this is induced  
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth  
 CC factor or especially vascular endothelial growth factor. note: this  
 CC sequence does not appear in the specification; it was created using  
 CC information provided

XX  
 SQ Sequence 152 AA;

Query Match 100.0%; Score 29; DB 2; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||  
 Db 23 KAVFFA 28

## RESULT 37

AAW41090

ID AAW41090 standard; protein; 193 AA.

XX AAW41090;

XX 08-JUN-1998 (first entry)

XX Chicken matrix metalloproteinase chMMP-2 (aa445-637).

XX Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;  
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.

OS Gallus sp.

XX WO9745137-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009158.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI ) SCRIPPS RES INST.

XX Brooks P, Cheres DA;

XX WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, betas  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.

XX Claim 2; Page 158-159; 234pp; English.

XX This polypeptide comprises amino acid residues 445-637 of chicken mature  
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by  
 CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2  
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for  
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.  
 CC The invention relates to the discovery that angiogenesis is mediated by  
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibitors of  
 CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of  
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human  
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see  
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or  
 CC organic mimetic compound. The antagonists are used to inhibit  
 CC angiogenesis in: inflamed tissue for treatment of arthritis or  
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce  
 CC tumour regression or inhibit growth of tumours; and in ocular disorders

CC such as diabetic retinopathy or macular degeneration (all claimed). They  
 CC can also be used to treat restenosis caused by migration of smooth muscle  
 CC cells following angioplasty and to reduce blood supply to selected  
 CC tissues (claimed). The new antagonists are highly selective for  
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature  
 CC vessels are unaffected, and the antagonists should be of low toxicity  
 XX

SQ Sequence 193 AA;  
 Query Match 100.0%; Score 29; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 |||||  
 Db 64 KAVFFA 69

RESULT 38  
 AAW41084  
 ID AAW41084 standard; protein; 193 AA.  
 XX  
 AC AAW41084;  
 XX  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Human matrix metalloproteinase huMMP-2 (aa439-631).  
 XX  
 KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;  
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;  
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;  
 KW macular degeneration; restenosis; therapy.  
 XX

OS Homo sapiens.  
 XX  
 PN WO9745137-A1.  
 XX  
 PD 04-DEC-1997.  
 XX  
 PF 30-MAY-1997; 97WO-US009158.  
 XX  
 PR 31-MAY-1996; 96US-0015869P.  
 PR 31-MAY-1996; 96US-0018733P.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheres DA;  
 XX  
 WPI; 1998-032334/03.  
 XX

PT Packaging material containing polypeptide antagonist of alphav, beta3  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.  
 XX

PS Claim 2; Page 152-153; 234pp; English.  
 XX  
 CC This polypeptide comprises amino acid residues 439-631 of human mature  
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant  
 CC methods such as PCR amplification (see AAV12510) of huMMP-2 coding  
 CC sequence and cloning into e.g. pGEX-3X vector for expression in E. coli  
 CC as a glutathione-S-transferase fusion protein. The invention relates to  
 CC the discovery that angiogenesis is mediated by the specific vitronectin  
 CC receptor alpha-v beta-3, and that inhibition of alpha-v beta-3 function  
 CC inhibits angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-  
 CC terminal fragments (see AAW1083-94) of human or chicken MMP-2, fusion  
 CC polypeptides, cyclic or linear polypeptides (see also AAW1098-110),  
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic  
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed  
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours  
 CC or metastases, particularly to induce tumour regression or inhibit growth  
 CC of tumours; and in ocular disorders such as diabetic retinopathy or  
 CC macular degeneration (all claimed). They can also be used to treat  
 CC restenosis caused by migration of smooth muscle cells following

CC angioplasty and to reduce blood supply to selected tissues (claimed). The  
 CC new antagonists are highly selective for angiogenesis. Only new blood  
 CC vessels express alpha-v beta-3, so mature vessels are unaffected, and the  
 CC antagonists should be of low toxicity  
 XX

SQ Sequence 193 AA;  
 Query Match 100.0%; Score 29; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 |||||  
 Db 64 KAVFFA 69

RESULT 39  
 AAW41229  
 ID AAW41229 standard; protein; 193 AA.  
 XX  
 AC AAW41229;  
 XX  
 DT 09-JUN-1998 (first entry)  
 XX  
 DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.  
 XX  
 KW Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;  
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;  
 KW restenosis; neovascularisation.  
 XX

OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9745447-A1.  
 XX  
 PD 04-DEC-1997.  
 XX  
 PF 30-MAY-1997; 97WO-US009099.  
 XX  
 PR 31-MAY-1996; 96US-0015869P.  
 PR 31-MAY-1996; 96US-0018733P.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheres DA, Friedlander M;  
 XX  
 WPI; 1998-041758/04.  
 XX

PT Packaging material containing polypeptide antagonist of alphav, beta5  
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
 PT inflammation, eye diseases etc.  
 XX  
 PS Claim 2; Page; 117pp; English.

CC Peptides AAW41228-33 are derived from the mature protein of human matrix  
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from  
 CC amino acids 439-631. The peptides are able to act as alpha-v-beta-5  
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of  
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a  
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an  
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-  
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The  
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid  
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.  
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal  
 CC transplants). They are particularly used to induce regression or to  
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be  
 CC used to treat restenosis caused by migration of smooth muscle cells  
 CC following angioplasty and to reduce blood supply to selected tissues. The  
 CC antagonists particularly inhibit neovascularisation where this is induced  
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth  
 CC factor or especially vascular endothelial growth factor. note: this  
 CC sequence does not appear in the specification; it was created using

CC information provided

XX Sequence 193 AA;

SQ Query Match 100.0%; Score 29; DB 2; Length 193;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;

SQ Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

DB 64 KAVFFA 69

RESULT 40

AAW41235 ID AAW41235 standard; protein; 193 AA.

XX AC AAW41235;

XX DT 09-JUN-1998 (first entry)

XX DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX KW Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;

XX KW vitronectin receptor; inhibition; angiogenesis; tumour growth;

XX KW resection; neovascularisation.

XX OS Synthetic.

XX OS Gallus sp.

XX OS WO9745447-A1.

XX PN 04-DEC-1997.

XX PD 30-MAY-1997; 97WO-US009099.

XX PF 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PS (SCRI ) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA, Friedlander M;

XX DR WPI; 1998-041758/04.

XX PT Packaging material containing polypeptide antagonist of alphav, betas

XX PT integrin - used for inhibition of angiogenesis, and for treating tumours,

XX PT inflammation, eye diseases etc.

XX PS Claim 2; Page; 117pp; English.

XX CC Peptides AAW41234-39 are derived from the chicken matrix metalloprotease-

XX CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino

XX CC acids 445-637. The peptides are able to act as alpha-v-beta-5

XX CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of

XX CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a

XX CC novel labelled package that contains an inhibitor of angiogenesis i.e. an

XX CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-

XX CC beta-5 and includes a part of the C-terminal domain of MMP-2. The

XX CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

XX CC tumours or metastases, and in a wide range of ocular disorders (e.g.

XX CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal

XX CC transplants). They are particularly used to induce regression or to

XX CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be

XX CC used to treat resection caused by migration of smooth muscle cells

XX CC following angioplasty and to reduce blood supply to selected tissues. The

XX CC antagonists particularly inhibit neovascularisation where this is induced

XX CC by cytokines, e.g. transforming growth factor alpha, epidermal growth

XX CC factor or especially vascular endothelial growth factor. note: this

XX CC sequence does not appear in the specification; it was created using

XX CC information provided

XX SQ Sequence 193 AA;

Query Match 100.0%; Score 29; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

DB 90 KAVFFA 95

RESULT 41

ADT05964 ID ADT05964 standard; protein; 193 AA.

XX AC ADT05964;

XX DT 30-DEC-2004 (first entry)

XX DE Human matrix metalloprotease (MMP-2) residues 439-631, SEQ ID NO:18.

XX KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;

XX KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;

XX KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;

XX KW resection; smooth muscle cell migration; angioplasty; antiangiogenic;

XX KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;

XX KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;

XX KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;

XX KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX OS Homo sapiens.

XX OS WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PS (SCRI ) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v

XX PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue

XX PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX PS Example 1A; SEQ ID NO 18; 184pp; English.

XX CC The invention relates to a method of inhibiting angiogenesis in a tissue

XX CC by the administration of a composition comprising an organic

XX CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin

XX CC receptor). The integrin alpha-V beta-3 antagonist and compositions

XX CC containing it are useful for inhibiting angiogenesis in a variety of

XX CC medical conditions. The antagonist may be used to inhibit the regression

XX CC of solid tumours or solid tumour metastases; to inhibit the growth of

XX CC solid tumours undergoing neovascularisation; to treat inflamed tissue in

XX CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to

XX CC treat neovascularisation in retinal tissue (e.g., in diabetic

XX CC retinopathy); to treat resection in a tissue by inhibiting smooth muscle

XX CC cell migration (such as that which occurs following angioplasty); and to

XX CC reduce the blood supply to a tissue required to support new growth of the

XX CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin

XX CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,

XX CC gelatinase) used in an example of the invention in assays of inhibition

XX CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-

XX CC receptor binding.

XX SQ Sequence 193 AA;

Query Match

100.0%; Score 29; DB 8; Length 193;

```
0; Gap= 0;
```

AAW41083:

DT 08-JUN-1998 (first entry)

KW Matrix metalloproteinase; MMP-2; huMMP-2; human; an

**OS Homo sapiens.**

PD 04-DEC-1997.

31-MAY-1996: 96US-0015869P-

PR 31-MAY-1996; 96US-0018/33P.  
YY

PA (Scripps Res Inst.

PI Brooks P, Cheres DA;

DR WPI; 1998-032334/03.

PT Packaging material con

inflammation, eye disease

PS Claim 2: Page 150-151: 234nn: English

PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue  
PT angiogenesis, retinal angiogenesis and tumor angiogenesis in a tissue.  
PT Administration of composition comprising organic peptidomimetic alpha-na-

CC methods such as PCR amplification of  
CC into e.g. pGEX-3X vector for expression

Sequence 222 AA:

Query Match 100.0% Score 29 DB 2: Length 222:

Query Match 100.0% Score 29. PG 8. Length 193.

Best Local Similarity 100.0%; pred: No. 2.1e+02;  
Matches 5; Concentrative 0; Mismatches 0.

```
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



Db |||||  
93 KAVFFA 98

## RESULT 44

AAW41228  
ID AAW41228 standard; protein; 222 AA.

AC  
XX AAW41228;

DT 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

XX Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;  
KW vitronectin receptor; inhibition; angiogenesis; tumour growth;  
KW restenosis; neovascularisation.

XX Synthetic.

OS Homo sapiens.

XX WO9745447-A1.

PN 04-DEC-1997.

PD 30-MAY-1997; 97WO-US009099.

PF 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI ) SCRIPPS RES INST.

PA Brooks P, Cheres DA, Friedlander M;

PI WPI; 1998-041759/04.

DR Packaging material containing polypeptide antagonist of alphav, betas  
PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
PT inflammation, eye diseases etc.

PS Claim 2; Page; 117pp; English.

CC Peptides AAW41228-33 are derived from the mature protein of human matrix  
CC metalloprotease-2 (MMP-2) (AAW41226). The present peptide is derived from  
CC amino acids 410-631. The peptides are able to act as alpha-v-beta-5  
CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of  
CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a  
CC novel labelled package that contains an inhibitor of angiogenesis i.e. an  
CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-  
CC beta-5 and includes a part of the C-terminal domain of MMP-2. The  
CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid  
CC tumours or metastases, and in a wide range of ocular disorders (e.g.  
CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal  
CC transplants). They are particularly used to induce regression or to  
CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be  
CC used to treat restenosis caused by migration of smooth muscle cells  
CC following angioplasty and to reduce blood supply to selected tissues. The  
CC antagonists particularly inhibit neovascularisation where this is induced  
CC by cytokines, e.g. transforming growth factor alpha, epidermal growth  
CC factor or especially vascular endothelial growth factor. note: this  
CC sequence does not appear in the specification; it was created using  
CC information provided

XX Sequence 222 AA;

Query Match 100.0%; Score 29; DB 2; Length 222;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 93 KAVFFA 98

## RESULT 45

ADT05963

ID ADT05963 standard; protein; 222 AA.

XX ADT05963;

XX 30-DEC-2004 (first entry)

DE Human matrix metalloprotease (MMP-2) residues 410-631, SEQ ID NO:17.

XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;

KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;

KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;

KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;

KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;

KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;

KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;

KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX Homo sapiens.

XX WO2004087057-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009321.

XX 28-MAR-2003; 2003US-00402212.

XX (SCRI ) SCRIPPS RES INST.

XX Brooks PC, Cheres DA;

XX WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v  
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue  
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

PS Example 1A; SEQ ID NO 17; 184pp; English.

CC The invention relates to a method of inhibiting angiogenesis in a tissue  
CC by the administration of a composition comprising an organic  
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin  
CC receptor). The integrin alpha-V beta-3 antagonist and compositions  
CC containing it are useful for inhibiting angiogenesis in a variety of  
CC medical conditions. The antagonist may be used to induce the regression  
CC of solid tumours or solid tumour metastases; to inhibit the growth of  
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in  
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to  
CC treat neovascularisation in retinal tissue (e.g., in diabetic  
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle  
CC cell migration (such as that which occurs following angioplasty); and to  
CC reduce the blood supply to a tissue required to support new growth of the  
CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin  
CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,  
CC gelatinase) used in an example of the invention in assays of inhibition  
CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-  
CC receptor binding.

XX Sequence 222 AA;

Query Match 100.0%; Score 29; DB 8; Length 222;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 93 KAVFFA 98

## RESULT 46



```

AAW41089
ID AAW41089 standard; protein; 228 AA.
XX
AC AAW41089;
XX
AC AAW41089;
XX
DT 08-JUN-1998 (first entry)
XX
DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.
XX
DE Chicken matrix metalloproteinase chMMP-2 (aa410-637).
XX
KW Matrix metalloproteinase; MMP-2; chMMP-2; Gelatinase; chicken;
KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW diabetic retinopathy; macular degeneration; restenosis; therapy.
XX
OS Gallus sp.
XX
PN WO9745137-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US009158.
XX
PR 31-MAY-1996; 96US-0015969P.
XX
PR 31-MAY-1996; 96US-0018733P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Brooks P, Cheres DA;
XX
PI WPI; 1998-032334/03.
XX
DR Packaging material containing polypeptide antagonist of alphav, beta3
XX integrin - used for inhibition of angiogenesis, and for treating tumours,
XX inflammation, eye diseases etc.
XX
PS Claim 2; Page 157-158; 234pp; English.
XX
CC This polypeptide comprises amino acid residues 410-637 of chicken mature
CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
CC recombinant methods such as PCR amplification (see AAV12501) of chMMP-2
CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
CC expression in E. coli as a fusion protein with glutathione-S-transferase.
CC The invention relates to the discovery that angiogenesis is mediated by
CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human
CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
CC organic mimetic compound. The antagonists are used to inhibit
CC angiogenesis in: inflamed tissue for treatment of arthritis or
CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
CC tumour regression or inhibit growth of tumours; and in ocular disorders
CC such as diabetic retinopathy or macular degeneration (all claimed). They
CC can also be used to treat restenosis caused by migration of smooth muscle
CC cells following angioplasty and to reduce blood supply to selected
CC tissues (claimed). The new antagonists are highly selective for
CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
CC vessels are unaffected, and the antagonists should be of low toxicity
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFFA 6
DB 99 KAVFFFA 104
RESULT 47
AAW41234
ID AAW41234 standard; protein; 228 AA.
XX
AC AAW41234;
XX
AC AAW41234;
XX
DT 09-JUN-1998 (first entry)
XX
DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.
XX
DE Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
KW restenosis; neovascularisation.
XX
OS Synthetic.
XX
OS Gallus sp.
XX
PN WO9745447-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US009099.
XX
PR 31-MAY-1996; 96US-0015869P.
XX
PR 31-MAY-1996; 96US-0018733P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Brooks P, Cheres DA, Friedlander M;
XX
PI WPI; 1998-041758/04.
XX
DR Packaging material containing polypeptide antagonist of alphav, beta5
XX integrin - used for inhibition of angiogenesis, and for treating tumours,
XX inflammation, eye diseases etc.
XX
PS Claim 2; Page; 117pp; English.
XX
CC Peptides AAW41234-39 are derived from the chicken matrix metalloproteinase-
CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
CC acids 410-637. The peptides are able to act as alpha-v-beta-5
CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
CC tumours or metastases, and in a wide range of ocular disorders (e.g.
CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
CC transplants). They are particularly used to induce regression or to
CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC used to treat restenosis caused by migration of smooth muscle cells
CC following angioplasty and to reduce blood supply to selected tissues. The
CC antagonists particularly inhibit neovascularisation where this is induced
CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
CC factor or especially vascular endothelial growth factor. note: this
CC sequence does not appear in the specification; it was created using
CC information provided
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFFA 6
DB 125 KAVFFFA 130
RESULT 48
ADT05969
ID ADT05969 standard; protein; 228 AA.
XX
AC ADT05969;
XX
AC ADT05969;
XX

```

DT	30-DEC-2004	(first entry)
XX		
DE	Chicken matrix metalloprotease (MMP-2) residues 410-637,	SEQ ID NO:23.
XX		
KW	Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;	
KW	vitronectin receptor antagonist; neovascularisation; cancer; tumour;	
KW	inflammation; rheumatoid arthritis; retina; diabetic retinopathy;	
KW	stenosis; smooth muscle cell migration; angioplasty; antiangiogenic;	
KW	cytostatic; antiinflammatory; antiarthritic; antirheumatic;	
KW	ophthalmological; antidiabetic; vasotropic; muscular-gen.;	
KW	peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;	
KW	hemopexin domain; cell attachment assay; ligand binding assay; chicken.	
XX		
OS	Gallus gallus.	
XX		
PN	WO2004087057-A2.	
XX		
PD	14-OCT-2004.	
XX		
PF	26-MAR-2004; 2004WO-US009321.	
XX		
PR	28-MAR-2003; 2003US-00402212.	
XX		
PA	(SCRI ) SCRIPTS RES INST.	
XX		
PI	Brooks PC, Cheresh DA;	
XX		
DR	WPI; 2004-737508/72.	
XX		
PT	Administration of composition comprising organic peptidomimetic alpha-v	
PT	beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue	
PT	angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.	
XX		
PS	Example 1A; SEQ ID NO 23; 184pp; English.	
XX		
CC	The invention relates to a method of inhibiting angiogenesis in a tissue	
CC	by the administration of a composition comprising an organic	
CC	peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin	
CC	receptor). The integrin alpha-v beta-3 antagonist and compositions	
CC	containing it are useful for inhibiting angiogenesis in a variety of	
CC	medical conditions. The antagonist may be used to induce the regression	
CC	of solid tumours or solid tumour metastases; to inhibit the growth of	
CC	solid tumours undergoing neovascularisation; to treat inflamed tissue in	
CC	which neovascularisation is occurring (e.g., in rheumatoid arthritis); to	
CC	treat neovascularisation in retinal tissue (e.g., in diabetic	
CC	retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle	
CC	cell migration (such as that which occurs following angioplasty); and to	
CC	reduce the blood supply to a tissue required to support new growth of the	
CC	tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin	
CC	domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,	
CC	gelatinase) used in an example of the invention in assays of inhibition	
CC	of integrin alpha-v beta-3-mediated cell attachment and of ligand-	
CC	receptor binding.	
XX		
SQ	Sequence 228 AA;	
	Query Match	100.0%; Score 29; DB 8; Length 228;
	Best Local Similarity	100.0%; Pred.No. 2.5e+02;
	Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 KAVFFA 6	
Dd	99 KAVFFA 104	
RESULT 49		
ADT05661		
ID	ADT05661 standard; protein; 261 AA.	
XX		
AC	ADT05661;	
XX		
DT	02-DEC-2004 (first entry)	
XX		

XX  
DR WPI; 1998-032334/03.  
XX  
PT Packaging material containing polypeptide antagonist of alphav, beta3  
PT integrin - used for inhibition of angiogenesis, and for treating tumours,  
PT inflammation, eye diseases etc.  
XX  
PS Example 4; Page 177-179; 234pp; English.  
XX  
CC This polypeptide comprises amino acid residues 203-631 of human mature  
CC matrix metalloproteinase 2 (hMMP-2). It was produced by recombinant  
CC methods involving PCR amplification (see AAV12509) of hMMP-2 coding  
CC sequence and cloning into e.g. pGEX-lambda vector for expression in E.  
CC coli as a glutathione-S-transferase fusion protein. The invention relates  
CC to the discovery that angiogenesis is mediated by the specific  
CC vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v beta-  
CC 3 function inhibits angiogenesis. Claimed antagonists of alpha-v beta-3  
CC comprise C-terminal fragments (see AAW1083-94) of human or chicken MMP-  
CC 2, fusion polypeptides, cyclic or linear polypeptides (see also AAW1098-  
CC 110), derivatised polypeptides, a monoclonal antibody or organic mimetic  
CC compound. The antagonists are used to inhibit angiogenesis in: inflamed  
CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours  
CC or metastases, particularly to induce tumour regression or inhibit growth  
CC of tumours; and in ocular disorders such as diabetic retinopathy or  
CC macular degeneration (all claimed). They can also be used to treat  
CC restenosis caused by migration of smooth muscle cells following  
CC angioplasty and to reduce blood supply to selected tissues (claimed). The  
CC new antagonists are highly selective for angiogenesis. Only new blood  
CC vessels express alpha-v beta-3, so mature vessels are unaffected, and the  
CC antagonists should be of low toxicity  
XX  
SQ Sequence 429 AA;  
Query Match 100.0%; Score 29; DB 2; Length 429;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAVFFPA 6  
Db 300 KAVFFPA 305  
|||||  
RESULT 51  
ADT05991  
ID ADT05991 standard; protein; 429 AA.  
AC  
AC ADT05991;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Human matrix metalloprotease (MMP-2) residues 203-631, SEQ ID NO:45.  
XX  
KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;  
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;  
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;  
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;  
KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;  
KW ophthalmologic; antidiabetic; vasotropic; muscular-gen.;  
KW peptidomimetic; matrix metalloprotease 2; MMP-2; progelatinase; human;  
KW C-terminal fragment; glutathione-S-transferase; GST fusion protein.  
XX  
OS Homo sapiens.  
XX  
XX WO2004087057-A2.  
XX  
XX 14-OCT-2004.  
XX  
XX 26-MAR-2004; 2004WO-US009321.  
PF  
XX  
XX 28-MAR-2003; 2003US-00402212.  
PR  
XX  
XX (SCRI ) SCRIPPS RES INST.  
PA  
XX

PI Brooks PC, Chereah DA;  
XX  
DR WPI; 2004-737508/72.  
XX  
PT Administration of composition comprising organic peptidomimetic alpha-v  
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue  
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.  
XX  
PS Example 2; SEQ ID NO 45; 184pp; English.  
XX  
CC The invention relates to a method of inhibiting angiogenesis in a tissue  
CC by the administration of a composition comprising an organic  
CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin  
CC receptor). The integrin alpha-v beta-3 antagonist and compositions  
CC containing it are useful for inhibiting angiogenesis in a variety of  
CC medical conditions. The antagonist may be used to induce the regression  
CC of solid tumours or solid tumour metastases; to inhibit the growth of  
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in  
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to  
CC treat neovascularisation in retinal tissue (e.g., in diabetic  
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle  
CC cell migration (such as that which occurs following angioplasty); and to  
CC reduce the blood supply to a tissue required to support new growth of the  
CC tissue. The present sequence represents residues 203-631 of human MMP-2  
CC which is a component of a glutathione-S-transferase (GST)/MMP-2 fusion  
CC protein produced in an example of the invention.  
XX  
SQ Sequence 429 AA;  
Query Match 100.0%; Score 29; DB 8; Length 429;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KAVFFPA 6  
Db 300 KAVFFPA 305  
|||||  
RESULT 52  
ABG24001  
ID ABG24001 standard; protein; 468 AA.  
XX  
AC ABG24001;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #23992.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
XX WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US008631.  
XX  
XX 31-MAR-2000; 2000US-00540217.  
PR  
XX 23-AUG-2000; 2000US-00649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Drmanac RT, Liu C, Tang YT;  
XX  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAS88188.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

XX PS Claim 20; SEQ ID NO 54360; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridization probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activities. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

XX SQ Sequence 468 AA;

Query Match 100.0%; Score 29; DB 4; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6  
 |||||  
 Db 361 KAVFFFA 366

RESULT 53

ABM84057

ID ABM84057 standard; protein; 623 AA.

XX AC ABM84057;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4306.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen SJ, Wu MC, Stuve LL; Legace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D; Patury S, Shi X, Suarez CJ;

XX PI Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;

XX PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

XX PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

XX PI Peralta CH, Anderson SB, Rioux P, Shen SJ, Wu MC, Stuve LL;

XX PI Legace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

XX PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX PI Patury S, Shi X, Suarez CJ;

XX PI WPI; 2004-329368/30.

DR N-PSDB; ACN42709.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

PT PS Claim 27; Page; 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX SQ Sequence 623 AA;

Query Match 100.0%; Score 29; DB 8; Length 623;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6  
 |||||  
 Db 494 KAVFFFA 499

RESULT 54

ADG17622

ID ADG17622 standard; protein; 626 AA.

XX AC ADG17622;

XX DT 26-FEB-2004 (first entry)

XX DE Modified amyloid beta precursor protein-related fusion protein SeqID13.

XX KW amyloid beta precursor protein; APP; beta-selectase cleavage; alpha-selectase cleavage; Alzheimer's disease; dementia.

XX OS Unidentified.

XX PN WO2003102177-A1.

XX PD 11-DEC-2003.

XX PF 21-MAY-2003; 2003WO-JP006319.

XX PR 31-MAY-2002; 2002JP-00159472.

XX (SAKA) OTSUKA PHARM CO LTD.

XX PA Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T; WPI; 2004-053473/05.

XX PT Amyloid beta precursor protein cleaved by beta- but not alpha-selectase for screening for treatments for Alzheimer's disease.

XX PS Claim 15; SEQ ID NO 13; 89pp; Japanese.

XX CC This invention relates to a novel modified amyloid beta precursor protein (APP) which contains a beta-selectase cleavage site and a modification which prevents cleavage by alpha-selectase. The invention may be useful for screening for, treating and preventing Alzheimer's disease and

CC dementia. The present sequence is that of a protein which is related to  
 CC the modified amyloid beta precursor proteins of the invention.

XX Sequence 626 AA;  
 SQ Query Match 100.0%; Score 29; DB 8; Length 626;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||||  
 Db 543 KAVFFA 548

RESULT 55

ADG17627  
 ID ADG17627 standard; protein; 626 AA.

XX AC ADG17627;

XX DT 26-FEB-2004 (first entry)

XX DE Modified amyloid beta precursor protein-related fusion protein SeqId18.

XX KW amyloid beta precursor protein; APP; beta-selectase cleavage;

XX KW alpha-selectase cleavage; Alzheimer's disease; dementia.

XX OS Unidentified.

XX PN WO2003102177-A1.

XX PD 11-DEC-2003.

XX PF 21-MAY-2003; 2003WO-JP006319.

XX PR 31-MAY-2002; 2002JP-00159472.

XX PA (SAKA ) OTSUKA PHARM CO LTD.

XX PI Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;

XX DR WPI; 2004-053473/05.

XX PT Amyloid beta precursor protein cleaved by beta- but not alpha-selectase  
 for screening for treatments for Alzheimers disease.

XX PS Claim 16; SEQ ID NO 18; 89pp; Japanese.

XX CC This invention relates to a novel modified amyloid beta precursor protein  
 (APP) which contains a beta-selectase cleavage site and a modification  
 which prevents cleavage by alpha-selectase. The invention may be useful  
 for screening for, treating and preventing Alzheimer's disease and  
 CC dementia. The present sequence is that of a protein which is related to  
 CC the modified amyloid beta precursor proteins of the invention.

XX SQ Sequence 626 AA;

Query Match 100.0%; Score 29; DB 8; Length 626;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 |||||  
 Db 543 KAVFFA 548

RESULT 56

AAP96143  
 ID AAP96143 standard; protein; 631 AA.

XX AC AAP96143;

XX DT 25-MAR-2003 (revised)

DT 09-MAY-1991 (first entry)

XX DE Sequence of human type IV collagenase (gelatinase) in pGEL 186.2.

XX KW Hypertrophic scar; keloid; intervertebral disc disease; enzyme.

XX OS Homo sapiens.

XX PN GB2209526-A.

XX PD 17-MAY-1989.

XX PF 02-SEP-1988; 88GB-00820803.

XX PR 04-SEP-1987; 87US-00093421.

XX PA (UNIW ) UNIV WASHINGTON.

XX PI Eisen AZ, Goldberg GI;

XX DR WPI; 1989-147011/20.

XX DR N-PSDB; AAN91700.

XX FT DNA encoding human type IV collagenase (gelatinase) - for use in the  
 treatment of hypertrophic scars, keloids and intervertebral disc disease.

XX PS Disclosure; Fig 3; 36pp; English.

XX CC The original source of the protein material was H-ras transformed human  
 bronchial epithelial cells (TBE-1). The AA sequence was then used to  
 develop oligonucleotide probes which were used to screen a cDNA library  
 of human skin fibroblast mRNA. The longest clone, pGEL 186.2, represented  
 CC almost the full gelatinase mRNA sequence except the leader sequence  
 CC encoding the first few AA's of the signal peptide. (Updated on 25-MAR-  
 CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 631 AA;

Query Match 100.0%; Score 29; DB 1; Length 631;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 502 KAVFFA 507

RESULT 57

AAP91139

ID AAP91139 standard; protein; 631 AA.

XX AC AAP91139;

XX DT 25-MAR-2003 (revised)

XX DT 18-DEC-1989 (first entry)

XX DE Human type IV collagenase (gelatinase).

XX KW Human type IV collagenase; gelatinase; hypertrophic scars; keloids;  
 intervertebral disc disease; extracellular matrix metalloprotease;  
 KW bronchial epithelial cells; TBE-1 cells; pGEL186.2; type II motif;  
 KW fibonectin; collagen-binding domain.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 Key Domain 1..192

FT Domain 193..367

FT Duplication 197..254

FT Duplication 255..312

FT Duplication 313..368

FT Domain 368..631

XX GB2209526-A.  
 XX 17-MAY-1989.  
 XX 02-SEP-1988; 88GB-00820803.  
 XX 04-SEP-1987; 87US-00093421.  
 XX (UNIW ) UNIV WASHINGTON.  
 XX Eisen AZ, Goldberg GI;  
 XX WPI; 1989-147011/20.  
 XX DNA encoding human type IV collagenase (gelatinase) - for use in the  
 XX treatment of hypertrophic scars, keloids and intervertebral disc disease.  
 XX Claim 2; Fig 6; 36pp; English.  
 XX Human type IV collagenase (gelatinase). Protein source was H-ras  
 CC transformed human bronchial epithelial cells (TBE-1). The sequence was  
 CC determined from clone pGel 186.2 which represents almost the full mRNA  
 CC sequence. Feature 1 is the N-terminal domain, I; feature 2 is a middle  
 CC domain, II, which is organised into 3 x 58 amino acid long head to tail  
 CC repeats (features 4,5, and 6). These show homology to the type II motif  
 CC collagen binding domain of fibronectin. Feature 3 is the C-terminal  
 CC domain. The enzyme could be used in the treatment of hypertrophic scars,  
 CC keloids, and intervertebral disc disease. See also AAN91700. (Updated on  
 CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX SQ Sequence 631 AA;

Query Match 100.0%; Score 29; DB 1; Length 631;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||  
 Db 502 KAVFFA 507

RESULT 58  
 AAR07969  
 ID AAR07969 standard; protein; 631 AA.  
 XX AAR07969;

XX 25-MAR-2003 (revised)  
 DT 17-DEC-2001 (revised)  
 DT 16-JAN-1991 (first entry)

DE Complete type IV collagenase.

XX Type IV collagenase; peptide fragments; metalloproteinase detection;  
 KW antibodies; metalloproteinase inhibition; angiogenesis; arthritis;  
 KW tumour growth; metastasis; granulomatous inflammatory conditions;  
 KW sarcoidosis.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1. .18  
 FT Peptide /label= 1  
 FT Peptide 19. .33  
 FT Peptide /label= 2  
 FT Peptide 26. .42  
 FT Peptide /label= 3  
 FT Protein 34. .50  
 FT Peptide /label= 4  
 FT Peptide 51. .66  
 FT Peptide /label= 5

FT Peptide 67. .89  
 FT Peptide /label= 7  
 FT Peptide 67. .80  
 FT Peptide /label= 6  
 FT Peptide 69. .75  
 FT Peptide /label= 8  
 FT Peptide 75. .94  
 FT Peptide /label= 9  
 FT Peptide 141. .150  
 FT Peptide /label= 10  
 FT Peptide 299. .307  
 FT Peptide /label= 11  
 FT Peptide 308. .318  
 FT Peptide /label= 12  
 FT Peptide 344. .368  
 FT Peptide /label= 13  
 FT Peptide 371. .386  
 FT Peptide /label= 14  
 FT Peptide 372. .375  
 FT Peptide /label= 15  
 FT Peptide 472. .491  
 FT Peptide /label= 16

USN7317407-N.

21-AUG-1990.

01-MAR-1989; 89US-00317407.

01-MAR-1989; 89US-00317407.

(USSH ) US NAT CANCER INST.

(USDC ) US SEC OF COMMERCE.

Liotta LA, Stetlerste W, Krutzsch H;

WPI; 1990-290093/38.

New type-IV collagenase peptide fragments - used for metallo-proteinase  
 detection and inhibition and for producing antibodies for enzyme  
 detection.

Disclosure; Fig 1; -pp; English.

XX Type IV procollagenase was purified from human A2058 melanoma cells. The  
 CC complete amino acid sequence was determined (see also Hoyhtya, M. et al,  
 CC (1988) FEBS Letters 233, 109-113). Based on this sequence, peptides were  
 CC synthesised (see features) having homology with a histidine contg. domain  
 CC at residues 371-386, a cysteine contg. domain at residues 200-370, the 80  
 CC residue amino terminus or a region 159 residues from the carboxy  
 CC terminus. These regions correspond to the domain of the enzyme involved  
 CC in enzyme activation and interaction of the enzyme with the substrate.  
 CC The peptides are useful in metalloproteinase detection and inhibition.  
 CC They can be used in the treatment of inappropriate angiogenesis,  
 CC arthritis, tumour growth, invasion and metastasis and granulomatous  
 CC inflammatory conditions such as sarcoidosis. The peptides can be used to  
 CC produce antibodies. Peptide 6, at concn. of 0.1 mM inhibited 80% of the  
 CC enzyme activity. See also US7494796-A and WO9010228. (Note: Revised entry  
 CC submitted to correct the patent number format of US Government-owned NTIS  
 CC applications to prevent clashes with ongoing US granted patent numbers.  
 CC For further information please visit the Derwent web site at  
 CC www.derwent.com/dwpi/updates/ntis\_us.html.) (Updated on 25-MAR-2003 to  
 CC correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX SQ Sequence 631 AA;

Query Match 100.0%; Score 29; DB 2; Length 631;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||

Db 502 KAVFFA 507

```

DE      Human mature matrix metalloprotease-2 (MMP-2) protein sequence.
XX
XX      Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
KW      vitronectin receptor; inhibition; angiogenesis; integrin; tumour growth;
KW      restenosis; neovascularisation.
XX
XX      Homo sapiens.
XX
XX      WO9745447-A1.
XX
XX      04-DEC-1997.
XX
XX      30-MAY-1997; 97WO-US009099.
XX
XX      31-MAY-1996; 96US-0015869P.
XX      31-MAY-1996; 96US-0018733P.
XX
XX      (SCRI ) SCRIPPS RES INST.
XX
XX      Brooks P, Chereah DA, Friedlander M;
XX      WPI; 1998-041758/04.
XX
XX      Packaging material containing polypeptide antagonist of alphav, beta5
XX      integrin - used for inhibition of angiogenesis, and for treating tumours,
XX      inflammation, eye diseases etc.
XX
XX      Disclosure; Fig 16; 117pp; English.
XX
XX      The present sequence represents the mature protein of human matrix
XX      metalloprotease-2 (MMP-2). Fragments of this protein (AAW41228-33) are
XX      able to act as alpha-v-beta-5 antagonists. Alpha-v-beta-5 is a
XX      vitronectin receptor. Inhibitors of alpha-v-beta-5 can inhibit
XX      angiogenesis. The specification describes a novel labelled package that
XX      contains an inhibitor of angiogenesis i.e. an alpha-v-beta-5 antagonising
XX      polypeptide that binds to integrin alpha-v-beta-5 and includes a part of
XX      the C-terminal domain of MMP. The antagonists are used to inhibit
XX      angiogenesis in inflamed tissue, in solid tumours or metastases, and in a
XX      wide range of ocular disorders (e.g. diabetic or other forms of
XX      retinopathy, neovascular glaucoma, or corneal transplants). They are
XX      particularly used to induce regression or to inhibit growth of tumours.
XX      The alpha-v-beta-5 antagonists can also be used to treat restenosis
XX      caused by migration of smooth muscle cells following angioplasty and to
XX      reduce blood supply to selected tissues. The antagonists particularly
XX      inhibit neovascularisation where this is induced by cytokines, e.g.
XX      transforming growth factor alpha, epidermal growth factor or especially
XX      vascular endothelial growth factor
XX
XX      Sequence 631 AA;
SQ
XX      Query Match 100.0%; Score 29; DB 2; Length 631;
XX      Best Local Similarity 100.0%; Pred. No. 6.8e+02;
XX      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      502 KAVFFA 507
      |||||

RESULT 61
ADM48668
ID      ADM48668 standard; protein; 631 AA.
XX
XX      ADM48668;
XX
XX      03-JUN-2004 (first entry)
XX
XX      Human matrix metalloproteinase-2 (MMP-2) protein.
XX
XX      Cancer; metastasis; matrix metalloproteinase-2; MMP-2; vaccine;
KW      immune response; gene therapy; cytostatic; enzyme; human.
XX
XX      Homo sapiens.

```

```

XX  US2003139345-A1.
XX  24-JUL-2003.
XX  23-JAN-2003; 2003US-00350258.
XX  23-JAN-2002; 2002US-0351317P.
XX  (NETK/) NETKE S.
XX  (NIED/) NIEDZWIECKI A.
XX  (RATH/) RATH M.
XX  Necke S, Niedzwiecki A, Rath M;
XX  WPI; 2003-897356/82.
XX  New synthetic oligopeptide, useful for blocking or treating cancer
XX  invasion and metastases in a human patient, particularly as a vaccine for
XX  treating or preventing diagnosing brain cancer, lung cancer, skin cancer
XX  or breast cancer.
XX  Example 1; Fig 1; 11pp; English.
XX  The present invention relates to novel synthetic oligopeptides effective
XX  in blocking cancer invasion and metastasis. The invention relates to
XX  matrix metalloproteinase-2 (MMP-2) peptides. The synthetic oligopeptides
XX  are useful as pharmaceutical compositions for blocking or treating cancer
XX  invasion and metastases in a human patient. In particular, they are
XX  useful for treating brain cancer, lung cancer, skin cancer or breast
XX  cancer. The oligopeptides are also useful as vaccines for preventing
XX  these cancers, enhancing immune response or raising antibodies for assays
XX  used to diagnose diseases involving matrix metalloproteinases or clinical
XX  monitoring of the progression or regression of disease. They are also
XX  useful in gene therapy. The present sequence is the human MMP-2 protein.
XX  Sequence 631 AA;
XX  Query Match 100.0%; Score 29; DB 7; Length 631;
XX  Best Local Similarity 100.0%; Pred. No. 6.8e+02;
XX  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  Qy 1 KAVPFA 6
XX  |||||
XX  502 KAVPFA 507
XX  Db
XX  RESULT 62
XX  ADT05996
XX  ID ADT05996 standard; protein; 631 AA.
XX  AC ADT05996;
XX  30-DEC-2004 (first entry)
XX  DE Human mature matrix metalloprotease (MMP-2).
XX  Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
XX  vitronectin receptor antagonist; neovascularisation; cancer; tumour;
XX  inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
XX  restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
XX  cytosstatic; antiinflammatory; antiarthritic; antirheumatic;
XX  ophthalmological; antidiabetic; vasotropic; muscular-gen.;
XX  peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase; human;
XX  enzyme.
XX  OS Homo sapiens.
XX  FH Key Location/Qualifiers
XX  FT Region 410..631
XX  FT Domain 439..631
XX  FT /note= "Corresponds to SEQ ID NO:17"
XX  FT /label = Hemopexin_domain

```

```

PT  Region /note = Corresponds to SEQ ID NO:18
FT 439..546
PT  Region /note= "Corresponds to SEQ ID NO:20"
FT 439..512
PT  Region /note= "Corresponds to SEQ ID NO:19"
FT 510..631
PT  Region /note= "Corresponds to SEQ ID NO:21"
FT 543..631
PT  Region /note= "Corresponds to SEQ ID NO:22"
XX WO2004087057-A2.
XX 14-OCT-2004.
XX 26-MAR-2004; 2004WO-US009321.
XX 28-MAR-2003; 2003US-00402212.
XX (SCRI ) SCRIPPS RES INST.
XX Brooks PC, Cheres DA;
XX WPI; 2004-737508/72.
XX Administration of composition comprising organic peptidomimetic alpha-v
XX beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
XX angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX Example 2; Fig 7A-C; 184pp; English.
XX The invention relates to a method of inhibiting angiogenesis in a tissue
XX by the administration of a composition comprising an organic
XX peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
XX receptor). The integrin alpha-V beta-3 antagonist and compositions
XX containing it are useful for inhibiting angiogenesis in a variety of
XX medical conditions. The antagonist may be used to induce the regression
XX of solid tumours or solid tumour metastases; to inhibit the growth of
XX solid tumours undergoing neovascularisation; to treat inflamed tissue in
XX which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
XX treat neovascularisation in retinal tissue (e.g., in diabetic
XX retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
XX cell migration (such as that which occurs following angioplasty); and to
XX reduce the blood supply to a tissue required to support new growth of the
XX tissue. The present sequence represents human mature matrix
XX metalloprotease 2 (MMP-2, gelatinase) used in an example of the
XX invention.
XX SQ Sequence 631 AA;
XX Query Match 100.0%; Score 29; DB 8; Length 631;
XX Best Local Similarity 100.0%; Pred. No. 6.8e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 KAVPFA 6
XX |||||
XX 502 KAVPFA 507
XX Db
XX RESULT 63
XX ADT05997
XX ID ADT05997 standard; protein; 633 AA.
XX AC ADT05997;
XX 30-DEC-2004 (first entry)
XX DE Mouse mature matrix metalloprotease (MMP-2).
XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
XX vitronectin receptor antagonist; neovascularisation; cancer; tumour;
XX inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
XX restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
XX cytosstatic; antiinflammatory; antiarthritic; antirheumatic;
XX metalloprotease 2; MMP-2; gelatinase; human;
XX enzyme.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 410..631
XX FT Domain 439..631
XX FT /note= "Corresponds to SEQ ID NO:17"
XX FT /label = Hemopexin_domain

```



KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;  
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase; mouse;  
 KW murine; enzyme.

XX Mus sp.

XX Key Location/Qualifiers  
 FH 441. .633  
 FT Domain /label = Hemopexin\_domain  
 XX

XX WO2004087057-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009321.

XX 28-MAR-2003; 2003US-00402212.

XX (SCRI ) SCRIPPS RES INST.

XX Brooks PC, Chereesh DA;

XX WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v  
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue  
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX Example 2; Fig 7A-C; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue  
 CC by the administration of a composition comprising an organic  
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin  
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions  
 CC containing it are useful for inhibiting angiogenesis in a variety of  
 CC medical conditions. The antagonist may be used to induce the regression  
 CC of solid tumours or solid tumour metastases; to inhibit the growth of  
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in  
 CC treat neovascularisation is occurring (e.g., in rheumatoid arthritis); to  
 CC treat neovascularisation in retinal tissue (e.g., in diabetic  
 CC retinopathy); to treat stenosis in a tissue by inhibiting smooth muscle  
 CC cell migration (such as that which occurs following angioplasty); and to  
 CC reduce the blood supply to a tissue required to support new growth of the  
 CC tissue. The present sequence represents mouse mature matrix  
 CC metalloprotease 2 (MMP-2, gelatinase) used in an example of the  
 CC invention.

XX Sequence 633 AA;

Query Match 100.0%; Score 29; DB 8; Length 633;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6

Db 504 KAVFFFA 509

RESULT 64

AAB20490

ID AAB20490 standard; protein; 644 AA.

XX AAB20490;

XX 21-JUN-2001 (first entry)

XX Human matrix metalloproteinase-2 (MMP-2).

XX Matrix metalloproteinase-2; MMP-2; human; pain; analgesic;  
 KW nerve tissue damage; stroke; haemorrhage; reperfusion injury;  
 KW cerebral ischaemia; cerebral infarction; narcotic tolerance;  
 KW narcotic withdrawal.

OS Homo sapiens.

XX WO200126671-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-US027949.

XX 12-OCT-1999; 99US-0158787P.

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX Romanic Arnold A, Barone FC, Bingham S;

XX WPI; 2001-290654/30.

XX N-PSDB; AAF30807.

XX Polypeptide for the treatment of pain and the reduction of tissue damage  
 PT comprises an inhibitor of human matrix metalloproteinase.

XX Claim 1; Fig 2; 61pp; English.

XX The present sequence is that of human matrix metalloproteinase-2 (MMP-2),  
 CC previously known as 72 kDa gelatinase and gelatinase A. MMP-2 is capable  
 CC of degrading the extracellular matrix components of the basement  
 CC membrane. The invention relates to methods for treating pain in a patient  
 CC by administering a dual inhibitor of MMP-2 and MMP-9 (see AAB20491). The  
 CC administration of an inhibitor of MMP-2 is useful for treating nerve  
 CC tissue damage (claimed), where the patient is suffering from a disease or  
 CC disorder selected from stroke, haemorrhage, reperfusion injury, cerebral  
 CC ischaemia and cerebral infarction (claimed). The method is useful for  
 CC treating a disease, disorder or nerve tissue damage selected from  
 CC enhanced or exaggerated sensitivity to acute pain, burn pain, atypical  
 CC facial pain, neuropathic pain, back pain, complex regional pain syndrome  
 CC I and II, arthritic pain, sports injury pain, pain related to virus  
 CC infection, post-herpetic neuralgia, phantom limb pain, labour pain,  
 CC cancer pain, post-chemotherapy pain, post-operative pain, post-stroke  
 CC pain, physiological pain, inflammatory pain, acute inflammatory  
 CC conditions/visceral pain, neuralgia, painful diabetic retinopathy,  
 CC traumatic nerve injury, and tolerance to narcotics or withdrawal from  
 CC narcotics (claimed). MMP-2 polypeptides can also be used to screen for  
 CC agonist or antagonist (inhibitor) compounds

XX Sequence 644 AA;

Query Match 100.0%; Score 29; DB 4; Length 644;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6

Db 515 KAVFFFA 520

RESULT 65

AAR06420

ID AAR06420 standard; protein; 660 AA.

XX AAR06420;

XX 25-MAR-2003 (revised)

XX 13-DEC-1990 (first entry)

XX Type IV collagenase cDNA product.

XX hypetrophic scars; keloids; intervertebral disc disease; ds.

XX Homo sapiens.

XX US4923818-A.

XX 08-MAY-1990.

XX PF 15-MAY-1989; 89US-00352069.  
 XX PR 15-MAY-1989; 89US-00352069.  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX PI Goldberg GL, Eisen AZ;  
 XX DR WPI; 1990-245482/32.  
 XX DR N-PSDB; AAO05620.  
 XX PT Recombinant human type IV collagenase - used in treatment of hypertrophic  
 XX PT scars, keloids and intervertebral disc disease.  
 XX PS Claim 3; Fig 9; 23pp; English.  
 XX CC cDNA clone enables production of type IV collagenase, useful in  
 XX CC catalyzing cleavage of extracellular matrix macromolecules, and in  
 XX CC treatment of hypertrophic scars, keloids and intervertebral disc disease.  
 XX CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX SQ Sequence 660 AA;  
 Query Match 100.0%; Score 29; DB 2; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KAVFFA 6  
 Db 531 KAVFFA 536  
 RESULT 66  
 AAB84607  
 ID AAB84607 standard; protein; 660 AA.  
 AC AAB84607;  
 XX 05-SEP-2001 (first entry)  
 XX Amino acid sequence of matrix metalloproteinase gelatinase A.  
 XX Growth factor; protein inhibitor; protease; damaged tissue;  
 XX platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;  
 XX connective tissue derived growth factor; CTGF; chrysalin; VEGF;  
 XX keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;  
 XX transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;  
 XX granulocyte macrophage colony stimulating factor; GM-CSF; uPA;  
 XX vascular endothelial growth factor; urokinase plasminogen activator;  
 XX dermal ulcer; wound.  
 XX Homo sapiens.  
 XX WO200149309-A2.  
 XX 12-JUL-2001.  
 XX 21-DEC-2000; 2000WO-IB001935.  
 XX 29-DEC-1999; 99GB-00030768.  
 XX (PFIZ ) PFIZER LTD.  
 XX (PFIZ ) PFIZER INC.  
 XX Davies MJ, Huggins JP, McIntosh PS, Occleston NL;  
 XX WPI; 2001-418351/44.  
 XX N-PSDB; AAB28222.  
 XX Composition for the treatment of damaged tissue i.e. chronic wounds and  
 XX dermal ulcers comprises an inhibitor agent i.e. a protease and a growth  
 XX factor.

XX PS Disclosure; Page 552; 572pp; English.  
 XX The specification describes a pharmaceutical composition, comprising a  
 XX growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent  
 XX inhibits the action of at least one specific adverse protein, i.e. a  
 XX protease, that is upregulated in a damaged tissue such as a wound  
 XX environment. Growth factors which are included in the composition of the  
 XX invention are platelet-derived growth factor (PDGF), fibroblast growth  
 XX factor (FGF), connective tissue derived growth factor (CTGF),  
 XX keratinocyte-derived growth factor (KGF), transforming growth factor-beta  
 XX (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),  
 XX epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),  
 XX and chrysalin. Inhibitors which are included in the composition of the  
 XX invention include inhibitors of urokinase-type plasminogen activator  
 XX (uPA) and matrix metalloproteinase (MMP). The composition is useful for  
 XX the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.  
 XX The present sequence represents a human MMP-2, and is used to produce the  
 XX composition of the invention  
 XX SQ Sequence 660 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KAVFFA 6  
 Db 531 KAVFFA 536  
 RESULT 67  
 AAE10431  
 ID AAE10431 standard; protein; 660 AA.  
 AC AAE10431;  
 XX 10-DEC-2001 (first entry)  
 XX Human matrix metalloproteinase-2 (MMP-2) protein.  
 XX Human; matrix metalloproteinase; MMP-2; hair growth; antisense therapy;  
 XX endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX Peptide 1..27  
 XX Protein 28..660  
 XX Domain 100..106  
 XX Domain 171..195  
 XX /label= Signal\_peptide  
 XX /label= Mature\_MMP\_2\_protein  
 XX /label= Cysteine\_switch\_domain  
 XX /note= "Zinc and calcium binding domain"  
 XX WO200166766-A2.  
 XX 13-SEP-2001.  
 XX 06-MAR-2001; 2001WO-US007167.  
 XX 06-MAR-2000; 2000US-0187196P.  
 XX (DARW-) DARWIN MOLECULAR CORP.  
 XX (SCHA/) SCHATZMAN R.  
 XX Fajardo M, Wang K, Smith R, Moss P;  
 XX WPI; 2001-582276/65.  
 XX Novel isolated matrix metalloproteinase-25 nucleic acid molecule and  
 XX proteins encoded by them whose inhibition is useful for modulation of



PR 11-APR-2001; 2001US-0282850P.  
XX  
XX PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX PI St Croix B, Kinzler KW, Vogelstein B;  
XX  
XX CC WPI; 2002-291856/33.  
DR N-PSDB; ABL92092.  
XX  
XX An isolated molecule comprising an antibody variable region which  
PT specifically binds to an extracellular domain of a tumor endothelial  
PT marker (TEM) protein, useful for inhibiting tumor growth.  
XX  
XX Claim 54; Page 166-168; 31pp; English.  
XX  
XX The invention relates to an isolated molecule comprising an antibody  
CC variable region which specifically binds to an extracellular domain of a  
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
CC are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995  
XX  
XX Sequence 660 AA;  
SQ

Query Match 100.0%; Score 29; DB 5; Length 660;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
Db |||||  
531 KAVFFA 536

RESULT 70  
AAU84348  
ID AAU84348 standard; protein; 660 AA.  
XX  
XX AC AAU84348;  
XX  
XX DT 08-MAY-2002 (first entry)  
XX  
XX DE Protein MMP2 differentially expressed in breast cancer tissue.  
XX  
XX KW Human; diagnosis of breast cancer; endometrial cancer; breast tumour;  
XX MAI; mitotic activity index; cytostatic.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200210436-A2.  
XX  
XX PD 07-FEB-2002.  
XX  
XX PP 27-JUL-2001; 2001WO-US023642.  
XX  
XX PR 28-JUL-2000; 2000US-0222093P.  
XX  
XX PA (BGMH ) BRIGHAM & WOMENS HOSPITAL INC.  
XX (BAAK/) BAAK J.  
XX  
XX FI Baak J, Mutter GL;  
XX  
XX DR WPI; 2002-180084/23.  
DR N-PSDB; ABK35568.  
XX  
XX PT Diagnosing breast cancer comprises determining expression of nucleic acid  
PT molecules or expression products that are differentially expressed in

PT normal and malignant tissue.  
XX  
XX PS Claim 37; Page 185-187; 21pp; English.  
XX  
XX The present invention relates to a method for diagnosing breast cancer in  
CC a subject suspected of having endometrial cancer. The method comprises  
CC determining the expression of a set of human genes or expression products  
CC in an endometrial sample suspected of being cancerous. The human genes of  
CC the invention are differentially expressed in breast tumours  
CC characterised as high or low MAI (mitotic activity index). These sets of  
CC genes can be used to discriminate between high and low MAI breast  
CC tumours. The invention also provides DNA and protein microarrays for  
CC analysing the expression of the human genes and their protein products.  
CC The methods and arrays are useful for the diagnosis and prognosis of  
CC endometrial cancer, selecting and monitoring treatment regimes, and  
CC identification of compounds useful for the treatment of endometrial  
CC cancer. AAU84311-AAU84361 represent the human proteins of the invention  
CC that are differentially expressed in breast cancer tissue  
XX  
XX Sequence 660 AA;  
SQ

Query Match 100.0%; Score 29; DB 5; Length 660;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
Db |||||  
531 KAVFFA 536

RESULT 71  
ABU54445  
ID ABU54445 standard; protein; 660 AA.  
XX  
XX AC ABU54445;  
XX  
XX DT 12-MAR-2003 (first entry)  
XX  
XX DE Human tumour endothelial marker TEM 7.  
XX  
XX KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
XX Tumour endothelial marker; normal endothelial marker; PEM;  
XX pan-endothelial marker; polycystic kidney disease; psoriasis;  
XX diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
XX neoangiogenesis; immune response; cytostatic; antidiabetic;  
XX ophthalmological; antirheumatic; antiarthritic; antipsoriatic.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200283874-A2.  
XX  
XX PD 24-OCT-2002.  
XX  
XX PP 10-APR-2002; 2002WO-US008253.  
XX  
XX PR 11-APR-2001; 2001US-0282850P.  
XX  
XX PR 06-FEB-2002; 2002US-0354262P.  
XX  
XX PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
XX  
XX DR WPI; 2003-093016/08.  
DR N-PSDB; ABX72017.  
XX  
XX PT New purified human transmembrane protein, designated as tumor endothelial  
XX marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
XX polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
XX psoriasis.  
XX  
XX PS Disclosure; Page 173-174; 374pp; English.  
XX  
XX CC The present invention relates to a novel method for the isolation of

CC endothelial cells (ECs), and the identification of genes expressed in  
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
 CC identified in human ECs. The human EC marker proteins and the  
 CC polynucleotide sequences encoding them are useful for detecting,  
 CC diagnosing or treating tumours as well as polycystic kidney disease,  
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
 CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for  
 CC inducing an immune response to tumour endothelial cells in a patient, or  
 CC for identifying candidate drugs for treating tumours. The present  
 CC sequence represents a human TEM or NEM protein of the invention  
 XX  
 SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6  
 |||||  
 Db 531 KAVFFFA 536

RESULT 72  
 ABP97136  
 ID ABP97136 standard; protein; 660 AA.  
 XX  
 AC ABP97136;  
 XX  
 DT 24-JUN-2003 (first entry)  
 XX  
 DE Human matrix metalloproteinase 2 protein SEQ ID NO:14.  
 XX  
 KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;  
 KW matrix metalloproteinase inhibitor; antitumour; angiogenic; cardiac;  
 KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;  
 KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;  
 KW dermatological; metastatic; non-metastatic; vascularised; heart disease;  
 KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;  
 KW macular degeneration; diabetic retinopathy; cleavage region.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003018748-A2.  
 XX  
 PD 06-MAR-2003.  
 XX  
 PF 15-AUG-2002; 2002WO-US026319.  
 XX  
 PR 16-AUG-2001; 2001US-0312726P.  
 PR 21-DEC-2001; 2001US-00032376.  
 PR 21-MAY-2002; 2002US-00153185.  
 XX  
 PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.  
 XX  
 PI Quirk S, Weart IF;  
 XX  
 DR WPI; 2003-381408/36.  
 XX  
 PS Anti-angiogenic composition comprising peptide inhibitor of matrix  
 PT metalloproteinase, useful for decreasing the expression of vascular  
 PT endothelial growth factor and treating cancers and tissue injuries.  
 XX  
 PS Example 1; Page 43-44; 103pp; English.  
 XX  
 CC The present invention describes an anti-angiogenic composition (I) for  
 CC inhibiting expression of vascular endothelial growth factor (VEGF). (I)  
 CC comprises an effective amount of a peptide inhibitor of matrix  
 CC metalloproteinase (MMP), where the peptide can inhibit the expression of  
 CC VEGF. (I) has cytostatic, vulnary, cardiac, cerebroprotective,  
 CC antidiabetic, ophthalmological and dermatological activities. (I) can be  
 CC used for inhibiting expression of VEGF, and so can be used for inhibiting  
 CC growth of tumours and diminishing tumours size. The tumour can be

CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.  
 CC (I) is also useful for treating injuries including wounds, surgical  
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful  
 CC for treating disorders characterised by excessive angiogenesis e.g.  
 CC macular degeneration and diabetic retinopathy. The present sequence  
 CC represents the human MMP-2 protein, which is used in the exemplification  
 XX  
 SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6  
 |||||  
 Db 531 KAVFFFA 536

RESULT 73  
 AAO16608  
 ID AAO16608 standard; protein; 660 AA.  
 XX  
 AC AAO16608;  
 XX  
 DT 08-MAY-2003 (first entry)  
 XX  
 DE Human matrix metalloproteinase 2 (MMP2) gelatinase protein.  
 XX  
 KW Human; enzyme; crystalline polypeptide; matrix metalloproteinase 9; MMP9;  
 KW gelatinase; metalloproteinase mediated disease; drug design; arthritis;  
 KW three-dimensional structure; MMP9 inhibitor; tumour growth;  
 KW cancer metastasis; osteoarthritis; atherosclerosis; restenosis;  
 KW periodontitis; multiple sclerosis; glomerulonephritis; MMP9 modulator;  
 KW graft-versus-host disease; non-insulin dependent diabetes; MMP2;  
 KW matrix metalloproteinase 2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003002729-A1.  
 XX  
 PD 09-JAN-2003.  
 XX  
 PF 24-JUN-2002; 2002WO-SE001266.  
 XX  
 PR 27-JUN-2001; 2001SE-00002298.  
 XX  
 PA (ASTR ) ASTRAZENCA AB.  
 XX  
 PI Jenson H, Minshull C, Paupit R, Rowsell S;  
 XX  
 DR WPI; 2003-201502/19.  
 XX  
 PT Novel crystalline form of a polypeptide corresponding to the catalytic  
 PT domain of matrix metalloproteinase 9 protein, useful for selecting or  
 PT designing chemical modulators which are used for treating diabetes,  
 PT cancer, arthritis.  
 XX  
 PS Disclosure; Fig 7; 227pp; English.  
 XX  
 CC The invention comprises a crystalline form of a polypeptide corresponding  
 CC to the catalytic domain of matrix metalloproteinase 9 (MMP9) protein - a  
 CC gelatinase. The crystalline polypeptide of the invention is useful for  
 CC treating a metalloproteinase mediated disease or condition in a warm-  
 CC blooded animal. The crystalline polypeptide is also useful for  
 CC determining the three-dimensional structure of the MMP9 catalytic domain  
 CC to high resolution. The three-dimensional structure of the MMP9 catalytic  
 CC domain is useful for rational drug design, and the atomic coordinates of  
 CC the catalytic domain of MMP9 are useful for selecting or designing  
 CC chemical modulators (preferably inhibitors) of MMP9. The crystalline  
 CC polypeptide of the invention is useful in the treatment of a  
 CC metalloproteinase mediated disease or condition, such as: tumour growth;  
 CC metastasis in cancer; arthritis; osteoarthritis; atherosclerosis;

CC reestenosis; periodontitis; multiple sclerosis; glomerulonephritis; graft-versus-host disease; and non-insulin dependent diabetes. The present amino acid sequence represents a human matrix metalloproteinase 2 (MMP2) protein

XX SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|||||  
Db 531 KAVFFA 536

RESULT 74

ABG76322 ID ABG76322 standard; protein; 660 AA.

XX AC ABG76322;

XX DT 10-MAY-2003 (first entry)

XX DE Human matrix metalloproteinase-2 (MMP-2).

XX KW Human; peptide inhibitor; matrix metalloproteinase-2; MMP-2; cleavage region; proenzyme form; cellular proliferation; fibroblast; keratinocyte; healthy skin development; wound healing; scarring; skin tone; wrinkle; anti-aging; vulnerary.

XX OS Homo sapiens.

XX PN WO2003016520-A1.

XX PD 27-FEB-2003.

XX PF 15-AUG-2002; 2002WO-US026198.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Malik S, Villanueva JM;

XX PS WPI; 2003-289980/28.

XX PT Novel peptide inhibitor of proteinase activity of matrix metalloproteinases, e.g. matrix metalloproteinase-2, useful for stimulating cellular proliferation of fibroblasts or keratinocytes.

XX PS Example 1; Page 41-42; 120pp; English.

XX CC The present invention relates to peptide inhibitors of metalloproteinases (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have peptide sequences related to the cleavage regions of the proenzyme forms of the MMPs. The peptide inhibitors are useful for stimulating cellular proliferation of fibroblasts or keratinocytes, promoting healthy skin development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for stimulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healing compounds. The present sequence represents human MMP-2

XX SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|||||

Db 531 KAVFFA 536

RESULT 75

ADD18578 ID ADD18578 standard; protein; 660 AA.

XX AC ADD18578;

XX DT 15-JAN-2004 (first entry)

XX DE Human disease related protein SeqID9.

XX KW human; disease state; cytostatic; antiinflammatory; ophthalmological; antiarteriosclerotic; vulnerary; gene therapy;  
XX KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;  
XX KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;  
XX KW glucose transport; catecholamine synthesis; iron transport;  
XX KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;  
XX KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;  
XX KW inflammatory condition; wound healing.

XX OS Homo sapiens.

XX PN WO2003018621-A2.

XX PD 06-MAR-2003.

XX PF 23-AUG-2002; 2002WO-GB003892.

XX PR 23-AUG-2001; 2001GB-00020558.

XX PR 05-OCT-2001; 2001GB-00024037.

XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.

XX PI Kingeman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX DR WPI; 2003-290046/28.

XX DR N-PSDB; ADD18579.

XX PT New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.

XX PS Claim 25; SEQ ID NO 9; 424pp; English.

XX CC This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, ophthalmological, antiarteriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, such as tumorigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transport, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein of the invention.

XX SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 7; Length 660;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|||||

Db 531 KAVFFA 536

Search completed: December 29, 2005, 17:33:36  
Job time : 91.7742 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds  
(without alignments)  
54.137 Million cell updates/sec

Title: US-10-009-122-4  
Perfect score: 31  
Sequence: 1 KVFVFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

UniProt\_05\_80:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	47	2	Q8G9Y9_fugu_rubrip
2	31	100.0	229	2	Q6R599_triticum tu
3	31	100.0	241	2	Q7XVC3_triticum ae
4	31	100.0	331	2	Q6K5X9_oryza sativ
5	31	100.0	331	2	Q84NE7_ORYSA
6	31	100.0	335	2	Q615W9_ORYSA
7	31	100.0	353	2	Q4HQ66_CAMUP
8	31	100.0	519	2	Q5ATG9_EMENI
9	31	100.0	935	2	Q7XM01_oryza sativ
10	31	100.0	3044	2	Q7QYR7_GIALA
11	30	96.8	224	2	Q84NG7_HORVU
12	30	96.8	395	2	Q98GC2_RHILO
13	30	96.8	397	2	Q2YIY6_RHIME
14	30	96.8	2643	2	Q5A3W3_CANAL
15	30	96.8	2643	2	Q4XXR5_PLACH
16	28	90.3	23	2	Q73M63_TREDE
17	28	90.3	43	2	Q73M63_TREDE
18	28	90.3	49	2	Q9KAX7_BACHD
19	28	90.3	150	2	Q7R979_PLAYO
20	28	90.3	152	2	Q4J1Z2_AZOVI
21	28	90.3	177	2	Q20070_CAEEL
22	28	90.3	199	2	Q6LSA9_PROPR
23	28	90.3	225	2	Q6UJY8_TRITU
24	28	90.3	226	2	Q8LKV8_AEGTA
25	28	90.3	241	2	Q7R8Y4_PLAYO
26	28	90.3	242	2	Q7RA05_PLAYO
27	28	90.3	250	2	Q7RNP5_PLAYO
28	28	90.3	251	2	Q7PDC0_PLAYO
29	28	90.3	251	2	Q7RPS1_PLAYO
30	28	90.3	252	2	Q7RA57_PLAYO
31	28	90.3	252	2	Q7RF37_PLAYO

32	28	90.3	255	2	Q7RLK2_PLAYO
33	28	90.3	262	2	Q7RCL4_PLAYO
34	28	90.3	265	2	Q7RC37_PLAYO
35	28	90.3	268	2	Q7RB86_PLAYO
36	28	90.3	285	2	Q529U4_MAGGR
37	28	90.3	293	2	Q94284_CAEEL
38	28	90.3	294	2	Q7RBU1_PLAYO
39	28	90.3	300	2	Q5UMP7_HALMA
40	28	90.3	321	2	Q7RBU3_PLAYO
41	28	90.3	326	2	P74429_SYNY3
42	28	90.3	380	2	Q6KI05_MYCNO
43	28	90.3	388	2	Q4MSJ5_BACCE
44	28	90.3	388	2	Q6HLH8_BACHK
45	28	90.3	388	2	Q73BD3_BACCL
46	28	90.3	388	2	Q63E03_BACCC
47	28	90.3	388	2	Q81T98_BACAN
48	28	90.3	391	2	Q81G40_BACCR
49	28	90.3	398	2	Q5NEA9_FRATT
50	28	90.3	409	2	Q73V08_MYCPA
51	28	90.3	421	2	Q7Z2C3_CAEEL
52	28	90.3	422	2	Q9PQ22_UREPA
53	28	90.3	430	2	Q8FW04_BRUSU
54	28	90.3	432	2	Q6Q8W8_9GAMM
55	28	90.3	436	2	Q8M9J3_9AQUA
56	28	90.3	452	2	Q44595_CAEEL
57	28	90.3	456	2	Q6GVJ4_9BURK
58	28	90.3	465	1	RBL_NEPAL
59	28	90.3	472	2	Q9NSQ8_CAEEL
60	28	90.3	480	2	Q625W2_CAEER
61	28	90.3	482	2	Q5JJ16_PYRKO
62	28	90.3	488	2	Q966D7_CAEEL
63	28	90.3	492	2	Q621X3_CAEER
64	28	90.3	506	2	Q38860_ARATH
65	28	90.3	508	1	MURE_BORBU
66	28	90.3	509	2	P93058_BRAJU
67	28	90.3	509	2	Q8LSC7_BRACM
68	28	90.3	509	2	Q8S384_BRAJU
69	28	90.3	517	2	Q80729_ARATH
70	28	90.3	529	2	Q6NI23_CORDI
71	28	90.3	538	2	Q7PQ20_ANOGA
72	28	90.3	558	2	Q5TTR3_ANOGA
73	28	90.3	571	2	Q97KU8_CLOAB
74	28	90.3	584	2	Q4UGB4_THEAN
75	28	90.3	615	2	Q7PS12_ANOGA
76	28	90.3	664	2	Q966D8_CAEEL
77	28	90.3	746	2	Q9NSQ9_CAEEL
78	28	90.3	802	2	Q7R8Y2_PLAYO
79	28	90.3	853	2	Q7QTQ4_GIALA
80	28	90.3	922	1	GYRA_AERSA
81	28	90.3	1072	2	Q94537_SCHPO
82	28	90.3	1165	2	Q962L9_PLAVI
83	28	90.3	1285	2	Q9WXU3_THEMA
84	28	90.3	1558	2	Q5RH87_BRARE
85	27	87.1	31	2	Q4YNS6_PLABE
86	27	87.1	36	2	Q4XBB3_PLACH
87	27	87.1	38	2	Q32187_EUGGR
88	27	87.1	46	2	Q867A4_TRAJA
89	27	87.1	60	2	Q4YKM8_PLABE
90	27	87.1	77	2	Q52R02_CHICK
91	27	87.1	90	2	Q4XC01_PLACH
92	27	87.1	92	2	Q8MPY0_CAEEL
93	27	87.1	96	2	Q61123_CAEEL
94	27	87.1	99	2	Q4T7Q1_TETTING
95	27	87.1	114	2	Q6ZB28_ORYSA
96	27	87.1	117	2	Q74KX8_LACJO
97	27	87.1	121	2	Q6R983_MAI2E
98	27	87.1	128	2	Q4MQN4_BACCE
99	27	87.1	128	2	Q6HNK6_BACHK
100	27	87.1	128	2	Q81116_BACCR
101	27	87.1	128	2	Q73DN7_BACCL
102	27	87.1	128	2	Q63G38_BACCC
103	27	87.1	128	2	Q81V92_BACAN
104	27	87.1	134	2	Q7R7Y0_PLAYO

Q7rlk2	plasmodium
Q7rc14	plasmodium
Q7rc37	plasmodium
Q7rb86	plasmodium
Q529u4	magnaporthe
Q94284	caenorhabdi
Q7rbu1	plasmodium
Q5ump7	haloarcula
Q7rbj3	plasmodium
P74429	mynechocyst
Q6ki05	mycoplasma
Q4msj5	bacillus ce
Q6hlh8	bacillus th
Q73bd3	bacillus ce
Q63e03	bacillus ce
Q81t98	bacillus an
Q81g40	bacillus ce
Q5nea9	francisella
Q73v08	mycobacteri
Q7z2c3	caenorhabdi
Q9pq22	ureaplasma
Q8fw04	brucella su
Q6q8w8	uncultured
Q8m9j3	illex pubesc
Q44595	caenorhabdi
Q6gvj4	burkholderi
P28434	nepeenthes a
Q9nsq8	caenorhabdi
Q625w2	caenorhabdi
Q5jj16	pyrococcus
Q966d7	caenorhabdi
Q621x3	caenorhabdi
Q38860	arabidopsis
Q51219	borrelia bu
P93058	brassica ju
Q8lsc7	brassica ca
Q8s384	brassica ju
Q80729	arabidopsis
Q6ni23	corynebacte
Q7p200	anopheles g
Q5ttr3	anopheles g
Q97ku8	clostridium
Q4ugb4	theileria a
Q7ps12	anopheles g
Q966d8	caenorhabdi
Q9nsq9	caenorhabdi
Q7r8y2	plasmodium
Q7gtq4	giardia lam
P48369	aeromonas s
Q94537	schizosacch
Q962l9	plasmodium
Q9wxu3	thermotoga
Q5rh87	brachydanio
Q4y6n6	plasmodium
Q4xb83	plasmodium
Q32187	euglena gra
Q867a4	tragulus ja
Q4ykm8	plasmodium
Q52r02	gallus gall
Q4xc01	plasmodium
Q8mpy0	caenorhabdi
Q61123	caenorhabdi
Q4t7q1	tetradon n
Q6zb28	oryza sativ
Q74kx8	lactobacill
Q6r983	zea mays (m
Q4mqn4	bacillus ce
Q6hnk6	bacillus th
Q81116	bacillus ce
Q73dn7	bacillus ce
Q63g38	bacillus ce
Q81v92	bacillus an
Q7r7y0	plasmodium



105	27	87.1	134	2	Q4XU22_PLACH	Q4xu22 plasmodium
106	27	87.1	135	2	Q8MYN0_CABEL	Q8myno caenorhabdi
107	27	87.1	136	2	O51365_BORBU	O51365 borrelia bu
108	27	87.1	137	2	Q9G4E5_FASGI	Q9g4e5 fasciola gi
109	27	87.1	138	2	O8I4D1_CABEL	O8i4d1 caenorhabdi
110	27	87.1	139	2	O8IWA3_HUMAN	O8iwa3 homo sapien
111	27	87.1	140	2	Q6MGH2_EDEBA	Q6mgm2 bdellovibri
112	27	87.1	141	2	Q6MUK5_MYCNS	Q6muk5 mycoplasma
113	27	87.1	142	2	Q6ZUC5_HUMAN	Q6zuc5 homo sapien
114	27	87.1	143	2	Q97657_CANFA	Q97657 canis fami
115	27	87.1	144	2	Q6QLX0_CANFA	Q6qlx0 canis fami
116	27	87.1	145	2	Q4WKU9_ASPFU	Q4wku9 aspergillus
117	27	87.1	146	2	Q6KAU3_MOUSE	Q6kau3 mus musculu
118	27	87.1	147	1	RT25_MOUSE	Q6kai25 mus musculu
119	27	87.1	148	2	Q4QRJ80_RAT	Q4qrj80 rattus norv
120	27	87.1	149	2	Q4RQW4_TETNG	Q4rjqv4 tetraodon n
121	27	87.1	150	1	RT25_HUMAN	P82663 homo sapien
122	27	87.1	151	2	Q63507_9TREM	O63507 echinostoma
123	27	87.1	152	2	Q63508_9TREM	O63508 echinostoma
124	27	87.1	153	2	Q4ZOC8_PLABE	Q4zoc8 plasmodium
125	27	87.1	154	2	Q63509_9TREM	P41026 bacillus am
126	27	87.1	155	1	LEP1_BACAM	O51736 borrelia bu
127	27	87.1	156	2	O51736_BORBU	P41025 bacillus am
128	27	87.1	157	1	LEP2_BACAM	P71013 bacillus eu
129	27	87.1	158	1	LEP1_BACSU	Q504j3 entamoeba h
130	27	87.1	159	1	Q50XJ3_ENTHI	O5nt24 entamoeba h
131	27	87.1	160	2	O5NT24_ENTHI	O6pb22 homo sapien
132	27	87.1	161	2	Q96B03_HUMAN	Q83455 porcine ade
133	27	87.1	162	2	O6PDB2_HUMAN	Q7rxj3 plasmodium
134	27	87.1	163	2	Q83455_ADEP3	O83455 thermotoga
135	27	87.1	164	2	Q7RMJ3_PLAYO	Q6pwq4 xenopus lae
136	27	87.1	165	2	Q6PMQ4_XENLA	Q9llm5 arabidopsis
137	27	87.1	166	2	Q9LHM5_ARATH	Q8zdv0 versinia pe
138	27	87.1	167	2	Q8ZDV0_YERPE	P42540 bacterioph
139	27	87.1	168	1	YO14_BFL2	O5hrc1 staphylococ
140	27	87.1	169	2	Q5HRC1_STAEO	Q8cns5 staphylococ
141	27	87.1	170	2	Q8CTN5_STAEP	O5b4b1 aspergillus
142	27	87.1	171	2	Q5B4B1_EMENI	Q4n8x3 theileria p
143	27	87.1	172	2	Q4N8X3_THEPA	Q8fb21 escherichia
144	27	87.1	173	2	Q8FB21_ECOL6	O8ib21 plasmodium
145	27	87.1	174	2	O8IB21_PLAF7	Q51209 geobacillus
146	27	87.1	175	2	O5L209_GEOKA	Q9c110 neurospora
147	27	87.1	176	2	Q9C110_NEUCR	O9bg13 ovis aries
148	27	87.1	177	2	Q9BGL3_SHEEP	O6pwg5 xenopus lae
149	27	87.1	178	2	Q6PMQ5_XENLA	Q9wz85 thermotoga
150	27	87.1	179	2	Q9WZ85_THEMA	O9u336 caenorhabdi
151	27	87.1	180	2	Q9U336_CABEL	Q72p77 leptospira
152	27	87.1	181	2	Q72P77_LEPIC	Q8f779 leptospira
153	27	87.1	182	2	Q8F779_LEPIN	Q34521 fasciola he
154	27	87.1	183	2	Q34521_FASHE	Q9bb94 fasciola he
155	27	87.1	184	2	Q9BB94_FASHE	O88xr9 lactobacill
156	27	87.1	185	2	Q88XR9_LACPL	Q7xji1 trifolium r
157	27	87.1	186	2	Q7XJ11_TRIPL	Q7xji6 triticum ae
158	27	87.1	187	2	Q7XJ11_WHEAT	Q7xji2 brassica na
159	27	87.1	188	2	Q7XJ12_ERANA	O66917 yersinia ps
160	27	87.1	189	2	Q66917_YERPS	O511s8 silicibacte
161	27	87.1	190	2	Q5LSH8_SILPO	Q8k9x4 buchnera ap
162	27	87.1	191	1	Y160_BUCAP	P48279 cyanophora
163	27	87.1	192	1	YCE39_CVAPA	Q6hxi3 bacillus th
164	27	87.1	193	2	Q6HKI3_BACHK	O818a4 bacillus an
165	27	87.1	194	2	Q818A4_BACAN	Q84rd6 cucumis sat
166	27	87.1	195	2	Q84RD6_CUCSA	Q7xji3 rosa davuri
167	27	87.1	196	2	Q7XJ13_9ROSA	Q7xji4 salix babyl
168	27	87.1	197	2	Q7XJ14_9ROSI	Q85fx6 cyanidiosch
169	27	87.1	198	1	ACSP_CYAME	O5l441 bacterioides
170	27	87.1	199	2	Q5LE41_BACFN	Q9f749 bacterioides
171	27	87.1	200	2	Q9F749_BACFR	O688q2 oryza sativ
172	27	87.1	201	2	Q688Q2_ORYSA	Q9xdj2 bacterioides
173	27	87.1	202	2	Q9XDJ2_BACFR	O5lgh6 bacterioides
174	27	87.1	203	2	Q5LGH6_BACFN	O5lir4 bacterioides
175	27	87.1	204	2	O5LIR4_BACFN	O64zv1 bacterioides
176	27	87.1	205	2	Q64ZV1_BACFR	Q6y7p5 staphylococ
177	27	87.1	206	2	Q6Y7P5_9VIRU	

178	27	87.1	345	2	Q4Z9Y8_9VIRU	Q4z9y8 bacterioph
179	27	87.1	346	2	Q8KZ48_9PROT	Q8kz48 uncultured
180	27	87.1	347	1	ACSF_GLOVI	Q7nfaf gloebacter
181	27	87.1	348	1	ACSF_GRATL	Q7nba1 gracilaria
182	27	87.1	349	1	ACSF_PORPU	P51277 porphyra pu
183	27	87.1	350	2	Q9Y370_HUMAN	Q9y370 homo sapien
184	27	87.1	351	2	Q8TCX1_HUMAN	Q8tcx1 homo sapien
185	27	87.1	352	2	Q96J00_HUMAN	Q96j00 homo sapien
186	27	87.1	353	2	O17576_CABEL	O17576 caenorhabdi
187	27	87.1	354	1	ACSF_CYACA	Q9t1r8 cyanidium c
188	27	87.1	355	1	ACSF_SYNPX	Q7u6y8 symnechococ
189	27	87.1	356	2	Q5NPT3_ZYMMO	Q5npt3 zymomonas m
190	27	87.1	357	1	ACSF1_SYNY3	P72584 synchocyst
191	27	87.1	358	1	ACSF3_ANASP	Q8y7z2 anaebaeia sp
192	27	87.1	359	2	Q75AT8_ASHGO	Q75at8 ashbya goss
193	27	87.1	360	2	Q7RGM5_PLAYO	Q7rgm5 plasmodium
194	27	87.1	361	1	ACSF_RHOPA	Q6n9j7 rhodospseudo
195	27	87.1	362	2	Q6ZM18_BRARE	Q6zm18 brachydanio
196	27	87.1	363	2	Q40093_IPONI	Q40093 ipomoea nil
197	27	87.1	364	2	Q8A715_BACTN	Q8a715 bacterioides
198	27	87.1	365	2	Q98QH7_MYCPU	Q98qh7 mycoplasma
199	27	87.1	366	2	Q84RD7_TOBAC	Q84rd7 nicotiana t
200	27	87.1	367	2	Q8FVI2_CANGA	Q8fvi2 candida gla
201	27	87.1	368	2	Q95NI2_CABEL	Q95ni2 caenorhabdi
202	27	87.1	369	2	Q8LEE4_ARATH	Q8lee4 arabidopsis
203	27	87.1	370	1	CRD1_EUPES	Q945b7 euphorbia e
204	27	87.1	371	1	CRD1_GOSHI	Q691v8 gossypium h
205	27	87.1	372	1	CTH1_CHLRE	Q9ar22 chlamydomon
206	27	87.1	373	2	O45653_CABEL	O45653 caenorhabdi
207	27	87.1	374	2	Q9SDJ2_ORYSA	Q9sdj2 oryza sativ
208	27	87.1	375	1	CRD1_ARATH	Q9m591 a magnesium
209	27	87.1	376	2	O5LH15_BACFN	Q5lhi5 bacterioides
210	27	87.1	377	2	Q64YF9_BACFR	Q64yf9 bacterioides
211	27	87.1	378	1	CRD1_HORVU	O5etu4 hordeum vul
212	27	87.1	379	2	Q6NKY4_ARATH	Q6nky4 arabidopsis
213	27	87.1	380	2	Q6OIR3_MYCHY	Q6oir3 mycoplasma
214	27	87.1	381	2	Q98TF3_ORYLA	Q98tf3 oryza lat
215	27	87.1	382	2	Q68IY3_ARATH	Q68iy3 arabidopsis
216	27	87.1	383	2	Q6XRC0_9BACT	Q6xrc0 uncultured
217	27	87.1	384	2	Q9C954_ARATH	Q9c954 arabidopsis
218	27	87.1	385	2	O5LEE2_ENTHI	O5lee2 entamoeba h
219	27	87.1	386	1	ENGA_CLOPE	Q8xfjk1 clostridium
220	27	87.1	387	2	Q9WZ33_THEMA	Q9wz33 thermotoga
221	27	87.1	388	2	Q8VUW4_STAHO	Q8vuw4 staphylococ
222	27	87.1	389	2	O51FM2_ENTHI	Q51fm2 entamoeba h
223	27	87.1	390	2	Q4UDY3_THEAN	Q4udy3 theileria a
224	27	87.1	391	2	Q6UR08_ANOGA	Q6ur08 anopheles g
225	27	87.1	392	2	Q7QCC7_ANOGA	Q7qcc7 anopheles g
226	27	87.1	393	2	Q18760_CABEL	Q18760 caenorhabdi
227	27	87.1	394	2	P87212_9APHY	P87212 polyporacea
228	27	87.1	395	2	Q8NKF3_9AGAR	Q8nkf3 termitomyce
229	27	87.1	396	2	Q6QNE9_CABEL	Q6qne9 caenorhabdi
230	27	87.1	397	2	Q9LPY0_ARATH	Q9lpy0 arabidopsis
231	27	87.1	398	2	Q75819_ASHGO	Q75819 ashbya goss
232	27	87.1	399	1	IPT1_YEAST	P38954 saccharomyc
233	27	87.1	400	2	Q7QX86_GIALA	Q7qx86 giardia lam
234	27	87.1	401	2	Q98TF2_ORYLA	Q98tf2 oryza lat
235	27	87.1	402	2	Q4SKD2_TETNG	Q4skd2 tetraodon n
236	27	87.1	403	2	Q4S0T5_TETNG	Q4s0t5 tetraodon n
237	27	87.1	404	2	Q7T2J2_BRARE	Q7t2j2 brachydanio
238	27	87.1	405	2	Q5USC3_XENLA	Q5usc3 xenopus lae
239	27	87.1	406	2	Q6DCW8_XENLA	Q6dcw8 xenopus lae
240	27	87.1	407	2	Q5BL52_XENTR	Q5bl52 xenopus tro
241	27	87.1	408	1	MMP14_FIG	O9xt90 sus scrofa
242	27	87.1	409	2	O68921_NEIGO	O68921 neisseria g
243	27	87.1	410	2	Q5F8K1_NEIGI	Q5f8k1 neisseria g
244	27	87.1	411	2	Q9U293_NEIMB	Q9u293 neisseria m
245	27	87.1	412	2	Q9JUB8_NEIMA	Q9jub8 neisseria m
246	27	87.1	413	2	MMP14_HUMAN	P50281 homo sapien
247	27	87.1	414	2	MMP14_MOUSE	P32690 mus musculu
248	27	87.1	415	2	MMP14_RABIT	P52220 rhyctolagus
249	27	87.1	416	2	MMP14_RAT	Q10739 rhyctolagus
250	27	87.1	417	2	Q6GSF3_HUMAN	Q6gsf3 homo sapien

251	27	87.1	582	2	Q9GLE4	BOVIN	Q9gle4	bos taurus
252	27	87.1	582	2	Q9RES1	PONPY	Q9resi	pongo pygma
253	27	87.1	582	2	Q9XSP0	CAPHY	Q9xsp0	capra hircu
254	27	87.1	582	2	Q99PG1	CRIGR	Q99pg1	cricetulus
255	27	87.1	582	2	Q9BTX2	MOUSE	Q9btx2	mus musculus
256	27	87.1	582	2	Q6DFU5	MOUSE	Q6dfu5	mus musculus
257	27	87.1	582	2	Q6IN06	RAT	Q6in06	rattus norv
258	27	87.1	585	2	Q7RDB0	PLAYO	Q7rdb0	plasmodium
259	27	87.1	585	2	Q4NRW3	THEPA	Q4nrw3	theileria p
260	27	87.1	592	2	Q4RWY3	TETNG	Q4rwy3	tetraodon n
261	27	87.1	599	2	Q752M5	ASHGO	Q752m5	ashbya goss
262	27	87.1	607	2	Q76LU7	ORYLA	Q76lu7	oryzias lat
263	27	87.1	610	2	Q4W889	ORYLA	Q4w889	oryzias lat
264	27	87.1	621	2	Q72TJ1	BRARE	Q72tj1	brachydanio
265	27	87.1	626	2	Q98HT9	RHIL0	Q98ht9	rhizobium l
266	27	87.1	689	1	SO1B2	HOUSE	Q9j1l3	mus musculus
267	27	87.1	695	2	Q419L8	GIBZE	Q419l8	gibberellia
268	27	87.1	698	2	Q5BD98	EMENI	Q5bd98	aspergillus
269	27	87.1	721	2	O16363	CABEL	O16363	caenorhabdi
270	27	87.1	732	2	Q4SKK7	TETNG	Q4skk7	tetraodon n
271	27	87.1	763	2	Q4Y784	PLACH	Q4y784	plasmodium
272	27	87.1	773	1	YOD3	CABEL	P34595	caenorhabdi
273	27	87.1	780	2	Q6A1B3	ECHMU	Q6a1b3	echinococcu
274	27	87.1	789	2	Q5AGA4	PLAYO	Q5aga4	candida alb
275	27	87.1	794	2	Q7RBG4	PLAYO	Q7rbg4	plasmodium
276	27	87.1	796	2	Q91SC5	9ALPH	Q91sc5	canine herp
277	27	87.1	833	1	HMDH	AGRIP	Q76819	agrotis ips
278	27	87.1	846	2	Q4SL98	TETNG	Q4sl98	tetraodon n
279	27	87.1	856	1	HMDH	BLAGE	P54960	blattella g
280	27	87.1	923	2	Q73L77	TREDE	Q73l77	treponema d
281	27	87.1	1024	1	CAR12	HUMAN	Q9app4	homo sapien
282	27	87.1	1049	2	Q528F0	MAGGR	Q528f0	magnaporthe
283	27	87.1	1068	2	Q55DX7	DICDI	Q55dx7	dictyosteli
284	27	87.1	1099	2	Q81E72	PLAF7	Q81e72	plasmodium
285	27	87.1	1126	2	Q73ME8	TREDE	Q73me8	treponema d
286	27	87.1	1144	2	Q86JE2	DICDI	Q86je2	dictyosteli
287	27	87.1	1145	2	Q5SA20	DICDI	Q5sa20	dictyosteli
288	27	87.1	1269	2	Q4YNH1	PLABE	Q4ynh1	plasmodium
289	27	87.1	1279	2	Q761L3	BRARE	Q761l3	brachydanio
290	27	87.1	1469	2	Q4YZQ1	PLABE	Q4yzq1	plasmodium
291	27	87.1	1508	2	Q7BHP5	PLAYO	Q7rbf5	plasmodium
292	27	87.1	1563	2	Q61CM5	CABER	Q61cm5	caenorhabdi
293	27	87.1	1897	2	Q81BK2	PLAF7	Q81bk2	plasmodium
294	27	87.1	1917	2	Q4X570	PLACH	Q4x570	plasmodium
295	27	87.1	2118	2	Q7RR57	PLAYO	Q7rr57	plasmodium
296	27	87.1	2921	2	Q5WNK5	CABER	Q5wnk5	caenorhabdi
297	27	87.1	3978	2	Q97236	PLAF7	Q97236	plasmodium
298	27	87.1	6739	2	Q7QVB8	GIALA	Q7qvb8	glardia lam
299	26	83.9	24	2	Q4X467	PLACH	Q4x467	plasmodium
300	26	83.9	27	2	Q4Z519	PLABE	Q4z519	plasmodium

## ALIGNMENTS

RESULT 1			
Q8QGY9_FUGRU			
ID	Q8QGY9_FUGRU	PRELIMINARY;	PRT; 47 AA.
AC	Q8QGY9;		
DT	01-JUN-2002	(T=EMBLrel. 21, Created)	
DT	01-JUN-2002	(T=EMBLrel. 21, Last sequence update)	
DT	01-JUN-2003	(T=EMBLrel. 24, Last annotation update)	
DE	Guanine nucleotide binding protein (Fragment).		
GN	Names=Gna12;		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;		
OC	Tetraodontidae; Tetraodontidae; Takifugu.		
OX	NCBI_TaxID=31033;		
OX	[1]		
RN	NUCLEOTIDE SEQUENCE.		
RP	MEDLINE=97129408; PubMed=8973916;		
RX			

```

OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Seed;
RA Li J.R., Wang F., Li Q.Z., Zhang X.S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF475121; AAP80642.1; -; mRNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp alpha amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
FT NON TER
SQ SEQUENCE 241 AA; 26139 MW; AAD8F2BB859DA016 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 15 KVFVFA 20

RESULT 4
Q6K5X9 ORYSA
ID Q6K5X9 ORYSA PRELIMINARY; PRT; 331 AA.
AC Q6K5X9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Transmembrane protein-like.
GN Name=OJ2055 H10.27-1; Synonyms=P0407A09.6-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005300; BAD19727.1; -; Genomic DNA.
DR EMBL; AF004747; BAD19452.1; -; Genomic DNA.
DR Gramene; Q6K5X9; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
KW Transmembrane.
SQ SEQUENCE 331 AA; 36397 MW; EACAC4769463E9EA CRC64;

Query Match 100.0%; Score 31; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 80 KVFVFA 85

RESULT 5
Q84NE7 ORYSA
ID Q84NE7 ORYSA PRELIMINARY; PRT; 331 AA.
AC Q84NE7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transmembrane protein.

```

```

OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Lee R.H., Chen S.C.G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY030360; AAKS0365.1; -; mRNA.
DR Gramene; Q84NE7; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
KW Transmembrane.
SQ SEQUENCE 331 AA; 36384 MW; 289C89F3D3F8229A CRC64;

Query Match 100.0%; Score 31; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 80 KVFVFA 85

RESULT 6
Q615W9 ORYSA
ID Q615W9 ORYSA PRELIMINARY; PRT; 335 AA.
AC Q615W9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transmembrane protein.
GN Name=OJ1076 H08.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsiang Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC108498; AAT47018.1; -; Genomic DNA.
DR Gramene; Q615W9; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
KW Transmembrane.
SQ SEQUENCE 335 AA; 36836 MW; 5A0EF43F8578B46F CRC64;

Query Match 100.0%; Score 31; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 80 KVFVFA 85

RESULT 7
Q4HQ66 CAMUP
ID Q4HQ66 CAMUP PRELIMINARY; PRT; 353 AA.
AC Q4HQ66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

```

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE GDP-fucose synthetase.  
 GN Name=fcl; ORFNames=CUP1255;  
 OS Campylobacter upsaliensis RP31195.  
 CC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 CC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=306264;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=RM31195;  
 RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,  
 RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,  
 RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,  
 RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,  
 RA Nelson K.E.;  
 RT "Major structural and novel potential virulence mechanisms from the  
 RT genomes of multiple Campylobacter species.";  
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAF01000007; EAL52977.1; -; Genomic DNA.  
 SQ SEQUENCE 353 AA; 39798 MW; 59CC8A432D31EPAE CRC64;  
  
 Query Match 100.0%; Score 31; DB 2; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 KFVFFA 6  
 DQ |||||  
 DB 58 KFVFFA 63  
  
 RESULT 8  
 Q5ATG9\_EMENT PRELIMINARY; PRT; 519 AA.  
 ID Q5ATG9\_EMENT PRELIMINARY;  
 AC Q5ATG9;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=AN8411.2;  
 OS Aspergillus nidulans FGSC A4.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=227321;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FGSC A4;  
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,  
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,  
 RA Borkhater B., Butler J., Calvo S.E., Camarata J., Chang J.,  
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArrellano K.,  
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,  
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,  
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,  
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,  
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,  
 RA Kells C., Landers T., Levine R., Maclean C., Macdonald P., Major J., Manning J.,  
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,  
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,  
 RA Mihova T., Mieng V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,  
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,  
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy N., Smirnov S.,  
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,  
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
 RA Lander E.;  
 RT "Genome Sequence of Aspergillus nidulans.";  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Hydroxylation of N-alkanes at the terminal  
 CC position.  
 CC -1- CATALYTIC ACTIVITY: Obtusifoliosin + 3 O(2) + 3 NADPH = 4-alpha-  
 CC methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate + 3  
 CC NADP(+) + 3 H(2)O.  
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
 DR EMBL; AACD01000153; EAA67033.1; -; Genomic DNA.  
 DR GO; GO:0048872; F:metal ion binding; IEA.  
 DR GO; GO:0004497; F:monooxygenase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR GO; GO:0016126; P:sterol biosynthesis; IEA.  
 DR InterPro; IPR001128; Cytochrome P450.  
 DR InterPro; IPR002974; EP450\_II\_CYP52.  
 DR InterPro; IPR002403; EP450IV.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR01239; EP450IICYP52.  
 DR PRINTS; PR00465; EP450IV.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.  
 KW Heme; Hypothetical protein; Iron; Lipid synthesis; Membrane;  
 KW Metal-binding; Monooxygenase; Oxidoreductase; Steroid biosynthesis;  
 KW Sterol biosynthesis.  
 SQ SEQUENCE 519 AA; 60440 MW; B367EE6EB6PFA287 CRC64;  
  
 Query Match 100.0%; Score 31; DB 2; Length 519;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 KFVFFA 6  
 DQ |||||  
 DB 26 KFVFFA 31  
  
 RESULT 9  
 Q7XM01\_ORYSA PRELIMINARY; PRT; 935 AA.  
 ID Q7XM01\_ORYSA PRELIMINARY;  
 AC Q7XM01;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE OSJNBa0086006.8 protein.  
 GN Names=OSJNBa0086006.8;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoidae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed=12447439; DOI=10.1038/nature01183;  
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,  
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,  
 RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,  
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,  
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,  
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,  
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,  
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,  
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,  
 RA Han B.;  
 RT "Sequence and analysis of rice chromosome 4.";  
 RL Nature 420:316-320(2002).  
 DR EMBL; AL662981; CAB04860.2; -; Genomic DNA.  
 DR Gramene; Q7XM01; -;  
 DR GO; GO:0006512; P:ubiquitin cycle; IEA.  
 DR InterPro; IPR001810; F-box.  
 DR Pfam; PF00646; F-box; 2.  
 DR SMART; SM00256; FBOX; 2.  
 DR PROSITE; PS50181; FBOX; 1.  
 SQ SEQUENCE 935 AA; 103910 MW; 735DD287C6E1BC69 CRC64;  
  
 Query Match 100.0%; Score 31; DB 2; Length 935;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0

QY 1 KVFVFA 6  
|||||  
Db 74 KVFVFA 79

## RESULT 10

Q7QYR7 GIALA  
ID Q7QYR7 GIALA PRELIMINARY; PRT; 3044 AA.  
AC Q7QYR7;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE GLP\_70\_49040\_39906.  
OS Giardia lamblia ATCC 50803.  
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.  
OX NCBI\_TaxID=184922;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=WB C6;  
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;  
RA "Draft sequence of the Giardia lamblia genome.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.  
CC EMBL: AACB0100048; EAA40229.1; -; Genomic\_DNA.  
DR InterPro; IPR012351; Cytochrome\_4\_hlx.  
KW Cytochrome.  
SQ SEQUENCE 3044 AA; 347085 MW; 24F737600F128C6D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 3044;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0

QY 1 KVFVFA 6  
|||||  
Db 382 KVFVFA 387

## RESULT 11

Q84NG7 HORVU  
ID Q84NG7 HORVU PRELIMINARY; PRT; 224 AA.  
AC Q84NG7;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Globulin.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC PubMed=14663527; DOI=10.1139/g03-071;  
RA Gu Y.Q., Anderson O.D., Londeore C.F., Kong X., Chibbar R.N., Lazo G.R.;  
RT "Structural organization of the barley D-hordein locus in comparison with its orthologous regions of wheat genomes.";  
RL Genome 46:1084-1097(2003).  
DR EMBL: AY268139; AAP31050.1; -; Genomic DNA.  
DR GO: 0045735; F.nutrient reservoir activity; IEA.  
DR InterPro; IPR003612; AAI.  
DR InterPro; IPR001419; Glutenin.  
DR Pfam; PF00234; Tryp\_alpha\_amy1; 1.  
DR PRINTS; PR00210; GLUTENIN-  
DR SMART; SM00499; AAI; 1.  
SQ SEQUENCE 224 AA; 24561 MW; 91A5BFF15C86394D CRC64;

Query Match 96.8%; Score 30; DB 2; Length 224;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
|||||  
Db 3 KVFVFA 8

## RESULT 12

Q98GC2 RHIL0  
ID Q98GC2 RHIL0 PRELIMINARY; PRT; 395 AA.  
AC Q98GC2;  
DT 01-OCT-2001 (TREMBlrel. 18, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Putative peptidase.  
GN OrderedLocusNames=ml13393;  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=MAFF303099;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideawawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";  
RL DNA Res. 7:331-338(2000).  
DR EMBL: BA000012; BAB50294.1; -; Genomic DNA.  
DR GO: 0001878; F:hydrolyase activity; IEA.  
DR GO: 00004239; F:methionyl aminopeptidase activity; IEA.  
DR GO: 00006508; F:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000994; Peptidase M24.  
DR InterPro; IPR001714; Pept\_M24\_MAP.  
DR Pfam; PF00557; Peptidase\_M24; 1.  
DR PRINTS; PR00599; MAPEPTIDASE.  
KW Complete proteome; Hydrolase.  
SQ SEQUENCE 395 AA; 43302 MW; E9ADFA4ADB1D472 CRC64;

Query Match 96.8%; Score 30; DB 2; Length 395;  
Best Local Similarity 83.3%; Pred. No. 2.9e+02; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
|||||  
Db 48 KVFVFA 53

## RESULT 13

Q92YY6 RHIME  
ID Q92YY6 RHIME PRELIMINARY; PRT; 397 AA.  
AC Q92YY6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Putative proline dipeptidase.  
GN OrderedLocusNames=RA0726; ORFNames=SM1329;  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OG Plasmid pSymA.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
OX NCBI\_TaxID=382;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=1021;  
RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798; Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

**\*\***

RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAJ01002391; CNH78296.1; -; Genomic\_DNA.

KW Hypothetical protein.  
 FT NON\_TER 1

SQ SEQUENCE 23 AA; 3051 MW; ECFB64E8BCC09AA0 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 23;  
 Best Local Similarity 83.3%; Pred. No. 74;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
 Db 16 KVFVFA 21  
 |||||

RESULT 17

ID Q73M63 TREDE PRELIMINARY; PRT; 43 AA.  
 AC Q73M63;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocusNames=TDE1646;  
 OS Treponema denticola.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
 OX NCBI\_TaxID=158;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 35405 / DSM 14222;  
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;  
 RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,  
 RA Dodson R.J., Davidson T.M., Deboy R.T., Fouts D.E., Haft D.H.,  
 RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,  
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,  
 RA Gebrgeorgis E., Geer K., Teagave G., Malek J.K.A., Ayodeji B.,  
 RA Shatman S., McLeod M.P., Smajs D., Howell J.K.A., Pal S., Amin A.,  
 RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,  
 RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;  
 RT "Comparison of the genome of the oral pathogen Treponema denticola  
 with other spirochete genomes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).  
 DR EMBL; AR017251; AAS12163.1; -; Genomic\_DNA.  
 DR TIGR; TDE1646; -.

KW Complete proteome.

SQ SEQUENCE 43 AA; 5202 MW; E1189303B62C9173 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 43;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
 Db 20 KVFVFA 25  
 |||||

RESULT 18

ID Q9KAX7 BACHD PRELIMINARY; PRT; 49 AA.  
 AC Q9KAX7;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE BH2159 protein.  
 GN OrderedLocusNames=BH2159;  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=86665;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C-125 / JCM 9153;  
 RX MEDLINE=205112582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 DR EMBL; BA000004; BAB05878.1; -; Genomic\_DNA.  
 DR PIR; G83919; G83919.  
 KW Complete proteome.

SQ SEQUENCE 49 AA; 5463 MW; D669731B6DCD0B1 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 49;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
 Db 34 KVFVFA 39  
 |||||

RESULT 19

Q7R979 PLAYO PRELIMINARY; PRT; 150 AA.  
 ID Q7R979;  
 AC Q7R979;  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=PY06986;  
 OS Plasmodium yoelii yoelii.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=73239;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=17XNL;  
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteu M.,  
 RA Silva J.C., Emolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidblyum S.L.,  
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,  
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RT "Genome sequence and comparative analysis of the model rodent malaria  
 RT parasite Plasmodium yoelii yoelii.";  
 RL Nature 419:512-519(2002).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABL01002464; EAA19320.1; -; Genomic\_DNA.  
 DR InterPro; IPR006484; PYST-B.  
 DR TIGRFAMs; TIGR01597; PYST-B; 1.  
 KW Hypothetical protein.

SQ SEQUENCE 150 AA; 17794 MW; DA68536D398B37AC CRC64;

Query Match 90.3%; Score 28; DB 2; Length 150;  
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
 Db 7 KVFVFA 12  
 |||||

RESULT 20

QAJ1Z2\_AZOVI



```

ID Q4J122_AZOVI PRELIMINARY; PRT; 152 AA.
AC Q4J122;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Glyoxalase/Bleomycin resistance protein/dioxygenase domain.
DE ORFNames=AVINDRAFT_6949;
GN Azotobacter vinelandii AVOP.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Ibrani S., Pitluck S., Richardson P.,
RA "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RA DOE Joint Genome Institute;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Ibrani S., Pitluck S., Richardson P.;
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAU03000001; EAM08399.1; -; Genomic_DNA.
KW Dioxygenase.
SQ SEQUENCE 152 AA; 16984 MW; 05A60BD5879ED93 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 152;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
DB 111 RFVFFA 116
|||||

RESULT 21
Q20070 CAEEL
ID Q20070_CAEEL PRELIMINARY; PRT; 177 AA.
AC Q20070;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Hypothetical protein F35H10.6.
DE ORFNames=F35H10.6;
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2; PubMed=9851916;
RX MEDLINE=99069613; PubMed=9851916;

```

```

RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; U40934; AAA81680.1; -; Genomic_DNA.
DR PIR; T16280; T16280.
DR Ensembl; F35H10.6; Caenorhabditis elegans.
DR GO; GO:0016272; C:prefoldin complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR004127; PFD_alpha_like.
DR Pfam; PF02996; Prefoldin; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 177 AA; 21142 MW; E8B71144250DB915 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
DB 10 KVFVFFS 15
|||||

RESULT 22
Q6LSA9_PROPR
ID Q6LSA9_PROPR PRELIMINARY; PRT; 199 AA.
AC Q6LSA9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocaNames=BPRA1406;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Cestaro A., Malacrida G., Simonati B., Cannata N.,
RA Ronuaidi C., Bartlett D.H., Valle G.;
RA "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis.";
RL Science 307:1459-1461(2005).
DR EMBL; CR378667; CAG19817.1; -; Genomic DNA.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf_1; 1.
DR Complete proteome.
SQ SEQUENCE 199 AA; 22203 MW; AF44E115663FD3F6 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 199;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
DB 47 KFLFFA 52
|||||

RESULT 23
Q6UJY8_TRITU
ID Q6UJY8_TRITU PRELIMINARY; PRT; 225 AA.
AC Q6UJY8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Globulin.
GN Triticum turgidum (Poulard wheat) (Rivet wheat).
OS Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; Pooideae;
OC Eukaryota; Viridiplantae; Streptophyta; Poales; Pooideae;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pooideae;

```



```

OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15159634; DOI=10.1023/B:PLAN.0000028768.21587.dg;
RA Kong X.Y., Gu Y.Q., You F.M., Dubcovsky J., Anderson O.D.;
RT "Dynamics of the evolution of orthologous and paralogous portions of a
complex locus region in two genomes of allopolyploid wheat.";
RL Plant Mol. Biol. 54:55-69(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kong X.-Y., Gu Y.Q., Anderson O.D.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY368673; AAQ93632.1; -; Genomic DNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha_amy1; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 225 AA; 24502 MW; 45F4D19403BCDCC2 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 225;
Best Local Similarity 83.3%; Pred. No. 4.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 KVFVFA 6
Db :|||||
3 RFVFFA 8

RESULT 24
Q8LKV8 AEGTA PRELIMINARY; PRT; 226 AA.
AC Q8LKV8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Seed globulin.
GN Names=Glo-2;
OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22478028; PubMed=12590343;
RA Anderson O.D., Rausch C., Moullet O., Lagudah E.S.;
RT "The wheat D-genome HMW-glutenin locus: BAC sequencing, gene
distribution, and retrotransposon clusters.";
RL Funct. Integr. Genomics 3:56-68(2003).
DR EMBL; AF497474; AAM77580.1; -; Genomic DNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha_amy1; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 226 AA; 24515 MW; 95397E83C63D50AD CRC64;

Query Match 90.3%; Score 28; DB 2; Length 226;
Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 KVFVFA 6
Db :|||||
3 RFVFFA 8

RESULT 25
Q7R8Y4 PLAYO PRELIMINARY; PRT; 241 AA.
ID Q7R8Y4_PLAYO PRELIMINARY; PRT; 242 AA.
AC Q7R8Y4
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY07086;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=17XNL;
RM MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabai A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01002524; EAA19443.1; -; Genomic DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 241 AA; 28789 MW; BE3AD8A3E5924873 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 241;
Best Local Similarity 83.3%; Pred. No. 5.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 KVFVFA 6
Db :|||||
7 KVFVFS 12

RESULT 26
Q7RA05 PLAYO PRELIMINARY; PRT; 242 AA.
AC Q7RA05
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06703;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=17XNL;
RM MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabai A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).

```

CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABL01002310; EAA18966.1; -; Genomic\_DNA.  
 DR InterPro; IPR006484; PYST-B.  
 DR TIGRFAMs; TIGR01597; PYST-B; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 242 AA; 28514 MW; FF31C7DBB82957BF CRC64;

Query Match 90.3%; Score 28; DB 2; Length 242;  
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVFVFA 6  
 Db 7 KVFVFS 12

RESULT 27  
 Q7RNP5 PLAYO PRELIMINARY; PRT; 250 AA.  
 AC Q7RNP5;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=PY01770;  
 OS Plasmodium yoelii yoelii.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=73239;  
 RN STRAIN=17XNL;  
 RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,  
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,  
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RT "Genome sequence and comparative analysis of the model rodent malaria  
 parasite Plasmodium yoelii yoelii.";  
 RL Nature 419:512-519(2002).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABL01000477; EAA21136.1; -; Genomic\_DNA.  
 DR InterPro; IPR006484; PYST-B.  
 DR TIGRFAMs; TIGR01597; PYST-B; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 250 AA; 29944 MW; EFPF3D5B5C001C8C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 250;  
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVFVFA 6  
 Db 7 KVFVFS 12

RESULT 28  
 Q7PDC0 PLAYO PRELIMINARY; PRT; 251 AA.  
 ID Q7PDC0;  
 AC Q7PDC0;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.

GN Name=PY00554; Synonym=PY01592;  
 OS Plasmodium yoelii yoelii.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=73239;  
 RN STRAIN=17XNL;  
 RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,  
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,  
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RT "Genome sequence and comparative analysis of the model rodent malaria  
 parasite Plasmodium yoelii yoelii.";  
 RL Nature 419:512-519(2002).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABL01000150; EAA16801.1; -; Genomic\_DNA.  
 DR InterPro; IPR006484; PYST-B.  
 DR TIGRFAMs; TIGR01597; PYST-B; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 251 AA; 30043 MW; 3D608A4EC7F432D5 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 251;  
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVFVFA 6  
 Db 7 KVFVFS 12

RESULT 29  
 Q7RPS1 PLAYO PRELIMINARY; PRT; 251 AA.  
 ID Q7RPS1;  
 AC Q7RPS1;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=PY01385;  
 OS Plasmodium yoelii yoelii.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=73239;  
 RN STRAIN=17XNL;  
 RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,  
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,  
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RT "Genome sequence and comparative analysis of the model rodent malaria  
 parasite Plasmodium yoelii yoelii.";  
 RL Nature 419:512-519(2002).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABL01000363; EAA20702.1; -; Genomic\_DNA.  
 DR InterPro; IPR006484; PYST-B.

```

DR TIGRFAMs: TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 251 AA; 30054 MW; 3D6A80BE6DFE9275 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 251;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db      |||||:
       7 KVFVFS 12

RESULT 30
Q7RA57_FPLAYO
ID Q7RA57_FPLAYO PRELIMINARY; PRT; 252 AA.
AC Q7RA57;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Names=PY06647;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Sedegh M., Shoaibi A., Cummings L.M.,
RA Cho J.K., Quackenbush J., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Florens L., van Aken S.E., Sedegh M., Shoaibi A., Cummings L.M.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01001507; EAA16812.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 29757 MW; 64EB5B4C1F49786D CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 252;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db      |||||:
       7 KVFVFS 12

RESULT 32
Q7RLK2_PLAYO
ID Q7RLK2_PLAYO PRELIMINARY; PRT; 255 AA.
AC Q7RLK2;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY02539;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Sedegh M., Shoaibi A., Cummings L.M.,
RA Cho J.K., Quackenbush J., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL0100695; EAA21989.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 255 AA; 30283 MW; 51F1D33FED980B3 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 255;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db      |||||:
       7 KVFVFS 12

RESULT 31
Q7RF37_FPLAYO
ID Q7RF37_FPLAYO PRELIMINARY; PRT; 252 AA.
AC Q7RF37;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Names=PY04873;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]

```

```
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 7 KFVFFS 12

RESULT 33
Q7RCL4 PLAYO
ID Q7RCL4 PLAYO PRELIMINARY; PRT; 262 AA.
AC Q7RCL4;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY05766;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT parasite Plasmodium yoelii yoelii.;
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01001873; EAA17841.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 7A520F097AEF0573 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 262;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 7 KFVFFS 12

RESULT 34
Q7RC37 PLAYO
ID Q7RC37 PLAYO PRELIMINARY; PRT; 265 AA.
AC Q7RC37;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY05947;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT parasite Plasmodium yoelii yoelii.;
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01001873; EAA17841.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 7A520F097AEF0573 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 262;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 7 KFVFFS 12

RESULT 35
Q7RB86 PLAYO
ID Q7RB86 PLAYO PRELIMINARY; PRT; 268 AA.
AC Q7RB86;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
GN Name=PY06262;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01002095; EAA18444.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
FT NON-TER 268
SQ SEQUENCE 268 AA; 32060 MW; D273B20B61AA181C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
```

```
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01001955; EAA18074.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 265 AA; 31511 MW; 7CCD7DBBCC3A26FF CRC64;

Query Match 90.3%; Score 28; DB 2; Length 265;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 7 KFVFFS 12

RESULT 35
Q7RB86 PLAYO
ID Q7RB86 PLAYO PRELIMINARY; PRT; 268 AA.
AC Q7RB86;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
GN Name=PY06262;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01002095; EAA18444.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
FT NON-TER 268
SQ SEQUENCE 268 AA; 32060 MW; D273B20B61AA181C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
```

```
Db      |||||:
        7 KVFVFS 12

RESULT 36
ID Q529U4_MAGGR PRELIMINARY; PRT; 285 AA.
AC Q529U4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG02290.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]

NUCLEOTIDE SEQUENCE.
RP STRAIN=70-15;
RC Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-zahra M., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Ambruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blithsteyn B., Bloom I., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
RA Kelis C., Kieu A., Kishner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Legler J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Maneus L.,
RA Mesirov J., Mihaliev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Picani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Teamlia T., Tsomo N., Vallée D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
[2]

NUCLEOTIDE SEQUENCE.
RP STRAIN=70-15;
RC Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
[3]

NUCLEOTIDE SEQUENCE.
RP STRAIN=70-15;
RC Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
```

```
DR EMBL; AACU01000444; EAA54305.1; -, Genomic_DNA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR007568; RTA1.
DR Pfam; PF04479; RTA1; 1.
KW Hypothetical protein.
SQ SEQUENCE 285 AA; 31531 MW; DCB48A5EB9E4D1BD CRC64;

Query Match          90.3%; Score 28; DB 2; Length 285;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
       |||||:
DB      6 KVFVFA 11

RESULT 37
Q94284_CAEEL
ID Q94284_CAEEL PRELIMINARY; PRT; 293 AA.
AC Q94284;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein M02B7.4.
GN ORFNames=M02B7.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Bristol N2;
RC MEDLINE=99069613; PubMed=9851916;
RX The C. elegans sequencing consortium;
RG "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; U70851; AAB09129.1; -, Genomic_DNA.
DR PIR; T29899; T29899.
DR Ensemble; M02B7.4; Caenorhabditis elegans.
DR WormBase; WEGene00019725; M02B7.4.
DR WormPep; M02B7.4; CRI2326.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 293 AA; 33247 MW; 90CEE020650E5065 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 293;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
       |||||:
DB     258 KVFVFS 263

RESULT 38
Q7RBUL_PLAYO
ID Q7RBUL_PLAYO PRELIMINARY; PRT; 294 AA.
AC Q7RBUL;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06045;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]

NUCLEOTIDE SEQUENCE.
RP STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
```

```

RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002005; EAA18193.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 294 AA; 34611 MW; 281A85D322236659 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 294;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 7 KVFVFS 12

RESULT 39
QSUMP7_HALMA PRELIMINARY; PRT; 300 AA.
AC QSUMP7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Sugar ABC transport system permease protein.
GN Name=malFG-9; OrderedLocNames=rrn80104;
OS Haloarcula marismortui (Halo bacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT the Dead Sea.";
RL Genome Res. 14:2221-2234(2004).
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; AY596298; AAV48306.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD transp.1; 1.
DR PROSITE; PS50928; ABC_TM1; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 300 AA; 32975 MW; 9C230B44EF19CE5A CRC64;

Query Match 90.3%; Score 28; DB 2; Length 300;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6

```

```

Db 86 KVFVFA 91

RESULT 40
Q7RBJ3_PLAYO PRELIMINARY; PRT; 321 AA.
AC Q7RBJ3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06150;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perlea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002053; EAA18307.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 38948 MW; E1127BA81EB58FDB CRC64;

Query Match 90.3%; Score 28; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 51 KVFVFS 56

RESULT 41
P74429_SYNV3 PRELIMINARY; PRT; 326 AA.
AC P74429;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ycf39 gene product.
GN Name=ycf39; OrderedLocNames=slr0399;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita A., Nakazaki S., Kimura T.,
RA Hosouchi T., Matsumoto A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the

```

RT entire genome and assignment of potential protein-coding regions. ";  
RL DNA Res. 3:109-136 (1996).  
DR EMBL; BA000022; BAA18529.1; -; Genomic\_DNA.  
DR PIR; S76400; S76400.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0051287; F:NAD binding; IEA.  
DR GO; GO:0009225; F:nucleotide-sugar metabolism; IEA.  
DR InterPro; IPR001509; Epimerase\_Dh.  
DR Pfam; PF01370; Epimerase; 1.  
KW Complete proteome.  
SQ SEQUENCE 326 AA; 36519 MW; 99F522C1E980B943 CRC64;  
  
Query Match 90.3%; Score 28; DB 2; Length 326;  
Best Local Similarity 83.3%; Pred. No. 6.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVFVFA 6  
|||||  
Db 104 KVFVFS 109  
  
RESULT 42  
Q6K105 MYCWO  
ID Q6K105 MYCWO PRELIMINARY; PRT; 380 AA.  
AC Q6K105  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Restriction-modification enzyme mpuUVIII 8 subunit (EC 3.1.21.3).  
GN Name=hds; OrderedLocusNames=MM02850;  
OS Mycoplasma mobile.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2118;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=163K / ATCC 43663;  
RX PubMed=15289470; DOI=10.1101/gr.2674004;  
RA Jaife J.D., Stange-Thomann N., Smith C., DeCaprio D., Fisher S.,  
RA Butler J., Calvo S., Elkins T., Fitzgerald M.G., Hafez N.,  
RA Kodira C.D., Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.,  
RA Birren B., Berg H.C., Church G.M.;  
RT "The complete genome and proteome of Mycoplasma mobile.";  
RL Genome Res. 14:1447-1461 (2004).  
DR EMBL; AS017338; AAT27771.1; -; Genomic\_DNA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0009035; F:type I site-specific deoxyribonuclease acti...; IEA.  
DR GO; GO:0006304; P:DNA modification; IEA.  
DR InterPro; IPR000055; Rest\_mod\_DNA.  
DR Pfam; PF01420; Methylase\_S; 2.  
KW Complete proteome; Hydrolase.  
SQ SEQUENCE 380 AA; 44463 MW; D42428E38774F9CE CRC64;  
  
Query Match 90.3%; Score 28; DB 2; Length 380;  
Best Local Similarity 83.3%; Pred. No. 7.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVFVFA 6  
|||||  
Db 294 KVFVFA 299  
  
RESULT 43  
Q4MSJ5 BACCE  
ID Q4MSJ5 BACCE PRELIMINARY; PRT; 388 AA.  
AC Q4MSJ5;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Basic membrane protein DtlB.  
GN Name=dtlB; ORFNames=BCE\_G9241\_1384;  
OS Bacillus cereus G9241.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

OC Bacillus cereus group.  
OX NCBI\_TaxID=269801;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=G9241;  
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;  
RA Hoffmaister A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,  
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,  
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,  
RA Rilestone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,  
RA Popovic T., Fraser C.M.;  
RT "Identification of anthrax toxin genes in a Bacillus cereus associated  
with an illness resembling inhalation anthrax.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454 (2004).  
CC -!- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
DR EMBL; AAEK0100009; EAL15142.1; -; Genomic\_DNA.  
DR EMBL; AAEK0100009; EAL15142.1; -; Genomic\_DNA.  
SQ SEQUENCE 388 AA; 45590 MW; E21AEA22BA0511CF CRC64;  
  
Query Match 90.3%; Score 28; DB 2; Length 388;  
Best Local Similarity 83.3%; Pred. No. 7.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVFVFA 6  
|||||  
Db 286 RVFVFA 291  
  
RESULT 44  
Q6HLH8 BACHK  
ID Q6HLH8 BACHK PRELIMINARY; PRT; 388 AA.  
AC Q6HLH8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE D-alanyl transfer protein.  
GN Name=ditB; OrderedLocusNames=BT9727\_1258;  
OS Bacillus thuringiensis (subsp. konkukian).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=180856;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=97-27;  
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Rice H.;  
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE017355; AAT61956.1; -; Genomic\_DNA.  
DR InterPro; IPR004299; MBOAT\_fam.  
DR Pfam; PF03062; MBOAT; 1.  
KW Complete proteome.  
SQ SEQUENCE 388 AA; 45999 MW; DFB6794B3247A66B CRC64;  
  
Query Match 90.3%; Score 28; DB 2; Length 388;  
Best Local Similarity 83.3%; Pred. No. 7.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVFVFA 6  
|||||  
Db 286 RVFVFA 291  
  
RESULT 45  
Q73BD3 BACC1  
ID Q73BD3 BACC1 PRELIMINARY; PRT; 388 AA.  
AC Q73BD3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE DltB protein.



```

GN Name=dltB; OrderedLocusNames=BCE1486;
OS Bacillus cereus (strain ATCC 10987);
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017269; AAS40415.1; -; Genomic_DNA.
DR TIGR; BCE1486; -.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 74CBF3D745A83EC6 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
Db 286 RFVFFA 291

RESULT 46
Q63E03 BACCZ
ID Q63E03 BACCZ PRELIMINARY; PRT; 388 AA.
AC Q63E03;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE D-alanyl transfer protein.
GN Name=dltB;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=286681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18989.1; -; Genomic_DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 009F62D46DF6FC7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
Db 286 RFVFFA 291

RESULT 47
Q81T98 BACAN
ID Q81T98 BACAN PRELIMINARY; PRT; 388 AA.
AC Q81T98; Q611H5; Q6KVC6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE DltB protein.

```

```

GN Name=dltB; OrderedLocusNames=BAL388, BAS1286, GBAA1388;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Ames / Isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oekstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Ames / Isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017028; AAP25332.1; -; Genomic_DNA.
DR EMBL; AE017334; AAT30485.1; -; Genomic_DNA.
DR EMBL; AE017225; AAT53606.1; -; Genomic_DNA.
DR TIGR; BAL388; -.
DR TIGR; GBAA1388; -.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 009F62D46DF6FC7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
Db 286 RFVFFA 291

RESULT 48
Q81G40 BACCR
ID Q81G40 BACCR PRELIMINARY; PRT; 391 AA.
AC Q81G40;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein dltB.
GN OrderedLocusNames=BC1371;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```



```

RX MEDLINE-22608415; PubMed-12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017002; AAP08353.1; -; Genomic_DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 391 AA; 46119 MW; B8755D0033C91C54 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 391;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 289 RFVFFA 294
:|||||

RESULT 49
QSNEA9 FRATT PRELIMINARY; PRT; 398 AA.
ID Q5NEA9;
AC Q5NEA9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Aromatic amino acid transporter of the HAAAP family.
GN OrderedLocusNames=FTII732c;
OS Francisella tularensis (subsp. tularensis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Francisellaceae; Francisella.
OX NCBI_TaxID=119856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCHU S4 / Schu 4;
RC PubMed=15640799; DOI=10.1038/ng1499;
RA Larsson P., Oyston P.C.F., Chain P., Chu M.C., Duffield M.,
RA Fuxelius H.-H., Garcia E., Haelterl G., Johansson D., Isherwood K.E.,
RA Karp P.D., Larsson E., Liu Y., Michell S., Prior J., Prior R.,
RA Malfatti S., Sjoestedt A., Svensson K., Thompson N., Vergez L.,
RA Wagg J.K., Wren B.W., Lindler L.E., Andersson S.G.E., Forsman M.,
RA Titball R.W.;
RT "The complete genome sequence of Francisella tularensis, the causative
RT agent of tularemia.";
RL Nat. Genet. 37:153-159(2005).
DR EMBL; AJ749949; CAG46365.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002293; AA/re1_permease1.
DR InterPro; IPR002422; AA/re1_permease2.
DR InterPro; IPR002091; ARAA_permease.
DR Pfam; PF03222; Txp_Typ_perm.1.
DR PRINTS; PR00166; AEOAPRMEASE.
KW Complete proteome; Transmembrane.
SQ SEQUENCE 398 AA; 44437 MW; 1A93FFD1D8AA4A38 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 398;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 152 KLFVFA 157
:|||||

RESULT 50

```

```

Q73V08 MYCPA
ID Q73V08 MYCPA PRELIMINARY; PRT; 409 AA.
AC Q73V08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nuoh.
GN Name=nuoh; OrderedLocusNames=MAP3208;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1770;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K10;
RA Li L., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017238; AAS05756.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Complete proteome.
SQ SEQUENCE 409 AA; 44971 MW; 693518B9DDF94B11 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 409;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 67 KFYVFA 72
:|||||

RESULT 51
Q722C3 CAEL
ID Q722C3 CAEL PRELIMINARY; PRT; 421 AA.
AC Q722C3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFName=Y19D10A.8;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AC006722; AAK68421.2; -; Genomic_DNA.
DR Ensembl; Y19D10A.8; Caenorhabditis elegans.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS.1.
DR Pfam; PF07690; MFS 1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 421 AA; 46361 MW; 75B7CF15ABE2C432 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 421;

```

Best Local Similarity 83.3%; Pred. No. 8.4e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KVFVFA 6  
Db 291 RFVFFA 296

## RESULT 52

ID Q9PG2\_UREPA PRELIMINARY; PRT; 422 AA.  
AC Q9PG2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Unique hypothetical.  
GN OrderedLocusNames=U0329;  
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.  
OX NCBI\_TaxID=134821;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 700970;  
RX MEDLINE=20500219; PubMed=11048724; DOI=10.1038/35037619;  
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,  
RA Caswell G.H.;  
RA "The complete sequence of the mucosal pathogen Ureaplasma  
RT urealyticum".  
RL Nature 407:757-762(2000).  
RW EMBL; AB002130; AAF30738.1; -; Genomic DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 422 AA; 49219 MW; 8EA05B3F2F76C8E8 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 422;  
Best Local Similarity 83.3%; Pred. No. 8.4e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KVFVFA 6  
Db 208 KVFVFA 213

## RESULT 53

ID Q8FW04\_BRUSU PRELIMINARY; PRT; 430 AA.  
AC Q8FW04;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Uracil-xanthine permease, putative.  
GN OrderedLocusNames=BRA0661;  
OS Brucella suis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29461;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=1330 / Biovar 1;  
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;  
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,  
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
RA Nelson W.C., Ayodeji B., Kaul M., Shetty J., Malek J.A.,  
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,  
RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,  
RA Fraser C.M.;  
RT "The Brucella suis genome reveals fundamental similarities between  
RT animal and plant pathogens and symbionts.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).  
DR EMBL; AE014292; AAN33850.1; -; Genomic DNA.  
DR TIGR; BRA0661; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR004711; Bene.  
DR InterPro; IPR006043; Xant/urac/vitc.  
DR Pfam; PF00860; Xan ux permease; 1.  
DR ProDom; PD024853; Bene; 1.  
KW Complete proteome.

SQ SEQUENCE 430 AA; 44661 MW; B69F2E03E9A28C39 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 430;  
Best Local Similarity 83.3%; Pred. No. 8.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
Db 424 RFVFFA 429

## RESULT 54

ID Q6QW8\_9GAMM PRELIMINARY; PRT; 432 AA.  
AC Q6QW8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 03-JUN-2004 (TrEMBLrel. 27, Last annotation update)  
DE Predicted preprotein translocase subunit SecY.  
GN ORFNames=Red20809\_103;  
OS uncultured marine gamma proteobacterium EBAC20E09.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; SAR86 cluster;  
OC environmental samples.  
OX NCBI\_TaxID=266134;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15305915; DOI=10.1111/j.1462-2920.2004.00676.x;  
RA Sabehi G., Beja O., Suzuki M.T., Preston C.M., DeLong E.P.;  
RT "Different SAR86 subgroups harbour divergent proteorhodopsins.";  
RL Environ. Microbiol. 6:903-910(2004).  
DR EMBL; AY552545; AAS73104.1; -; Genomic DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0015450; F:protein translocase activity; IEA.  
DR GO; GO:0009306; P:protein secretion; IEA.  
DR GO; GO:0006605; P:protein targeting; IEA.  
DR GO; GO:0015031; P:protein transport; IEA.  
DR InterPro; IPR002208; SecY.  
DR Pfam; PF00344; SecY; 1.  
DR PRINTS; PR00303; SECYTRNLCASE.  
DR TIGRPFAMs; TIGR00967; 3a05018007; 1.  
DR PROSITE; PS00756; SECY\_2; 1.  
KW Protein transport; Translocation; Transmembrane; Transport.  
SQ SEQUENCE 432 AA; 47276 MW; CC0F2DA782EB8F79 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 432;  
Best Local Similarity 83.3%; Pred. No. 8.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
Db 15 RFVFFA 20

## RESULT 55

ID Q8M9J3\_9AQUA PRELIMINARY; PRT; 436 AA.  
AC Q8M9J3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribulose-bisphosphate carboxylase (EC 4.1.1.39) (Fragment).  
GN Name=rbcl;  
OS Ilex pubescens.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC asterids; campanulids; Aquifoliales; Aquifoliaceae; Ilex.  
 OX NCBI\_TaxID=185543;  
 RN [1]  
 RA NUCLEOTIDE SEQUENCE.  
 RA Manen J.F.;  
 RT "The complex history of the genus Ilex L. (Aquifoliaceae): evidence  
 RT from the comparison of plastid and nuclear DNA sequences and from  
 RT fossil data.";   
 RL Plant Syst. Evol. 0:0-0(0).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Manen J.F.;  
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -I- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-  
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic  
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic  
 CC carbon dioxide fixation, as well as the oxidative fragmentation of  
 CC carbon dioxide fixation, as well as the oxidative fragmentation of  
 CC the pentose substrate in the photorepiration process (By  
 CC similarity).  
 CC -I- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-  
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic  
 CC carbon dioxide fixation, as well as the oxidative fragmentation of  
 CC the pentose substrate in the photorepiration process. Both  
 CC reactions occur simultaneously and in competition at the same  
 CC active site (By similarity).  
 CC -I- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =  
 CC 2 3-phospho-D-glycerate.  
 CC -I- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-  
 CC phospho-D-glycerate + 2-phosphoglycolate.  
 CC -I- SUBUNIT: 8 large chains + 8 small chains (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Chloroplast (By similarity).  
 CC -I- SIMILARITY: Belongs to the RuBisCO large chain family.  
 DR EMBL; AJ492722; CAD37439.1; -; Genomic\_DNA.  
 DR SMR; Q8M9J3; 9-436.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .); IEA.  
 DR GO; GO:0016829; F:lyase activity; IEA.  
 DR GO; GO:0004497; F:monooxygenase activity; IEA.  
 DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.  
 DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.  
 DR GO; GO:0009853; P:photorepiration; IEA.  
 DR GO; GO:0015979; P:photosynthesis; IEA.  
 DR InterPro; IPR000685; RuBisCO\_large.  
 DR Pfam; PF00016; RuBisCO\_large; 1.  
 DR Pfam; PF02788; RuBisCO\_large; 1.  
 KW Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;  
 KW Oxidoreductase; Photorepiration; Photosynthesis.  
 FT NON\_TER 436 436  
 SQ SEQUENCE 436 AA; 48367 MW; E1A65FFCF93985A1 CRC64;  
 Query Match 90.3%; Score 28; DB 2; Length 436;  
 Best Local Similarity 83.3%; Pred. No. 8.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVFA 6  
 Db :|||||  
 217 RVVFFA 222  
 RESULT 56  
 ID O44595\_CABEL PRELIMINARY; PRT; 452 AA.  
 AC O44595;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein F56A4.10.  
 GN ORFNames=F56A4.10;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RG The C. elegans sequencing consortium;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology.";   
 RL Science 282:2012-2018(1998).  
 DR EMBL; AC006645; AAF39848.1; -; Genomic\_DNA.  
 DR FIR; C88969; C88969.  
 DR Ensembl; F56A4.10; Caenorhabditis elegans.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005215; F:transporter activity; IEA.  
 DR GO; GO:0006810; F:transport; IEA.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR011701; MFS.  
 DR Pfam; PF07690; MFS\_1; 1\_  
 DR PROSITE; PS50850; MFS; 1\_  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 452 AA; 49858 MW; F1BED2FBE60CAE59 CRC64;  
 Query Match 90.3%; Score 28; DB 2; Length 452;  
 Best Local Similarity 83.3%; Pred. No. 8.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVFA 6  
 Db :|||||  
 291 RVVFFA 296  
 RESULT 57  
 Q6GVJ4\_9BURK PRELIMINARY; PRT; 456 AA.  
 ID Q6GVJ4\_9BURK PRELIMINARY; PRT; 456 AA.  
 AC Q6GVJ4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Glycosyltransferase.  
 GN Name=wbc8;  
 OS Burkholderia cenocepacia.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.  
 OX NCBI\_TaxID=95486;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K56-2;  
 RX PubMed=15687196; DOI=10.1128/JB.187.4.1324-1333.2005;  
 RA Ortega X., Hunt T.A., Loutet S., Vinion-Dubiel A.D., Datta A.,  
 RA Choudhury B., Goldberg J.B., Carlson R., Valvano M.A.;  
 RT "Reconstitution of O-Specific Lipopolysaccharide Expression in  
 RT Burkholderia cenocepacia Strain J2315, Which Is Associated with  
 RT Transmissible Infections in Patients with Cystic Fibrosis.";   
 RL J. Bacteriol. 187:1324-1333(2005).  
 DR EMBL; AY633623; AAT48329.1; -; Genomic\_DNA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0009058; F:biosynthesis; IEA.  
 DR InterPro; IPR001296; Glyco\_transf\_1.  
 DR Pfam; PF00534; Glycos\_transf\_1; 1\_  
 KW Transferase.  
 SQ SEQUENCE 456 AA; 50801 MW; E5B3648E1BE54A54 CRC64;  
 Query Match 90.3%; Score 28; DB 2; Length 456;  
 Best Local Similarity 83.3%; Pred. No. 8.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVFVFA 6  
 Db :|||||  
 6 KFLFFA 11  
 RESULT 58  
 REL\_NEPAL  
 ID REL\_NEPAL STANDARD; PRT; 465 AA.  
 AC P28434;

DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Ribulose biphosphate carboxylase large chain (EC 4.1.1.39) (RuBisCO  
 DE large subunit) (Fragment).  
 GN Name:rbcl;  
 OS Nepenthes alata (Winged pitcher plant).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Caryophyllales; Nepenthaceae; Nepenthes.  
 OX NCBI\_TaxID=4376;  
 RN [1]

NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=32397008; PubMed=1523408;  
 RA Albert V.A., Williams S.E., Chase M.W.;  
 RT "Carnivorous plants: phylogeny and structural evolution.";   
 RL Science 257:1491-1495(1992);

CC -1- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-  
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic  
 CC carbon dioxide fixation, as well as the oxidative fragmentation of  
 CC the pentose substrate in the photorespiration process. Both  
 CC reactions occur simultaneously and in competition at the same  
 CC active site.  
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =  
 CC 2 3-phospho-D-glycerate + 2 H(+).  
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-  
 CC phospho-D-glycerate + 2-phosphoglycolate.  
 CC -1- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).  
 CC -1- SUBUNIT: Heterohexameric of 8 large chains and 8 small chains;  
 CC disulfide-linked. The disulfide link is formed within the large  
 CC subunit homodimers (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Chloroplast.  
 CC -1- DOMAIN: The basic functional RuBisCO is composed of a large chain  
 CC homodimer in a "head-to-tail" conformation. In form I RuBisCO this  
 CC homodimer is arranged in a barrel-like tetramer with the small  
 CC subunits forming a tetrameric "cap" on each end of the "barrel"  
 CC (By similarity).  
 CC -1- PTM: The disulfide bond which can form in the large chain dimeric  
 CC partners within the hexadecamer appears to be associated with  
 CC oxidative stress and protein turnover (By similarity).  
 CC -1- SIMILARITY: Belongs to the RuBisCO large chain family. Type I  
 CC subfamily.

-----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

-----  
 DR EMBL; L01936; AAA84502.2; -; Genomic\_DNA.  
 DR HSSP; P00875; LAUS.  
 DR SWP; P28434; 1-465.  
 DR HAWAP; MF\_01338; -; 1.  
 DR InterPro; IPR000685; RuBisCO\_large.  
 DR Pfam; PF00016; RuBisCO\_large; 1.  
 DR Pfam; PF02788; RuBisCO\_large; 1.  
 DR PROSITE; PS00157; RUBISCO\_LARGE; 1.  
 KW Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Magnesium;  
 KW Metal-binding; Methylation; Monooxygenase; Oxidoreductase;  
 KW Photorespiration; Photosynthesis.  
 FT ACT SITE 165 165 Proton acceptor (By similarity).  
 FT ACT SITE 284 284 Proton acceptor (By similarity).  
 FT ACT SITE 191 191 Magnesium (via carboxylate group) (By  
 FT METAL similarity).  
 FT METAL 193 193 Magnesium (By similarity).  
 FT METAL 194 194 Magnesium (By similarity).  
 FT BINDING 113 113 Substrate (in homodimeric partner) (By  
 FT similarity).  
 FT BINDING 163 163 Substrate; C1 phosphate group (By  
 FT similarity).  
 FT BINDING 167 167 Substrate (By similarity).  
 FT BINDING 285 285 Substrate; C5 phosphate group (By

FT BINDING 317 317 Substrate; C5 phosphate group (By  
 FT similarity).  
 FT BINDING 369 369 Substrate; C5 phosphate group (By  
 FT similarity).  
 FT SITE 324 324 Transition state stabilizer (By  
 FT similarity).  
 FT MOD\_RES 4 4 N6,N6,N6-trimethyllysine (By similarity).  
 FT MOD\_RES 191 191 N6-carboxyllysine (By similarity).  
 FT DISULFID 237 237 Interchain (in linked form) (By  
 FT similarity).  
 FT NON\_TER 1 1'  
 SQ SEQUENCE 465 AA; 51614 MW; 29E322894FE92451 CRC64;  
 Query Match 90.3%; Score 28; DB 1; Length 465;  
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KFVFFA 6  
 Db 207 RFVFFA 212

RESULT 59  
 Q9N5Q8\_CABE1 CABE1 PRELIMINARY; PRT; 472 AA.  
 ID Q9N5Q8\_CABE1 PRELIMINARY;  
 AC Q9N5Q8;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein F56A4.12.  
 DE ORFNames=F56A4.12;  
 GN Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RG The C. elegans sequencing consortium;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology.";   
 RL Science 282:2012-2018(1998).  
 DR EMBL; AC006645; AAF39850.1; -; Genomic DNA.  
 DR Ensembl; F56A4.12; Caenorhabditis elegans.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005215; P:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR011701; MFS\_1.  
 DR Pfam; PF07690; MFS\_1; 1.  
 DR PROSITE; PS50850; MFS; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 472 AA; 52251 MW; C06DFDB6AA6755AE CRC64;  
 Query Match 90.3%; Score 28; DB 2; Length 472;  
 Best Local Similarity 83.3%; Pred. No. 9.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KFVFFA 6  
 Db 340 RFVFFA 345

RESULT 60  
 Q625W2\_CABE1 CABE1 PRELIMINARY; PRT; 480 AA.  
 ID Q625W2\_CABE1 PRELIMINARY;  
 AC Q625W2;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein CBG01115.

```

GN Name=CBG01115;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAAC0100007; CAE58039.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 53324 MW; BDC735BE20A6CC51 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 480;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 343 RVFVFA 348

RESULT 61
Q5JJ16_PYRKO
ID Q5JJ16_PYRKO PRELIMINARY; PRT; 482 AA.
AC Q5JJ16;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical membrane protein, conserved.
GN OrderedLocusNames=TK1728;
OS Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=69014;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KOD1;
RA Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
RT "Complete genome sequence of the hyperthermophilic archaeon
Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
genomes."
RL Genome Res. 15:352-363(2005).
DR EMBL; AP006878; BAD85917.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 482 AA; 54068 MW; 097052348C3BB4D CRC64;

Query Match 90.3%; Score 28; DB 2; Length 482;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 336 RVFVFA 341

RESULT 62
Q966D7_CABEL
ID Q966D7_CABEL PRELIMINARY; PRT; 488 AA.
AC Q966D7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Y19D10A.11;

```

```

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AC006722; AAK68411.2; -; Genomic DNA.
DR Ensembl; Y19D10A.11; Caenorhabditis elegans.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 488 AA; 54121 MW; A14501A124DB716 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 488;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 356 RVFVFA 361

RESULT 63
Q621X3_CAEBR
ID Q621X3_CAEBR PRELIMINARY; PRT; 492 AA.
AC Q621X3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG02310 (Fragment).
GN Name=CBG02310;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAAC01000012; CAE59030.1; -; Genomic DNA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtase.
DR Pfam; PF00328; Acid_phosphat_A; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 492
SQ SEQUENCE 492 AA; 57471 MW; 4F1D61BB64DC5CFB CRC64;

Query Match 90.3%; Score 28; DB 2; Length 492;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 188 RVFVFA 193

```

RESULT 64

```

Q38860 ARATH
ID Q38860 ARATH PRELIMINARY; PRT; 506 AA.
AC Q38860;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE Fatty acid elongase 1.
GN Name=fael; Synonym=AT4g34520, T4L20.100;
OS Arabidopsis thaliana (Mousse-gar cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=95252821; PubMed=7734965; DOI=10.1105/tpc.7.3.309;
RA James D.W. Jr., Lim E., Keller J., Plooy I., Ralston E., Dooner H.K.;
RT "Directed tagging of the Arabidopsis FATTY ACID ELONGATION1 (FAE1)
RT gene with the maize transposon activator.";
RL Plant Cell 7:309-319(1995).
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Terryn N., Ardiles W., Buyssehaert C., Dasseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Gielen J., Van Montagu M., Jesse T., Heijnen L., Vos P.,
RA Hohelsel J., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA Terryn N., Ardiles W., Buyssehaert C., Dasseville R., De Clerck R.,
RA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarroel R.,
RA Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U29142; AAA70154.1; -; Genomic DNA.
DR EMBL; AL023094; CAA18831.1; -; Genomic DNA.
DR EMBL; AL161585; CAB80169.1; -; Genomic DNA.
DR PIR; T05272; T05272.
DR GO; GO:0008415; P:acyltransferase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 506 AA; 56263 MW; 4516D0EF8E453D18 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 9.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 356 KFLVFA 361

RESULT 65
MURE BORBU
ID MURE BORBU STANDARD; PRT; 508 AA.
AC O51219;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase
DE (EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
DE diaminopimelate-adding enzyme) (UDP-MurNAC-tripeptide synthetase).
GN Name=mure; OrderedLocName=BB0201;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;

Borrelia burgdorferi group.
NCBI_TaxID=139;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Winn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Utterback T.R., Wathey L., McDonald L.A.,
RA Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586 (1997).
CC -1- FUNCTION: Cell wall formation. Diaminopimelic acid adding enzyme
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
CC glutamate + meso-2,6-diaminoheptanedioate = ADP + phosphate + UDP-
CC N-acetylmuramoyl-L-alanyl-D-gamma-glutamyl-meso-2,6-diamino-
CC heptanedioate.
CC -1- PATHWAY: Peptidoglycan biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the murCDF family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AE001130; AAC65588.1; -; Genomic DNA.
DR PIR; A70125; A70125.
DR TIGR; BB0201; -.
DR HAMAP; MF_00208; -; 1.
DR InterPro; IPR004101; Mur_ligase_C.
DR InterPro; IPR00713; Mur_ligase_N.
DR InterPro; IPR005761; MurE.
DR InterPro; IPR012237; UDP-NACM_Align.
DR Pfam; PF01225; Mur_ligase_1.
DR Pfam; PF02875; Mur_ligase_C_1.
DR TIGRFAMs; TIGR01085; mure; 1.
DR KEGG; K00841; Cell cycle; Cell division; Cell shape; Cell wall;
KW ATP-binding; Cell cycle; Cell division; Nucleotide-binding;
KW Peptidoglycan synthesis.
FT NE_BIND 118 124 ATP (Potential).
SQ SEQUENCE 508 AA; 57149 MW; 44043B05F3683B8C CRC64;

Query Match 90.3%; Score 28; DB 1; Length 508;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 41 RLVVFA 46

RESULT 66
P93058 BRAJU
ID P93058 BRAJU PRELIMINARY; PRT; 509 AA.
AC P93058;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Fatty acid elongation 1.
GN Name=fael;
OS Brassica juncea (Leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Brassica.

```

```

OX NCBI_TaxID=3707;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypocotyl;
RA Venkateswari J., Kantar S., Kirti P.B., Malathi V.G., Chopra V.L.;
RT "Molecular cloning and characterization of fatty acid elongation 1
RT (fae 1) gene of Brassica juncea cv. Pusa Bold.";
RL J. Plant Biochem. Biotechnol. 8:53-55(1999).
DR EMBL; Y11007; CAA71898.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56663 MW; B204DASAB5987C5C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 359 KLFVFA 364

RESULT 67
Q8LSC7_BRACM
ID Q8LSC7_BRACM PRELIMINARY; PRT; 509 AA.
AC Q8LSC7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fatty acid elongase.
OS Brassica campestris (field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Yadav P., Bhat S., Chopra V.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF491878; AAM33539.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56661 MW; 59ED8F07457CB6F5 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 358 KLFVFA 363

RESULT 68
Q8S384_BRAJU
ID Q8S384_BRAJU PRELIMINARY; PRT; 509 AA.
AC Q8S384;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fatty acid elongase.
GN Name=Fael.2; Synonyms=fae 1.1;
OS Brassica juncea (leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Yadav P., Bhat S., Chopra V.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

```

```

DR EMBL; AF491877; AAM11648.1; -; Genomic DNA.
DR EMBL; AF491876; AAM34043.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56616 MW; F6C553739AD86C23 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 358 KLFVFA 363

RESULT 69
O80729_ARATH
ID O80729_ARATH PRELIMINARY; PRT; 517 AA.
AC O80729;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative cytochrome P450 (At2g46950).
GN Name=At2g46950;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Renning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RC NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RC NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RC NUCLEOTIDE SEQUENCE.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: belongs to the cytochrome P450 family.
DR EMBL; AC004411; AAC34228.1; -; Genomic DNA.
DR EMBL; BT014808; AAT41791.1; -; mRNA.
DR EMBL; BT011625; AAS47631.1; -; mRNA.
DR PIR; T02192; T02192.
DR HSP; P14779; 1JZP.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PRO0463; EP4501.
DR PRINTS; PRO0385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
KW Transmembrane.
SQ SEQUENCE 517 AA; 59021 MW; 3963BCEC988C19A2 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 517;
Best Local Similarity 83.3%; Pred. No. 9.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 123 KVFVFA 128

```







```

DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTPHPPTASE.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC_motif; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 1.
KW Hydrolase.
FT NON TER 1 1
FT NON TER 558 558
SQ SEQUENCE 558 AA; 63773 MW; 2EC7E5D5BAFE310 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 558;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 519 KVFVFA 524

RESULT 73
Q97K08 CLOAB
ID Q97K08_CLOAB PRELIMINARY; PRT; 571 AA.
AC Q97K08;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Diguanilate cyclase/phosphodiesterase domain (GGDEF) containing
DE protein.
GN OrderedLocusNames=CAC0818;
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
DOI=10.1128/JB.183.16.4823-4838.2001;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe P., Doucette-Stamm L.A., Soucaille F.,
RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AS007597; AAK78794.1; -; Genomic_DNA.
DR PIR; G97000; G97000.
DR InterPro; IPR011623; 7TMR-DISM_7TM.
DR InterPro; IPR000160; GGDEF.
DR Pfam; PF07695; 7TMR-DISM_7TM; 1.
DR Pfam; PF00990; GGDEF; 1.
DR SMART; SM00267; DJF1; 1.
DR TIGRFAMs; TIGR00254; GGDEF; 1.
DR PROSITE; PS00887; GGDEF; 1.
KW Complete proteome.
SQ SEQUENCE 571 AA; 66225 MW; 64B51A5D9F5BD23F CRC64;

Query Match 90.3%; Score 28; DB 2; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 314 KVFVFA 319

Pfam; PF00017; SH2; 1.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTPHPPTASE.
PRINTS; PR00401; SH2DOMAIN.
ProDom; PD000093; SH2; 1.
SMART; SM00194; PTPC; 1.
SMART; SM00404; PTPC_motif; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS00001; SH2; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 1.
Hydrolase.
NON TER 1 1
NON TER 558 558
SEQUENCE 558 AA; 63773 MW; 2EC7E5D5BAFE310 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 584;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 13 RVVFFA 18

RESULT 74
Q4UGB4 THEAN PRELIMINARY; PRT; 584 AA.
AC Q4UGB4;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Seryl-trna synthetase, putative (EC 6.1.1.11).
GN ORFNames=TA19195;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RT "The chromosome 1 sequence of Theileria annulata.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940347; CAI73875.1; -; Genomic_DNA.
KW Aminoacyl-tRNA synthetase; Ligase.
SQ SEQUENCE 584 AA; 66617 MW; 76FEB10EEF7C6691 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 584;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 13 RVVFFA 18

RESULT 75
Q7PS12 ANOGA PRELIMINARY; PRT; 615 AA.
ID Q7PS12_ANOGA PRELIMINARY;
AC Q7PS12;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ENSANGP00000017331.
GN ORFNames=ENSANGG00000021622;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RT The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100846; EAA06305.3; -; Genomic_DNA.
DR SMR; Q7PS12; 1-355.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008092; F:cytoskeletal protein binding; IEA.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR011174; ERM_4.1.
DR InterPro; IPR011259; ERM_C.
DR InterPro; IPR000798; Ez/Fad/moesin.
DR Pfam; PF00373; Band_41; 1.
DR Pfam; PF00769; ERM; 1.

```

DR PIRSF; PIRSF002305; ERM; 1.  
 DR PRINTS; PR00661; ERMFAMILY.  
 DR SMART; SM00295; B41; 1.  
 DR PROSITE; PS00661; FERM\_2; 1.  
 DR PROSITE; PS50057; FERM\_3; 1.  
 SQ SEQUENCE 615 AA; 72579 MW; 804168798B4C5DDC CRC64;  
 Query Match 90.3%; Score 28; DB 2; Length 615;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVFPPA 6  
 Db 96 KVFPPS 101

Search completed: December 29, 2005, 17:47:10  
 Job time : 90.1936 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds  
(without alignments)  
44.518 Million cell updates/sec

Title: US-10-009-122-4  
Perfect score: 31  
Sequence: 1 KVFPPA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : PIR 80.\*

- 1: piri.\*
- 2: pir2.\*
- 3: pir3.\*
- 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	96.8	397	2	P95352
2	28	90.3	49	2	G8319
3	28	90.3	177	2	T16280
4	28	90.3	293	2	T29899
5	28	90.3	326	2	S76400
6	28	90.3	422	2	E82904
7	28	90.3	452	2	C89699
8	28	90.3	506	2	T05272
9	28	90.3	508	2	A70125
10	28	90.3	517	2	T02192
11	28	90.3	571	2	G97000
12	28	90.3	1072	2	T37742
13	28	90.3	1285	2	B72420
14	27	87.1	38	4	S07937
15	27	87.1	138	2	C70150
16	27	87.1	185	2	I40051
17	27	87.1	185	2	C70199
18	27	87.1	193	2	S45022
19	27	87.1	193	2	G69707
20	27	87.1	232	2	AH0299
21	27	87.1	274	2	E72329
22	27	87.1	298	2	T29189
23	27	87.1	321	2	T06845
24	27	87.1	349	2	S73198
25	27	87.1	358	2	S74431
26	27	87.1	358	2	A82218
27	27	87.1	370	2	H90559
28	27	87.1	408	2	T23285
29	27	87.1	409	2	T47754
30	27	87.1	436	2	E96635
31	27	87.1	459	2	B72361
32	27	87.1	488	2	T20124
33	27	87.1	522	2	H86248
34	27	87.1	527	2	S49827
35	27	87.1	581	2	B81107
36	27	87.1	581	2	B81909
37	27	87.1	582	2	I38028
38	27	87.1	582	2	I84471
39	27	87.1	689	2	JC7286
40	27	87.1	856	2	S30338
41	27	87.1	857	2	S44883
42	27	87.1	870	2	T31795
43	26	83.9	107	2	S56500
44	26	83.9	127	2	G87731
45	26	83.9	171	2	C81280
46	26	83.9	183	2	T47707
47	26	83.9	188	2	A86806
48	26	83.9	203	2	S73449
49	26	83.9	216	2	G70437
50	26	83.9	218	2	F86844
51	26	83.9	243	2	T22101
52	26	83.9	255	2	B81693
53	26	83.9	265	2	T44414
54	26	83.9	289	2	B81857
55	26	83.9	289	2	D81085
56	26	83.9	294	2	A27692
57	26	83.9	294	2	B36351
58	26	83.9	297	2	S75656
59	26	83.9	323	2	D86216
60	26	83.9	324	2	T24424
61	26	83.9	337	2	S08459
62	26	83.9	344	2	E90564
63	26	83.9	381	2	T34333
64	26	83.9	389	2	S68155
65	26	83.9	390	2	T22810
66	26	83.9	395	2	T00516
67	26	83.9	395	2	D81040
68	26	83.9	395	2	B81986
69	26	83.9	397	2	T46710
70	26	83.9	397	2	AE1613
71	26	83.9	397	2	AI1250
72	26	83.9	398	2	T44331
73	26	83.9	401	2	H69833
74	26	83.9	404	2	C95990
75	26	83.9	405	1	CEQFR
76	26	83.9	406	2	T43120
77	26	83.9	416	2	T23977
78	26	83.9	431	2	B81254
79	26	83.9	432	2	AD3311
80	26	83.9	436	2	H82974
81	26	83.9	438	2	H82974
82	26	83.9	443	2	AB2841
83	26	83.9	443	2	D97618
84	26	83.9	462	2	AF0057
85	26	83.9	483	2	T20895
86	26	83.9	486	2	S50644
87	26	83.9	503	2	AC3296
88	26	83.9	544	2	T40058
89	26	83.9	664	2	T14132
90	26	83.9	749	2	S62171
91	26	83.9	780	2	T02939
92	26	83.9	841	2	T48508
93	26	83.9	884	2	T25205
94	26	83.9	903	2	G82516
95	26	83.9	1772	2	N45532
96	26	83.9	1785	2	A45546
97	26	83.9	2149	2	C96695
98	26	83.9	2948	2	T22664
99	25	80.6	33	2	S23094
100	25	80.6	42	2	PN0512
101	25	80.6	50	2	A69055
102	25	80.6	57	2	A60045

hypothetical prote  
conserved hypothet  
hypothetical prote  
protein T23J18.22  
probable membrane  
exodeoxyribonuclea  
exodeoxyribonuclea  
matrix metalloprot  
liver-specific org  
hydroxymethylgluta  
ZC62.3 protein -  
hypothetical prote  
probable membrane  
protein W10C8.3 li  
probable periplasm  
hypothetical prote  
transcription regu  
MG028 homolog B01  
soluble hydrogenas  
hypothetical prote  
hypothetical prote  
conserved hypothet  
hypothetical prote  
probable acetyltra  
HcrB/MsbB family p  
sarcotoxin IIA pre  
sarcotoxin II-2 -  
hypothetical prote  
hypothetical prote  
potassium channel  
hypothetical prote  
ubiquinol-cytochro  
hypothetical prote  
hypothetical prote  
cytochrome c-type  
probable membrane  
multidrug resistanc  
multidrug-efflux t  
multidrug-efflux t  
hypothetical prote  
conserved hypothet  
probable sugar upt  
ubiquinol-cytochro  
conserved hypothet  
hypothetical prote  
probable transmembr  
ubiquinol-cytochro  
probable transmembr  
probable MFS trans  
MFS permease/proli  
probable mfs trans  
probable transport  
hypothetical prote  
cytochrome oxidase  
proline/betaine tr  
NADH2 dehydrogenas  
probable membrane  
chloride channel p  
beta-adaptin-like  
hypothetical prote  
hypothetical prote  
major merozoite su  
ribulose biphosph  
hypothetical prote  
beta-amyloloid prote  
beta-amyloloid prote  
hypothetical prote  
Alzheimer's disease

103	25	80.6	57	2	F60045	Alzheimer's diseases	176	25	80.6	711	2	C49219	toxin apxIII secre
104	25	80.6	57	2	D60045	Alzheimer's diseases	177	25	80.6	747	2	JH0773	Alzheimer's diseases
105	25	80.6	57	2	E60045	Alzheimer's diseases	178	25	80.6	764	2	T48446	hypothetical prote
106	25	80.6	57	2	G60045	Alzheimer's diseases	179	25	80.6	770	1	QRHUA4	Alzheimer's diseases
107	25	80.6	57	2	B60045	Alzheimer's diseases	180	25	80.6	771	2	AD3126	ATP-dependent DNA
108	25	80.6	78	2	E69969	hypothetical prote	181	25	80.6	771	2	E98161	probable ATP-depen
109	25	80.6	82	2	FQ0438	Alzheimer's diseases	182	25	80.6	841	2	A43254	protein-tyrosine-p
110	25	80.6	114	2	T33289	hypothetical prote	183	25	80.6	901	2	D70116	transcription elon
111	25	80.6	152	2	T06645	hypothetical prote	184	25	80.6	942	2	T20287	hypothetical prote
112	25	80.6	159	2	T30445	hypothetical prote	185	25	80.6	962	2	G86479	FlaDP7.6 protein -
113	25	80.6	169	2	T15611	hypothetical prote	186	25	80.6	975	2	T22788	hypothetical prote
114	25	80.6	174	2	T15658	hypothetical prote	187	25	80.6	1016	2	S30236	genome polyprotein
115	25	80.6	177	2	T22603	hypothetical prote	188	25	80.6	1046	2	F71432	hypothetical prote
116	25	80.6	179	2	T17915	hypothetical prote	189	25	80.6	1436	2	S67655	probable membrane
117	25	80.6	191	2	A96765	hypothetical prote	190	25	80.6	1549	2	T13940	ankyrin - fruit fl
118	25	80.6	198	2	H84646	hypothetical prote	191	25	80.6	1683	2	S56811	probable membrane
119	25	80.6	210	2	F64609	conserved hypotet	192	25	80.6	1717	2	T50247	probable helicase
120	25	80.6	210	2	B71906	hypothetical prote	193	25	80.6	1848	2	S37771	ankyrin, erythrocy
121	25	80.6	220	2	T41562	hypothetical prote	194	25	80.6	1856	2	B35049	ankyrin 1, erythro
122	25	80.6	222	2	AB3114	hypothetical wtf p	195	25	80.6	1862	2	I49502	ankyrin - mouse
123	25	80.6	231	2	H85138	hypothetical prote	196	25	80.6	1880	2	A35049	ankyrin 1, erythro
124	25	80.6	237	2	AC1953	hypothetical prote	197	25	80.6	1881	1	SJHUK	ankyrin 1, erythro
125	25	80.6	242	2	A82512	rubrerythrin limpo	198	24	77.4	39	2	S00318	photosystem I chai
126	25	80.6	267	2	A40269	cyclin C - fruit f	199	24	77.4	47	2	G70191	hypothetical prote
127	25	80.6	270	2	H98172	amino acid ABC tra	200	24	77.4	51	2	T07326	hypothetical prote
128	25	80.6	273	2	B85896	probable dimethyl	201	24	77.4	71	2	T26661	hypothetical prote
129	25	80.6	273	2	F91051	probable dimethyl	202	24	77.4	71	2	T26663	hypothetical prote
130	25	80.6	277	2	E75187	sugar abc transpor	203	24	77.4	72	2	T26662	hypothetical prote
131	25	80.6	277	2	D71220	probable sugar tra	204	24	77.4	84	2	S77771	probable ribonucle
132	25	80.6	286	2	H86564	outer membrane lip	205	24	77.4	93	2	A89057	protein K09H11.5 l
133	25	80.6	288	2	T37709	hypothetical prote	206	24	77.4	94	2	F90448	hypothetical prote
134	25	80.6	300	2	T26245	hypothetical prote	207	24	77.4	109	2	S57547	hypothetical prote
135	25	80.6	303	2	T25501	hypothetical prote	208	24	77.4	113	2	PN0091	pullulanase (EC 3.
136	25	80.6	327	2	A83766	hypothetical prote	209	24	77.4	126	2	G69330	glyoxalase I (glyo
137	25	80.6	339	2	A30754	hypothetical prote	210	24	77.4	134	2	G89382	response regulator
138	25	80.6	342	2	A48454	cathepsin B-like c	211	24	77.4	134	2	B83804	small multidrug ex
139	25	80.6	342	2	T09355	hypothetical prote	212	24	77.4	139	2	T35620	hypothetical prote
140	25	80.6	346	2	A83686	hypothetical prote	213	24	77.4	139	2	G69543	conserved hypotet
141	25	80.6	349	2	T26247	hypothetical prote	214	24	77.4	140	2	H81959	patch repair prote
142	25	80.6	352	2	T48903	wax synthase limpo	215	24	77.4	143	2	S20937	photosystem I chai
143	25	80.6	356	2	G72386	conserved hypotet	216	24	77.4	143	2	A89093	hypothetical prote
144	25	80.6	361	2	T32411	hypothetical prote	217	24	77.4	143	2	F85938	hypothetical prote
145	25	80.6	389	2	T20811	hypothetical prote	218	24	77.4	143	2	B65069	hypothetical prote
146	25	80.6	397	2	A69525	uncharacterized co	219	24	77.4	149	2	A13586	xanthine/uracil pe
147	25	80.6	404	2	F87753	protein C43E11.7 l	220	24	77.4	156	2	T43957	hypothetical prote
148	25	80.6	406	2	C86904	transporter yxbD l	221	24	77.4	161	2	F72861	AcOrf-93 protein -
149	25	80.6	421	2	A93109	membrane transport	222	24	77.4	161	2	T41833	AcMNPV orf93 - Bom
150	25	80.6	428	2	T48008	hypothetical prote	223	24	77.4	167	1	F1SP5	photosystem I chai
151	25	80.6	439	2	E70371	apolipoprotein N-a	224	24	77.4	171	2	C86367	protein F26F24.18
152	25	80.6	497	2	AD3514	D-serine/D-alanine	225	24	77.4	171	2	D86475	unknown protein, 3
153	25	80.6	501	2	C70420	NADH2 dehydrogenas	226	24	77.4	176	2	G90120	hypothetical prote
154	25	80.6	508	2	T05156	probable Glucose t	227	24	77.4	177	2	S34499	hypothetical prote
155	25	80.6	516	2	S34525	hypothetical prote	228	24	77.4	177	2	AE1410	hypothetical prote
156	25	80.6	520	2	D90014	hypothetical prote	229	24	77.4	184	2	S23361	signal peptidase 1
157	25	80.6	534	2	E82269	conserved hypotet	230	24	77.4	186	1	WMR219	19K globulin precu
158	25	80.6	543	2	S62012	probable membrane	231	24	77.4	186	2	JC4784	alpha-globulin pre
159	25	80.6	568	2	D90525	hypothetical prote	232	24	77.4	188	2	B85481	yaah protein [simi
160	25	80.6	573	2	AB2401	hypothetical prote	233	24	77.4	188	2	B90630	yaah protein [simi
161	25	80.6	582	2	E71052	hypothetical prote	234	24	77.4	188	2	E56688	protein yaah - Esc
162	25	80.6	584	2	F75090	archaeosine tna-r	235	24	77.4	191	2	T09553	conserved hypotet
163	25	80.6	616	2	B90554	lipoprotein limpo-r	236	24	77.4	197	2	S42129	light-harvesting c
164	25	80.6	632	2	A25784	hypothetical 70K p	237	24	77.4	197	2	T33525	hypothetical prote
165	25	80.6	663	2	C287835	hypothetical prote	238	24	77.4	211	2	T05276	hypothetical prote
166	25	80.6	692	2	C87644	fatty oxidation co	239	24	77.4	211	2	T12013	cuticular protein
167	25	80.6	695	1	A49795	Alzheimer's diseases	240	24	77.4	217	2	T1830	hypothetical prote
168	25	80.6	695	2	A27485	Alzheimer's diseases	241	24	77.4	219	2	C85834	hypothetical prote
169	25	80.6	695	2	S00550	Alzheimer's diseases	242	24	77.4	219	2	A98989	hypothetical prote
170	25	80.6	703	2	H45456	NADH2 dehydrogenas	243	24	77.4	220	2	S62598	cuticular protein
171	25	80.6	707	1	LEEBBV	hemolysin secretio	244	24	77.4	220	2	C98900	conserved hypotet
172	25	80.6	707	1	LEECB	hemolysin secretio	245	24	77.4	231	2	T12012	cuticular protein
173	25	80.6	707	2	A61378	leukotoxin express	246	24	77.4	236	2	A97233	uncharacterized co
174	25	80.6	707	2	D43599	hemolysin I secret	247	24	77.4	239	2	S27789	hypothetical prote
175	25	80.6	708	2	C30169	leukotoxin express	248	24	77.4	250	2	F84977	deoxyribonuclease

249 24 77.4 255 2 E82813  
250 24 77.4 257 2 AC1290  
251 24 77.4 257 2 A11661  
252 24 77.4 259 2 E72218  
253 24 77.4 263 2 D72303  
254 24 77.4 267 2 S52347  
255 24 77.4 268 2 A82498  
256 24 77.4 270 2 T44049  
257 24 77.4 277 2 T50722  
258 24 77.4 279 2 E97849  
259 24 77.4 284 2 H86183  
260 24 77.4 285 2 F71851  
261 24 77.4 286 2 A82943  
262 24 77.4 294 2 G81318  
263 24 77.4 297 2 T25817  
264 24 77.4 298 2 H95195  
265 24 77.4 298 2 E98062  
266 24 77.4 301 2 S50737  
267 24 77.4 307 2 C90549  
268 24 77.4 312 2 G70114  
269 24 77.4 313 2 B98339  
270 24 77.4 314 2 G86835  
271 24 77.4 315 2 T07314  
272 24 77.4 317 2 B98208  
273 24 77.4 317 2 AG3078  
274 24 77.4 319 2 S73159  
275 24 77.4 320 2 T16311  
276 24 77.4 321 2 H71729  
277 24 77.4 327 2 AH2312  
278 24 77.4 328 2 AH2399  
279 24 77.4 334 2 T19127  
280 24 77.4 335 2 T04029  
281 24 77.4 340 1 M8B8E5  
282 24 77.4 345 2 C45456  
283 24 77.4 347 2 T15672  
284 24 77.4 348 2 T20167  
285 24 77.4 358 2 A64424  
286 24 77.4 358 2 T50897  
287 24 77.4 361 2 A86841  
288 24 77.4 364 2 T16376  
289 24 77.4 368 2 D90596  
290 24 77.4 375 2 A39622  
291 24 77.4 385 2 T05049  
292 24 77.4 391 2 T20752  
293 24 77.4 394 2 T19028  
294 24 77.4 397 2 T19029  
295 24 77.4 398 2 F72335  
296 24 77.4 401 2 S49393  
297 24 77.4 404 2 T32998  
298 24 77.4 405 2 B97171  
299 24 77.4 406 2 T32922  
300 24 77.4 409 2 E97218

## ALIGNMENTS

## RESULT 1

probable proline dipeptidase [imported] - Sinorhizobium meliloti (strain 1021) megaplasm  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: F95352  
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bower  
Proc. Natl. Acad. Sci. U.S.A. 96, 9883-9886, 2001  
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: F95352  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-397 <KUR>  
A:Cross-references: UNIPROT:Q92YY6; UNIPARC:UPI00000CB1AA; GB:AB006469; PIDN:AAK65384.1

A:Experimental source: strain 1021, megaplasmid pSymbA  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler  
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure  
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: SMal329  
A:Genome: plasmid

Query Match 96.8%; Score 30; DB 2; Length 397;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFFA 6  
|||:  
Db 25 KFIFFA 30

## RESULT 2

G83919  
hypothetical protein BH2159 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: G83919  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: G83919  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-49 <STO>  
A:Cross-references: UNIPROT:Q9KAX7; UNIPARC:UPI000000C3E07; GB:AP001514; GB:BA0000004; I  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH2159

Query Match 90.3%; Score 28; DB 2; Length 49;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFFA 6  
|||:  
Db 34 KFPVFFS 39

## RESULT 3

T16280  
hypothetical protein F35H10.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T16280  
R:Woesner, J.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid F35H10.  
A:Reference number: Z18490  
A:Accession: T16280  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-177 <WOB>  
A:Cross-references: UNIPROT:Q20070; UNIPARC:UPI0000007F0D0; EMBL:U40934; NID:g1072149; I  
C:Genetics:  
A:Gene: CESP:F35H10.6  
A:Introns: 18/1, 39/2, 74/3, 97/2

Query Match 90.3%; Score 28; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 43;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
 |||||:  
 Db 10 KFVFFS 15

RESULT 4  
 T29899  
 hypothetical protein M02B7.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T29899  
 R;Nelson, J.; Wohlmann, P.  
 submitted to the EMBL Data Library, September 1996  
 A:Description: The sequence of C. elegans cosmid M02B7.  
 A:Reference number: Z20706  
 A:Accession: T29899  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-293 <NEL>  
 A:Cross-references: UNIPROT:Q94284; UNIPARC:UPI0000078391; EMBL:U70851; PIDN:AAB09129.1;  
 A:Experimental source: strain Bristol N2; clone M02B7  
 C:Genetics:  
 A:Gene: CESP:M02B7.4  
 A:Map position: 4  
 A:Introns: 42/3; 150/2; 198/1; 230/3; 276/3

Query Match 90.3%; Score 28; DB 2; Length 293;  
 Best Local Similarity 83.3%; Pred. No. 69;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
 |||||:  
 Db 258 KFVFFS 263

RESULT 5  
 S76400  
 hypothetical protein - Synechocystis sp. (strain PCC 6803)  
 C:Species: Synechocystis sp.  
 A:Variety: PCC 6803  
 C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C:Accession: S76400  
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
 DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
 sp.  
 A:Reference number: S74322; MUID:97061201; PMID:8905231  
 A:Accession: S76400  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-326 <KAN>  
 A:Cross-references: UNIPROT:P74429; UNIPARC:UPI00000C1025; EMBL:D90915; GB:AB001339; NID  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 90.3%; Score 28; DB 2; Length 326;  
 Best Local Similarity 83.3%; Pred. No. 76;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
 |||||:  
 Db 104 KFVFFS 109

RESULT 6  
 E82904  
 hypothetical protein UV329 [imported] - Ureaplasma urealyticum  
 C:Species: Ureaplasma urealyticum  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C:Accession: E82904  
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi  
 A:Reference number: A82870  
 A:Accession: E82904  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-422 <GLA>  
 A:Cross-references: UNIPARC:UPI00000C1C1F; GB:AE002130; GB:AF222894; NID:g6899302; PIDN  
 A:Experimental source: serovar 3; biovar 1  
 C:Genetics:  
 A:Gene: UV329  
 A:Genetic code: SGC3

Query Match 90.3%; Score 28; DB 2; Length 422;  
 Best Local Similarity 83.3%; Pred. No. 96;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
 |||||:  
 Db 208 KYVFFA 213

RESULT 7  
 C88969  
 protein F15E11.8 [imported] - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C:Accession: C88969  
 R:Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo  
 A:Reference number: A75000; MUID:99069613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_el  
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an  
 A:Accession: C88969  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-452 <STO>  
 A:Cross-references: UNIPROT:O44595; UNIPARC:UPI0000075D10; GB:chr\_V; PIDN:AAB94205.1; P  
 C:Genetics:  
 A:Gene: F15E11.8  
 A:Map position: 5

Query Match 90.3%; Score 28; DB 2; Length 452;  
 Best Local Similarity 83.3%; Pred. No. 1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6  
 |||||:  
 Db 291 RFVFFA 296

RESULT 8  
 T05272  
 fatty acid elongase 1 - Arabidopsis thaliana  
 N:Alternate names: protein T4L20.100  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: T05272  
 R;Sevan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De  
 ewes, H.W.; Mayer, K.F.X.; Schueller, C.  
 submitted to the Protein Sequence Database, September 1998  
 A:Reference number: Z15406  
 A:Accession: T05272  
 A:Molecule type: DNA  
 A:Residues: 1-506 <BEV>  
 A:Cross-references: UNIPROT:Q38860; UNIPARC:UPI0000047264; EMBL:AL023094  
 A:Experimental source: cultivar Columbia; BAC clone T4L20  
 C:Genetics:  
 A:Map position: 4  
 A:Note: T4L20.100  
 C:Superfamily: very-long-chain 3-ketoacyl-CoA synthase

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6  
|||  
356 KFLFFA 361

Db

RESULT 9

A70125  
UDP-N-acetylmuramoyl-D-glutamate-2,6-diaminopimelate ligase (murE) homolog - Lyme  
C;Species: Borrelia burgdorferi (Lyme disease spirochete)  
C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 05-Oct-2004  
C;Accession: A70125  
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
A;Authors: Smith, H.O.; Venter, J.C.  
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
A;Reference number: A70100; MUID:98065943; PMID:9403685  
A;Accession: A70125  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-508 <KLE>  
A;Cross-references: UNIPROT:O51219; UNIPARC:UPI00000573B3; GB:AE001130; GB:AE000783; NID  
A;Experimental source: strain B31  
C;Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 90.3%; Score 28; DB 2; Length 508;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6  
|||  
41 RFVFFA 46

Db

RESULT 10

T02192  
probable cytochrome P450 At2g46950 [imported] - Arabidopsis thaliana  
N;Alternate names: cytochrome P450 homolog F14M4.22  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C;Accession: T02192; C84909  
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ron  
submitted to the EMBL Data Library, September 1998  
A;Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.  
A;Reference number: Z14609  
A;Accession: T02192  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-517 <ROU>  
A;Cross-references: UNIPROT:O80729; UNIPARC:UPI00000A147A; EMBL:AC004411; NID:G3522932;  
A;Experimental source: cultivar Columbia  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: C84909  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-517 <STO>  
A;Cross-references: UNIPARC:UPI00000A147A; GB:AE002093; NID:G3522946; PIDN:AAC34228.1; G  
C;Genetics:  
A;Map position: 2  
A;Gene: At2g46950; F14M4.22  
A;Introns: 95/1, 169/3; 252/2; 374/3  
C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology  
C;Keywords: heme; iron; metalloprotein  
F;321-485/Domain: cytochrome P450 homology <P45>

F;463/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.3%; Score 28; DB 2; Length 517;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6  
|||  
123 KVFVFFS 128

Db

RESULT 11

G97000  
diguanilate cyclase/phosphodiesterase domain (GGDEF) containing protein [imported] - Cl  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: G97000  
R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee  
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: G97000  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-571 <KUR>  
A;Cross-references: UNIPROT:Q97KUS; UNIPARC:UPI000000C9FBF; GB:AE001437; PIDN:AAK78794.1  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC0818

Query Match 90.3%; Score 28; DB 2; Length 571;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6  
|||  
314 KFMFFA 319

Db

RESULT 12

T37742  
serine threonine-protein kinase - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 05-Oct-2004  
C;Accession: T37742  
R;Rieger, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, January 1999  
A;Reference number: Z21743  
A;Accession: T37742  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1072 <RIE>  
A;Cross-references: UNIPROT:O94537; UNIPARC:UPI00000069EBD; EMBL:AL035248; PIDN:CRAA22846  
A;Experimental source: strain 972h-; cosmid c167  
C;Genetics:  
A;Gene: spac167.01; SPDB:SPAC167.01  
A;Map position: 1  
A;Introns: 1015/3

Query Match 90.3%; Score 28; DB 2; Length 1072;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6  
|||  
13 KVFVFFS 18

Db

RESULT 13

B72420  
hypothetical protein TM0088 - Thermotoga maritima (strain MSB8)  
C;Species: Thermotoga maritima



C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C;Accession: B72420  
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
 C.M.  
 Nature 399, 323-329, 1999  
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
 A;Reference number: A72200; MUID:99287316; PMID:10360571  
 A;Accession: B72420  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1285 <ARN>  
 A;Cross-references: UNIPROT:Q9WUX3; UNIPARC:UPI0000003DA9B; GB:AE001695; GB:AE000512; NID  
 A;Experimental source: strain MSB8  
 C;Genetics:  
 A;Gene: TW0088

Query Match 90.3%; Score 28; DB 2; Length 1285;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
 |||||  
 Db 341 KVFVFA 346

RESULT 14  
 S07937  
 hypothetical protein atpH 5'-region - Euglena gracilis chloroplast (fragment)  
 C;Species: chloroplast Euglena gracilis  
 C;Date: 06-Nov-1998 #sequence\_revision 06-Nov-1998 #text\_change 09-Jul-2004  
 C;Accession: S07937  
 R;Passavant, C.W.; Hallick, R.B.  
 Plant Mol. Biol. 4, 347-354, 1985  
 A;Title: Location, nucleotide sequence and expression of the proton-translocating subunit  
 A;Reference number: S07400  
 A;Accession: S07937  
 A;Molecule type: DNA  
 A;Residues: 1-38 <PAS>  
 A;Cross-references: UNIPROT:Q32187; UNIPARC:UPI00000965CB; EMBL:M16844; NID:g336867; PID  
 C;Comment: This is the hypothetical translation of a sequence that was not reported as a  
 C;Genetics:  
 A;Genome: chloroplast  
 C;Keywords: chloroplast

Query Match 87.1%; Score 27; DB 4; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5  
 |||||  
 Db 18 KVFVFF 22

RESULT 15  
 C70150  
 hypothetical protein BB0404 - Lyme disease spirochete  
 C;Species: Borrelia burgdorferi (Lyme disease spirochete)  
 C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
 C;Accession: C70150  
 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
 Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
 Nature 390, 580-586, 1997  
 A;Authors: Smith, H.O.; Venter, J.C.  
 A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
 A;Reference number: A70100; MUID:98065943; PMID:9403685  
 A;Accession: C70150  
 A;Status: preliminary;  
 A;Molecule type: DNA  
 A;Residues: 1-138 <KLE>  
 A;Cross-references: UNIPROT:O51135; UNIPARC:UPI000005747C; GB:AE001146; GB:AE000783; NID  
 A;Experimental source: strain B31

C;Superfamily: Borrelia burgdorferi hypothetical protein BB0404  
 Query Match 87.1%; Score 27; DB 2; Length 138;  
 Best Local Similarity 66.7%; Pred. No. 57;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6  
 |||||  
 Db 40 KVFVFA 45

RESULT 16  
 I40051  
 signal peptidase I (EC 3.4.21.89) - Bacillus amyloliquefaciens  
 N;Alternate names: leader peptidase  
 C;Species: Bacillus amyloliquefaciens  
 C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
 C;Accession: I40051; S3885  
 R;Tomlinson, I.M.; Cook, G.P.; Carter, N.P.; Elaszarapu, R.; Smith, S.; Walter, G.; Bul  
 Hum. Mol. Genet. 3, 853-860, 1994  
 A;Title: Human immunoglobulin VH and D segments on chromosomes 15q11.2 and 16p11.2.  
 A;Reference number: I37619; MUID:95038735; PMID:7951227  
 A;Accession: I40051  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-185 <RES>  
 A;Cross-references: UNIPROT:P41026; UNIPARC:UPI000012E452; EMBL:Z27458; NID:g429069; PFI  
 C;Genetics:  
 A;Gene: sipa  
 A;Start codon: TTG  
 C;Superfamily: signal peptidase I sips  
 C;Keywords: hydrolase; serine proteinase

Query Match 87.1%; Score 27; DB 2; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5  
 |||||  
 Db 172 KVFVFF 176

RESULT 17  
 C70199  
 hypothetical protein BB0796 - Lyme disease spirochete  
 C;Species: Borrelia burgdorferi (Lyme disease spirochete)  
 C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
 C;Accession: C70199  
 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
 Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
 Nature 390, 580-586, 1997  
 A;Authors: Smith, H.O.; Venter, J.C.  
 A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
 A;Reference number: A70100; MUID:98065943; PMID:9403685  
 A;Accession: C70199  
 A;Status: preliminary;  
 A;Molecule type: DNA  
 A;Residues: 1-185 <KLE>  
 A;Cross-references: UNIPROT:O51736; UNIPARC:UPI00000575FE; GB:AE001178; GB:AE000783; NIT  
 A;Experimental source: strain B31

Query Match 87.1%; Score 27; DB 2; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5  
 |||||  
 Db 7 KVFVFF 11

RESULT 18  
 S45022

signal peptidase I (EC 3.4.21.89) - Bacillus amyloliquefaciens

N;Alternate names: leader peptidase

C;Species: Bacillus amyloliquefaciens

C;Date: 06-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S59966; S45022

R;Hoang, V.; Hofemeister, J.

Biochim. Biophys. Acta 1269, 64-68, 1995

A;Title: Bacillus amyloliquefaciens possesses a second type I signal peptidase with exte

A;Reference number: S59965; MUID:96049527; PMID:7578273

A;Accession: S59966

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-193 <HO2>

A;Cross-references: UNIPROT:P41025; UNIPARC:UPI000012E454; EMBL:Z33640; NID:9562273; PID

C;Genetics:

A;Start codon: TTG

C;Superfamily: signal peptidase I sips

C;Keywords: hydrolase; serine proteinase; transmembrane protein

Query Match 87.1%; Score 27; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

Db 180 KFVFF 184

RESULT 19

G69707 signal peptidase I sipT - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C;Accession: G69707

R;Kunst, F.; Ogasawara, N.; Mozer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, K.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A;Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Banchin, A. Bacillus subtilis.

A;Title: The complete genome sequence of the Gram-positive bacterium

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69707

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-193 <KUN>

A;Cross-references: UNIPROT:P71013; UNIPARC:UPI000006032F; GB:Z99111; GB:AL009126; NID:9

A;Experimental source: strain 168

C;Genetics:

A;Gene: sipT

C;Superfamily: signal peptidase I sips

Query Match 87.1%; Score 27; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

Db 180 KFVFF 184

RESULT 20

AH0299

probable membrane protein YPO2455 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AH0299

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0299

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-232 <KUR>

A;Cross-references: UNIPROT:Q8ZDV0; UNIPARC:UPI000000DCD3E; GB:AL590842; PIDN:CAC91260.1

C;Genetics:

A;Gene: YPO2455

Query Match 87.1%; Score 27; DB 2; Length 232;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

Db 19 KFVFF 23

RESULT 21

E72329

hypothetical protein TM0818 - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: E72329

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

Garrett, M.E.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: E72329

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-274 <ARN>

A;Cross-references: UNIPROT:Q9WZS5; UNIPARC:UPI000000D3985; GB:AE001749; GB:AE0000512; NI

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM0818

Query Match 87.1%; Score 27; DB 2; Length 274;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

Db 260 KFVFF 264

RESULT 22

T29189

hypothetical protein C55C3.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T29189

R;Woessne, J.; Steillyes, L.

submitted to the EMBL Data Library, April 1996

A;Description: The sequence of C. elegans cosmid C55C3.

A;Reference number: Z20585

A;Status: T29189

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-298 <MOE>

A;Cross-references: UNIPROT:Q18868; UNIPARC:UPI00000074B15; EMBL:U53335; PIDN:AAA96172.1

A;Experimental source: strain Bristol N2; clone C55C3

C;Genetics:

A;Gene: C55C3.2



A;Residues: 1-370 <KUR>  
A;Cross-references: UNIPROT:Q9QNH7; UNIPARC:UPI00000C807C; GB:AL445566; PID:g14089798; R  
A;Experimental source: strain UAB CTIP  
C;Genetics:  
A;Gene: MYPU 3840  
A;Genetic code: SGC3

Query Match 87.1%; Score 27; DB 2; Length 370;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6  
|:|:|  
Db 23 KYIFFA 28

RESULT 28  
T23285  
hypothetical protein K03D7.8 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T23285  
R;Matthews, L.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19721  
A;Accession: T23285  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-408 <WIL>  
A;Cross-references: UNIPROT:O45653; UNIPARC:UPI00000610BB; EMBL:Z81562; PIDN:CAB04555.1;  
A;Experimental source: clone K03D7  
C;Genetics:  
A;Gene: CESP:K03D7.8  
A;Map position: 5  
A;Introns: 117/3; 304/1

Query Match 87.1%; Score 27; DB 2; Length 408;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5  
|:|:|  
Db 243 KFVFF 247

RESULT 29  
T47754  
leucine zipper-containing protein AT103 - Arabidopsis thaliana  
N;Alternate names: PNL134 protein homolog; protein F24I3.20  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T47754; S71218  
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Stert, W.; Holland, R.; Weichselgartner, M.;  
submitted to the Protein Sequence Database, February 2000  
A;Reference number: Z24475  
A;Accession: T47754  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-409 <NYA>  
A;Cross-references: UNIPROT:Q9MIK4; UNIPARC:UPI00000A741A; EMBL:AL1138655  
A;Experimental source: cultivar Columbia; BAC clone F24I3  
R;Zheng, C.C.; O'Neill, S.D.  
submitted to the EMBL Data Library, October 1995  
A;Description: Molecular analysis of a novel phytochrome-regulated Pharbitis cDNA and its  
A;Reference number: S71218  
A;Accession: S71218  
A;Molecule type: mRNA  
A;Residues: 37-156; 'S', 158-409 <ZHE>  
A;Cross-references: UNIPARC:UPI00000A9BBC; EMBL:U38232; NID:g1033194; PID:g1033195  
C;Genetics:  
A;Gene: AT103  
A;Map position: 3  
A;Introns: 158/3; 180/2; 289/3; 322/3

A;Note: F24I3.20  
C;Superfamily: leucine zipper-containing protein AT103

Query Match 87.1%; Score 27; DB 2; Length 409;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6  
|:|:|  
Db 210 KFIFYA 215

RESULT 30  
E96635  
hypothetical protein T7P1.13 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: E96635  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso  
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
Chin, C.W.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: E96635  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-436 <STO>  
A;Cross-references: UNIPROT:Q9C954; UNIPARC:UPI00000483C7; GB:AE005173; NID:g6751689; P  
C;Genetics:  
A;Gene: T7P1.13  
A;Map position: 1

Query Match 87.1%; Score 27; DB 2; Length 436;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6  
|:|:|  
Db 185 KYIFFA 190

RESULT 31  
B72361  
conserved hypothetical protein - Thermotoga maritima (strain MSB8)  
C;Species: Thermotoga maritima  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: B72361  
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
C.M.  
Nature 399, 323-329, 1999  
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se  
A;Reference number: A72200; MUID:99287316; PMID:10360571  
A;Accession: B72361  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-459 <ARN>  
A;Cross-references: UNIPROT:Q9WZ33; UNIPARC:UPI00000C13F0; GB:AE001731; GB:AE0000512; N  
C;Genetics:  
A;Gene: TM0563

Query Match 87.1%; Score 27; DB 2; Length 459;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

```

Db          210 KFVFF 214
|||||
RESULT 32
T20124
hypothetical protein C50H2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20124
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19226
A:Accession: T20124
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-488 <N1>
A:CROSS-references: UNIPROT:Q18760; UNIPARC:UPI000007F0DB; EMBL:Z73971; PIDN:CAA98250.1;
A:Experimental source: clone C50H2
C:Genetics:
A:Gene: CESP:C50H2.2
A:Map position: 5
A:Introns: 67/2; 107/3; 138/3; 180/3; 337/2; 391/3; 445/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C50H2.2

Query Match      87.1%; Score 27; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||||
Db 203 KFVFF 207

RESULT 33
H86248
protein T23J18.22 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86248
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-522 <STO>
A:CROSS-references: UNIPROT:Q9LPY0; UNIPARC:UPI00000A13DA; GB:AE005172; NID:g6554189; PI
C:Genetics:
A:Gene: T23J18.22
A:Map position: 1

Query Match      87.1%; Score 27; DB 2; Length 522;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||||
Db 257 KFVFF 261

RESULT 34
S49827
probable membrane protein YDR072c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D4405; hypothetical protein YD8554.05c

```

```

C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: S49827; S48758; S55820; S67889; S67888
R:Richards, C.; Harris, D.E.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49823
A:Accession: S49827
A:Molecule type: DNA
A:Residues: 1-527 <RIC>
A:CROSS-references: UNIPROT:P38954; UNIPARC:UPI000012D81A; EMBL:Z46796; NID:g577794; PI
R:Coster, P.; Jonniaux, J.L.; Goffeau, A.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48758
A:Accession: S48758
A:Molecule type: DNA
A:Residues: 1-524 <COS>
A:CROSS-references: UNIPARC:UPI0000168B70; EMBL:X82086; NID:g558241; PID:g558243
R:Coster, P.; Jonniaux, J.L.; Goffeau, A.
Yeast 11, 673-679, 1995
A:Title: Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading f
A:Reference number: S55819; MUID:96093910; PMID:7483840
A:Accession: S55820
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-525 <COM>
A:CROSS-references: UNIPARC:UPI000017B30A; EMBL:X82086
R:Poury, P.; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67889
A:Accession: S67889
A:Molecule type: DNA
A:Residues: 1-524 <FOU>
A:CROSS-references: UNIPARC:UPI0000168B70; EMBL:Z74368; MIPS:YDR072C
A:Experimental source: strain S288C
R:Blocker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67587
A:Accession: S67888
A:Molecule type: DNA
A:Residues: 417-527 <ELO>
A:CROSS-references: UNIPARC:UPI000017B30B; EMBL:Z74368; MIPS:YDR072C
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:SYR4
A:CROSS-references: SGD:S0002479; MIPS:YDR072C
A:Map position: 4R
C:Keywords: transmembrane protein
F124-40/Domain: transmembrane #status predicted <TM1>
F101-117/Domain: transmembrane #status predicted <TM2>
F153-169/Domain: transmembrane #status predicted <TM3>
F194-210/Domain: transmembrane #status predicted <TM4>
F294-310/Domain: transmembrane #status predicted <TM5>
F462-478/Domain: transmembrane #status predicted <TM6>

Query Match      87.1%; Score 27; DB 2; Length 527;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFVFF 6
|||||
Db 62 KPAPFA 67

RESULT 35
B81107
exodeoxyribonuclease V, alpha chain NMB1233 [imported] - Neisseria meningitidis (strain
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81107
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000

```

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V  
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
A;Reference number: A81000; MUID:20175755; PMID:10710307  
A;Accession: B81107  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-581 <FET>  
A;Cross-references: UNIPROT:Q9J293; UNIPARC:UPI000000C4671; GB:AE002471; GB:AE002098; NID  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
C;Superfamily: exodeoxyribonuclease V 67K chain

Query Match 87.1%; Score 27; DB 2; Length 581;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5  
Db 546 KFVFF 550

RESULT 36  
B81909  
exodeoxyribonuclease V alpha subunit NMA1401 [Imported] - *Neisseria meningitidis* (strain  
C;Species: *Neisseria meningitidis*  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C;Accession: B81909  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jørgels, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
A;Reference number: A81775; MUID:20222556; PMID:10761919  
A;Accession: B81909  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-581 <PAR>  
A;Cross-references: UNIPROT:Q9JUB8; UNIPARC:UPI000000C4BB0; GB:AL162755; GB:AL157959; NID  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: recD; NMA1401  
C;Superfamily: exodeoxyribonuclease V 67K chain

Query Match 87.1%; Score 27; DB 2; Length 581;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5  
Db 546 KFVFF 550

RESULT 37  
I38028  
matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human  
N;Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteinase  
C;Species: *Homo sapiens* (man)  
C;Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 09-Jul-2004  
C;Accession: I38028; G02274; I38046; S78011; S45341; S71384  
R;Will, H.; Hinzmann, B.  
Eur. J. Biochem. 231, 602-608, 1995  
A;Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloprote  
A;Reference number: I38028; MUID:95377289; PMID:7649159  
A;Accession: I38028  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-582 <WILL>  
A;Cross-references: UNIPROT:P50281; UNIPARC:UPI00000048136; EMBL:Z48481; NID:G963053; PID  
R;Luo, G.  
submitted to the EMBL Data Library, November 1995  
A;Reference number: H00963  
A;Accession: G02274  
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA  
A;Residues: 1-582 <DUO>  
A;Cross-references: UNIPARC:UPI00000048136; EMBL:U41078; NID:G1127836; PIDN:AAA83770.1; I  
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, I  
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995  
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal c  
A;Reference number: I38046; MUID:95224014; PMID:7708715  
A;Accession: I38046  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-7,'S',9-582 <OKA>  
A;Cross-references: UNIPARC:UPI000003096F; EMBL:X83535; NID:G804993; PIDN:CAA58519.1; P  
R;Seiki, M.  
submitted to the EMBL Data Library, January 1994  
A;Reference number: S78011  
A;Accession: S78011  
A;Molecule type: mRNA  
A;Residues: 1-7,'S',9-337,'K',339-582 <SEI>  
A;Cross-references: UNIPARC:UPI000003DC76; EMBL:D26512; NID:G793762; PIDN:BAA05519.1; P  
R;Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shingawa, A.; Yamamoto, E.; Seiki, M.  
Nature 370, 61-65, 1994  
A;Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.  
A;Reference number: S45341; MUID:94286011; PMID:8015608  
A;Accession: S45341  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-7,'S',9-188,'R',190,'A',192-267,'K',269-272,'HY',275,'P',277-285,'KQ',288  
A;Cross-references: UNIPARC:UPI0000157586; EMBL:D26512  
R;Sato, H.; Kinoshita, T.; Takino, T.; Nakayama, K.; Seiki, M.  
FEBS Lett. 393, 101-104, 1996  
A;Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)  
A;Reference number: S71384; MUID:96397540; PMID:8804434  
A;Accession: S71384  
A;Molecule type: protein  
A;Residues: 112-116 <SAW>  
A;Cross-references: UNIPARC:UPI0000175D8E  
C;Genetics:  
A;Gene: GDB:MMP14; MT1-MMP  
A;Cross-references: GDB:375731; OMIM:600754  
A;Map position: 14q11-14q12  
C;Superfamily: interstitial collagenase; metalloproteinase; zinc; zymogen  
C;Keywords: glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-97/Domain: activation peptide #status predicted <PRO>  
F;61-284/Domain: matrix metalloproteinase homology <MMP>  
F;98-582/Product: matrix metalloproteinase 14 membrane type #status predicted <MAT>  
F;285-313/Domain: hinge #status predicted <HNG>  
F;314-508/Domain: hemopexin repeat homology <PXN>  
F;539-562/Domain: transmembrane #status predicted <TMW>  
F;93,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F;130/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted  
F;240/Active site: Glu #status predicted  
F;319-508/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 2; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5  
Db 378 KFVFF 382

RESULT 38  
I84471  
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat  
N;Alternate names: membrane-type metalloproteinase  
C;Species: *Rattus norvegicus* (Norway rat)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I84471; I61946  
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset,  
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995

A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells  
A;Reference number: I38046; MUID:95224014; PMID:7708715  
A;Accession: I84471  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-582 <RES>  
A;Cross-references: UNIPROT:Q10739; UNIPARC:UPI0000030970; EMBL:X83537; NID:g805012; PID:161946  
A;Accession: I61946  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-67, 'M', '69-254, 'A', '256-582 <RES>  
A;Cross-references: UNIPARC:UPI00001679D1; EMBL:X91785; NID:g1001926; PIDN:CAA62897.1; F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted  
C;Genetics:  
A;Gene: mt-mmp  
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase  
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-97/Domain: activation peptide #status predicted <PRO>  
F:61-284/Domain: matrix metalloproteinase homology <MMP>  
F:313-508/Domain: hemopexin repeat homology <PXN>  
F:93,239,243,249/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted  
F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted  
F:240/Active site: Glu #status predicted

Query Match 87.1%; Score 27; DB 2; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5  
|||||  
378 KFVFF 382

Db

RESULT 39  
JC7286  
liver-specific organic anion transporter-1 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: JC7286  
R;Ogura, K.; Choudhuri, S.; Klaassen, C.D.  
Biochem. Biophys. Res. Commun. 272, 563-570, 2000  
A;Title: Full-length cDNA cloning and genomic organization of the mouse liver-specific organic anion transporter-1  
A;Reference number: JC7286  
A;Accession: JC7286  
A;Molecule type: mRNA  
A;Residues: 1-689 <OGU>  
A;Cross-references: UNIPROT:Q5JUL3; UNIPARC:UPI0000023434; DDBJ:AB031959  
C;Genetics:  
A;Gene: lat-1  
C;Keywords: glycolysis; transmembrane protein

Query Match 87.1%; Score 27; DB 2; Length 689;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5  
|||||  
404 KFVFF 408

Db

RESULT 40  
S30338  
hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - German cockroach  
C;Species: Blattella germanica (German cockroach)  
C;Date: 02-Dec-1993 #sequence\_revision 03-Aug-1995 #text\_change 27-Oct-2003  
C;Accession: S30338  
R;Martinez-Gonzalez, J.; Buesa, C.; Piulachs, M.D.; Belles, X.; Hegardt, F.G.  
Eur. J. Biochem. 213, 233-241, 1993  
A;Title: Molecular cloning, developmental pattern and tissue expression of 3-hydroxy-3-methylglutaryl-CoA reductase (HMG-CoA) reductase  
A;Reference number: S30338; MUID:93238692; PMID:8477698  
A;Accession: S30338  
A;Molecule type: mRNA  
A;Residues: 1-856 <MAR>

A;Cross-references: UNIPARC:UPI0000174BF6  
C;Superfamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase  
C;Keywords: coenzyme A; NADP; oxidoreductase

Query Match 87.1%; Score 27; DB 2; Length 856;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5  
|||||  
360 KFVFF 364

Db

RESULT 41  
S44883  
ZC262.3 protein - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004  
C;Accession: S44883  
R;Anderson, K.  
submitted to the EMBL Data Library, September 1993  
A;Description: Sequence of the C. elegans cosmid ZC262.  
A;Reference number: S44818  
A;Accession: S44883  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-857 <AND>  
A;Cross-references: UNIPROT:P34595; UNIPARC:UPI0000179325; EMBL:L23647; NID:g388612; PID:72/2; 145/1; 191/1; 263/3; 297/1; 363/2; 403/2; 448/2; 523/2; 563/2; 613/2; 643/3; 643/3; 643/3;  
C;Genetics:  
C;Superfamily: Caenorhabditis elegans ZC262.3 protein

Query Match 87.1%; Score 27; DB 2; Length 857;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5  
|||||  
87 KFVFF 91

Db

RESULT 42  
T31795  
hypothetical protein R02F11.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T31795  
R;Davidson, S.; Wohlmann, P.  
submitted to the EMBL Data Library, July 1997  
A;Description: The sequence of C. elegans cosmid R02F11.  
A;Reference number: Z21087  
A;Accession: T31795  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-870 <DAV>  
A;Cross-references: UNIPROT:O16363; UNIPARC:UPI000016423C; EMBL:AF016439; PIDN:AAB65898.  
C;Genetics:  
A;Gene: CESP:R02F11.2  
A;Map position: 5  
A;Introns: 44/2; 116/2; 164/3; 265/2; 335/2; 380/1; 397/1; 419/3; 475/1; 582/2; 643/3; 643/3; 643/3;

Query Match 87.1%; Score 27; DB 2; Length 870;  
Best Local Similarity 66.7%; Pred. No. 3.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 6  
|||||  
2 RFVFF 7

Db

RESULT 43  
SS6900



probable membrane protein YJL119c - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein J0738

C:Species: *Saccharomyces cerevisiae*

C>Date: 08-Jul-1995 #sequence\_revision 08-Sep-1995 #text\_change 09-Jul-2004

C:Accession: S56900

R:Czepluch, C.; Kordes, E.; Pujol, A.; Jauniaux, J.C.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56891

A:Accession: S56900

A:Molecule type: DNA

A:Residues: 1-107 <CZI>

A:Cross-references: UNIPROT:P47021; UNIPARC:UPI000013B5E8; EMBL:Z49394; NID:gl008309; P

C:Genetics:

A:Gene: MIPS:YJL119c

A:Cross-references: SGD:S0003655

A:Map position: 10L

C:Superfamily: *Saccharomyces* probable membrane protein YJL119c

C:Keywords: transmembrane protein

Query Match 83.9%; Score 26; DB 2; Length 107;  
Best Local Similarity 83.3%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KFVFFA 6

Db 102 KFFFFA 107

#### RESULT 44

G87731 protein W10C8.3 [imported] - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C:Accession: G87731

R:anonymous; The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: G87731

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-127 <STO>

A:Cross-references: UNIPARC:UPI0000164023; GB:chr\_I; PIDN:AAB97593.1; PID:g2804486; GSP

C:Genetics:

A:Gene: W10C8.3

A:Map position: 1

Query Match 83.9%; Score 26; DB 2; Length 127;  
Best Local Similarity 80.0%; Pred. No. 89;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

Db 83 KPIFF 87

#### RESULT 45

C81280 probable periplasmic cytochrome C Cj1358c [imported] - *Campylobacter jejuni* (strain NCTC

C:Species: *Campylobacter jejuni*

C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 05-Oct-2004

C:Accession: C81280

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Bagham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: C81280

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-171 <PAR>

A:Cross-references: UNIPROT:Q9PMU1; UNIPARC:UPI000000C1EDC; GB:AL1139078; GB:AL1111168; NI  
A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj1358c

C:Superfamily: denitrification system component NapC/NirT (membrane-bound tetraheme cyto

Query Match 83.9%; Score 26; DB 2; Length 171;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6

Db 24 FVFFA 28

#### RESULT 46

T47707

hypothetical protein Fli16.90 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C:Accession: T47707

R:Benes, V.; Wurnbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.

submitted to the Protein Sequence Database, March 2000

A:Reference number: Z24473

A:Accession: T47707

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-183 <BEN>

A:Cross-references: UNIPROT:Q9M054; UNIPARC:UPI000000A218E; EMBL:AL161667

A:Experimental source: cultivar Columbia; BAC clone Fli16

C:Genetics:

A:Map position: 3

A:Introns: 70/3

A:Note: Fli16.90

Query Match 83.9%; Score 26; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6

Db 18 FVFFA 22

#### RESULT 47

A86806

transcription regulator [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)

C:Species: *Lactococcus lactis* subsp. *lactis*

C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004

C:Accession: A86806

R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrh

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: A86806

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-188 <STO>

A:Cross-references: UNIPROT:Q9CFL8; UNIPARC:UPI000000C6A3D; GB:AE005176; PID:g12724440;

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: yohC

Query Match 83.9%; Score 26; DB 2; Length 188;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

Db 170 KPIFF 174

#### RESULT 48



S73449  
MG028 homolog B01\_orf203 - Mycoplasma pneumoniae (strain ATCC 29342)  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C:Date: 26-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 05-Oct-2004  
C:Accession: S73449  
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirk1, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
A:Reference number: S73327; MUID:97105885; PMID:8948633  
A:Accession: S73449  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-203 <HIM>  
A:Cross-references: UNIPROT:P75083; UNIPARC:UPI000013912P; EMBL:AE000015; GB:U00089; NID  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Genetic code: SGC3  
C:Superfamily: uncharacterized conserved protein

Query Match 83.9%; Score 26; DB 2; Length 203;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||  
DB 89 FVFFA 93

RESULT 49  
G70437  
soluble hydrogenase small subunit - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Oct-2004  
C:Accession: G70437  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98156666; PMID:9537320  
A:Accession: G70437  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-216 <AQF>  
A:Cross-references: UNIPROT:O67529; UNIPARC:UPI0000056670; GB:AE000746; NID:g2983925; PI  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: shyS  
C:Superfamily: serine-pyruvate/aspartate aminotransferase

Query Match 83.9%; Score 26; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||  
DB 61 FVFFA 65

RESULT 50  
F86844  
hypothetical protein ybbD [imported] - Lactococcus lactis subsp. lactis (strain ILL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: F86844  
R:Solotkin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: F86844  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-218 <STO>

A:Cross-references: UNIPROT:Q9CES6; UNIPARC:UPI00000C6AFC; GB:AE005176; PID:g12724779; I  
A:Experimental source: strain ILL1403  
C:Genetics:  
A:Gene: ybbD  
C:Superfamily: dedA protein

Query Match 83.9%; Score 26; DB 2; Length 218;  
Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5  
|||  
DB 155 KPIFF 159

RESULT 51  
T22101  
hypothetical protein F42F12.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T22101  
R:Lloyd, C.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: Z19514  
A:Accession: T22101  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-243 <WIL>  
A:Cross-references: UNIPROT:Q20344; UNIPARC:UPI000007AEF3; EMBL:Z68116; PIDN:CAA92173.1;  
A:Experimental source: clone F42F12  
C:Genetics:  
A:Gene: CESP:F42F12.3  
A:Map position: X  
A:Introns: 85/2; 138/1; 222/2  
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

Query Match 83.9%; Score 26; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||  
DB 18 FVFFA 22

RESULT 52  
B81693  
conserved hypothetical protein TC0525 [imported] - Chlamydia muridarum (strain Nigg)  
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: B81693  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255; PMID:10684935  
A:Accession: B81693  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <TET>  
A:Cross-references: UNIPROT:Q9PKE0; UNIPARC:UPI0000057969; GB:AE002321; GB:AE002160; NIT  
A:Experimental source: strain Nigg (MoPn)  
C:Genetics:  
A:Gene: TC0525  
C:Superfamily: Chlamydia trachomatis hypothetical protein CT254

Query Match 83.9%; Score 26; DB 2; Length 255;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||  
DB 68 FVFFA 72

D81085  
 Htrb/MebB family protein NMB1418 [imported] - Neisseria meningitidis (strain MC58 serog  
 C;Species: Neisseria meningitidis  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 05-Oct-2004  
 C;Accession: D81085  
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. G.  
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.  
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.  
 Science 287, 1809-1815, 2000  
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V  
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
 A;Reference number: A81000; MUID:20175755; PMID:10710307  
 A;Accession: D81085  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-289 <TEST>  
 A;Cross-references: UNIPROT:Q9JYV2; UNIPARC:UPI00000C46B0; GB:AE002491; GB:AE002098; NI  
 A;Experimental source: serogroup B, strain MC58  
 C;Genetics:  
 A;Gene: NMB1418  
 C;Superfamily: lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase  
  
 Query Match 83.9%; Score 26; DB 2; Length 289;  
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 KFVFF 5  
 ||:||  
 Db 2 KFIFF 6

RESULT 56  
 A27692  
 sarcotoxin IIA precursor - flesh fly (Sarcophaga peregrina)  
 C;Species: Sarcophaga peregrina  
 C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 09-Jul-2004  
 C;Accession: A27692  
 R;Ando, K.; Natori, S.  
 Biochemistry 27, 1715-1721, 1988  
 A;Title: Molecular cloning, sequencing, and characterization of cDNA for sarcotoxin IIA  
 A;Reference number: A27692; MUID:88209545; PMID:2452654  
 A;Accession: A27692  
 A;Molecule type: mRNA  
 A;Residues: 1-294 <AND>  
 A;Cross-references: UNIPROT:P14667; UNIPARC:UPI0000135ECC; GB:M18873; NID:g161272; PID  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-294/Product: sarcotoxin IIA #status predicted <MAT>

Query Match 83.9%; Score 26; DB 2; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 FVFPA 6  
 |||||  
 Db 35 FVFPA 39

RESULT 54  
 B81857  
 probable acetyltransferase NMA1630 [imported] - Neisseria meningitidis (strain Z2491 ser  
 C;Species: Neisseria meningitidis  
 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-Oct-2004  
 C;Accession: B81857  
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 i; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A;Reference number: A81775; MUID:20225556; PMID:10761919  
 A;Accession: B81857  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-289 <PAR>  
 A;Cross-references: UNIPROT:Q9JUT4; UNIPARC:UPI00000C4C38; GB:AL162756; GB:AL157959; NID  
 A;Experimental source: serogroup A, strain Z2491  
 C;Genetics:  
 A;Gene: NMA1630  
 C;Superfamily: lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase

Query Match 83.9%; Score 26; DB 2; Length 289;  
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 KFVFF 5  
 ||:||  
 Db 2 KFIFF 6

RESULT 55

D81085  
 Htrb/MebB family protein NMB1418 [imported] - Neisseria meningitidis (strain MC58 serog  
 C;Species: Neisseria meningitidis  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 05-Oct-2004  
 C;Accession: D81085  
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. G.  
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.  
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.  
 Science 287, 1809-1815, 2000  
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V  
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
 A;Reference number: A81000; MUID:20175755; PMID:10710307  
 A;Accession: D81085  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-289 <TEST>  
 A;Cross-references: UNIPROT:Q9JYV2; UNIPARC:UPI00000C46B0; GB:AE002491; GB:AE002098; NI  
 A;Experimental source: serogroup B, strain MC58  
 C;Genetics:  
 A;Gene: NMB1418  
 C;Superfamily: lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase  
  
 Query Match 83.9%; Score 26; DB 2; Length 289;  
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 KFVFF 5  
 ||:||  
 Db 2 KFIFF 6

RESULT 56  
 A27692  
 sarcotoxin IIA precursor - flesh fly (Sarcophaga peregrina)  
 C;Species: Sarcophaga peregrina  
 C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 09-Jul-2004  
 C;Accession: A27692  
 R;Ando, K.; Natori, S.  
 Biochemistry 27, 1715-1721, 1988  
 A;Title: Molecular cloning, sequencing, and characterization of cDNA for sarcotoxin IIA  
 A;Reference number: A27692; MUID:88209545; PMID:2452654  
 A;Accession: A27692  
 A;Molecule type: mRNA  
 A;Residues: 1-294 <AND>  
 A;Cross-references: UNIPROT:P14667; UNIPARC:UPI0000135ECC; GB:M18873; NID:g161272; PID  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-294/Product: sarcotoxin IIA #status predicted <MAT>

Query Match 83.9%; Score 26; DB 2; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPA 6  
 |||||  
 Db 4 FVFPA 8

RESULT 57  
 B36351  
 sarcotoxin II-2 - flesh fly (Sarcophaga peregrina)  
 C;Species: Sarcophaga peregrina  
 C;Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 09-Jul-2004  
 C;Accession: B36351  
 R;Kanai, A.; Natori, S.  
 Mol. Cell. Biol. 10, 6114-6122, 1990  
 A;Title: Analysis of a gene cluster for sarcotoxin II, a group of antibacterial protein  
 A;Reference number: A36351; MUID:91061717; PMID:2247051  
 A;Accession: B36351  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-294 <KAN>  
 A;Cross-references: UNIPROT:P24489; UNIPARC:UPI0000135EC9; GB:D90153; NID:g217388; PID

```

Query Match      83.9%; Score 26; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
DB      4 FVFFA 8

RESULT 58
S75656
hypothetical protein slr1980 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75656
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75656
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-297 <KAN>
A:Cross-references: UNIPROT:P74131; UNIPARC:UPI00000C100A; EMBL:D90912; GB:AB001339; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      83.9%; Score 26; DB 2; Length 297;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFF 5
DB     104 KFIFP 108

RESULT 59
D86216
protein T23G18.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86216
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86216
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <STO>
A:Cross-references: UNIPROT:Q9SGD8; UNIPARC:UPI000009EE07; GB:AE005172; NID:G6579209; PI
C:Genetics:
A:Gene: T23G18.8
A:Map position: 1

Query Match      83.9%; Score 26; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
DB     99 FVFFA 103

```

```

RESULT 60
T24424
hypothetical protein T04A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24424
R:Palmer, S.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19889
A:Accession: T24424
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-324 <WIL>
A:Cross-references: UNIPROT:P46568; UNIPARC:UPI000006112C; EMBL:Z35663; PIDN:CAA84725.1
C:Experimental source: clone T04A8
C:Genetics:
A:Gene: CESP:T04A8.1
A:Map position: 3
A:Introns: 77/3; 150/3; 198/3; 259/3

Query Match      83.9%; Score 26; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
DB     262 FVFFA 266

RESULT 61
S08459
hypothetical protein 2 - Spiroplasma virus 1
C:Species: Spiroplasma virus 1, SpV1
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 02-Mar-2001
C:Accession: S08459; S08447
R:Renaudin, J.; Aulio, P.; Vignault, J.C.; Bove, J.M.
Nucleic Acids Res. 18, 1293, 1990
A:Title: Complete nucleotide sequence of the genome of Spiroplasma citri virus SpV1-R8A2
A:Reference number: S08447; MUID:90206799; PMID:2320423
A:Accession: S08459
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-337 <REN>
A:Cross-references: UNIPARC:UPI0000138546; EMBL:X51344
A:Accession: S08447
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 262-337 <RE2>
A:Cross-references: UNIPARC:UPI0000161B8D; EMBL:X51344; NID:G61993; PIDN:CAA35725.1; PID
C:Genetics:
A:Genetic code: SGC3

Query Match      83.9%; Score 26; DB 2; Length 337;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFF 5
DB      3 KFIFP 7

RESULT 62
E90564
potassium channel protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: E90564
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:1133084
A:Accession: E90564
A>Status: preliminary

```

A;Molecule type: DNA  
A;Residues: 1-344 <KUR>  
A;Cross-references: UNIPROT:Q98QES; UNIPARC:UPI00000D45DF; GB:AL445566; PID:gl4089835; R  
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion  
C;Experimental source: strain UAB CTIP  
C;Genetics:  
A;Gene: MYP1 4210  
A;Genetic code: SGC3

Query Match 83.9%; Score 26; DB 2; Length 344;  
Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5  
|||:  
315 KPIFF 319

Db

RESULT 63  
T34333  
hypothetical protein K06A1.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T34333  
R;Fulton, L.  
submitted to the EMBL Data Library, July 1995  
A;Description: The sequence of C. elegans cosmid K06A1.  
A;Reference number: Z21507  
A;Accession: T34333  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-381 <FUL>  
A;Cross-references: UNIPROT:Q09585; UNIPARC:UPI000007A4D5; EMBL:U23449; PIDN:AAC24296.1;  
A;Experimental source: strain Bristol N2; clone K06A1  
C;Genetics:  
A;Gene: CESP:K06A1.1  
A;Map position: 2  
A;Introns: 142/1; 214/2; 254/1; 343/3

Query Match 83.9%; Score 26; DB 2; Length 381;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPA 6  
|||:  
152 FVFPA 156

Db

RESULT 64  
S68155  
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - slime mold (Dictyostelium  
C;Species: mitochondrion Dictyostelium discoideum  
C;Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S68155; T43757  
R;Angata, K.; Kuroe, K.; Yanagisawa, K.; Tanaka, Y.  
Curr. Genet. 27, 249-256, 1995  
A;Title: Codon usage, genetic code and phylogeny of Dictyostelium discoideum mitochondria  
A;Reference number: S68155; MUID:95254668; PMID:7736610  
A;Accession: S68155  
A;Molecule type: DNA  
A;Residues: 1-389 <ANG>  
A;Cross-references: UNIPROT:Q37311; UNIPARC:UPI00001289A6; EMBL:D16466; NID:g6959590; PID  
A;Experimental source: strain AX3  
R;Ogawa, S.; Yoshino, R.; Angata, K.; Pi, M.; Iwamoto, M.; Kuroe, K.; Matsuo, K.; Morio,  
submitted to the EMBL Data Library, December 1996  
A;Description: The mitochondrial DNA of Dictyostelium discoideum. Complete sequence, gen  
A;Reference number: Z22666  
A;Accession: T43757  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-389 <OGA>  
A;Cross-references: UNIPARC:UPI00001289A6; EMBL:AB000109; PIDN:BAA78061.1  
C;Genetics:  
A;Gene: cytb

A;Genome: mitochondrion  
C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinone  
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion  
F;10-340/Domain: cytochrome b6 homology <CBH>  
F;10-210/Domain: cytochrome b6 homology <CB6>  
F;35-51/Domain: transmembrane #status predicted <TM1>  
F;80-98/Domain: transmembrane #status predicted <TM2>  
F;118-134/Domain: transmembrane #status predicted <TM3>  
F;179-201/Domain: transmembrane #status predicted <TM4>  
F;222-340/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>  
F;230-246/Domain: transmembrane #status predicted <TM5>  
F;289-305/Domain: transmembrane #status predicted <TM6>  
F;324-344/Domain: transmembrane #status predicted <TM7>  
F;354-370/Domain: transmembrane #status predicted <TM8>  
F;82,183/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted  
F;96,197/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 83.9%; Score 26; DB 2; Length 389;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPA 6  
|||:  
243 FVFPA 247

Db

RESULT 65  
T22810  
hypothetical protein F56H9.4 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T22810  
R;Burton, J.  
submitted to the EMBL Data Library, June 1996  
A;Reference number: Z19618  
A;Accession: T22810  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-390 <WIL>  
A;Cross-references: UNIPROT:Q20910; UNIPARC:UPI000007F97A; EMBL:Z74473; PIDN:CAA98953.1  
A;Experimental source: clone F56H9  
C;Genetics:  
A;Gene: CESP:F56H9.4  
A;Map position: 5  
A;Introns: 51/1; 65/2; 112/3; 229/2; 247/3; 278/3; 330/1; 370/3  
C;Superfamily: GTP-binding regulatory protein Gs alpha chain

Query Match 83.9%; Score 26; DB 2; Length 390;  
Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5  
|||:  
229 KPIFF 233

Db

RESULT 66  
T00516  
hypothetical protein At2g23160 [imported] - Arabidopsis thaliana  
N;Alternate names: hypothetical protein T20D16.21  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 31-Dec-2004  
C;Accession: T00516; C84621  
R;Roundley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau  
submitted to the EMBL Data Library, November 1997  
A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.  
A;Reference number: Z14164  
A;Accession: T00516  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-395 <ROU>  
A;Cross-references: UNIPROT:O22191; UNIPARC:UPI00000AAAFDA; EMBL:AC002391; NID:g2642427;  
A;Experimental source: cultivar Columbia

R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84621

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <STO>

A;Cross-references: UNIPARC:UPI00000A0A0A; GB:AE002093; NID:g2642447; PIDN:AAB87115.1; C

C;Genetics:

A;Gene: AC2923160; T20D16.21

A;Map position: 2

A;Introns: 295/3

A;Note: T20D16.21

C;Superfamily: hypothetical protein containing F-box domain

Query Match 83.9%; Score 26; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5

Db 245 KVFVF 249

RESULT 67

D81040

Cytochrome c-type biogenesis protein, probable NMB1803 [imported] - Neisseria meningitidis

C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C;Accession: D81040

R;Fetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Olin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: D81040

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <TET>

A;Cross-references: UNIPROT:Q9JY05; UNIPARC:UPI00000C47CE; GB:AE002530; GB:AE002098; NID

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB1803

Query Match 83.9%; Score 26; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFVFA 6

Db 120 FVFVFA 124

RESULT 68

B81986

Probable membrane protein NMA0660 [imported] - Neisseria meningitidis (strain Z2491 sero

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004

C;Accession: B81986

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel i Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Accession: B81986

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <PAR>

A;Cross-references: UNIPROT:Q9JVV9; UNIPARC:UPI00000C4A09; GB:AL162753; GB:AL157959; NID

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: NMA0660

Query Match 83.9%; Score 26; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFVFA 6

Db 120 FVFVFA 124

## RESULT 69

T46710

multidrug resistance transporter [imported] - Listeria monocytogenes

C;Species: Listeria monocytogenes

C;Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004

C;Accession: T46710

R;Huillet, E.E.H.; Larpin, S.; Pardon, P.; Berche, P.

FEMS Microbiol. Lett. 174, 265-272, 1999

A;Title: Identification of a new locus in Listeria monocytogenes involved in cellobiose-

A;Reference number: Z23136; MUID:99271176; PMID:10339818

A;Accession: T46710

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-397 &lt;HUI&gt;

A;Cross-references: UNIPROT:Q9X769; UNIPARC:UPI0000055470; EMBL:AJ009627; NID:g4914621;

C;Genetics:

A;Gene: lltB

Query Match 83.9%; Score 26; DB 2; Length 397;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFVFA 6

Db 245 FVFVFA 249

## RESULT 70

AE1613

multidrug-efflux transporter homolog lin1446 [imported] - Listeria innocua (strain Clip1

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AE1613

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AE1613

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-397 &lt;GLA&gt;

A;Cross-references: UNIPROT:Q92B08; UNIPARC:UPI00000CC57B; GB:AL592022; PIDN:CAC96677.1;

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: lin1446

Query Match 83.9%; Score 26; DB 2; Length 397;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFVFA 6

Db 245 FVFVFA 249

RESULT 71  
A11250  
multidrug-efflux transporter homolog lmo1409 [imported] - Listeria monocytogenes (strain  
C;Species: Listeria monocytogenes  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: A11250  
R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Feihl, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A;Title: Comparative Genomics of Listeria species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: A11250  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-397 <GLA>  
A;Cross-references: UNIPROT:Q9X769; UNIPARC:UPI0000055470; GB:NC\_003210; PIDN:CAC99487.1  
A;Experimental source: strain EGD-e  
C;Genetics:  
A;Gene: lmo1409

Query Match 83.9%; Score 26; DB 2; Length 397;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||||  
DB 245 FVFFA 249

RESULT 72  
T44331  
hypothetical protein wbld [imported] - Vibrio cholerae  
C;Species: Vibrio cholerae  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T44331  
R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.  
Gene 237, 321-332, 1999  
A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae O139 are close  
A;Reference number: 222749; MUID:99453293; PMID:10521656  
A;Accession: T44331  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-398 <YAM>  
A;Cross-references: UNIPROT:O87160; UNIPARC:UPI00000B5419; EMBL:AB012957; NID:G4115688;  
A;Experimental source: strain 022  
C;Genetics:  
A;Note: wbld

Query Match 83.9%; Score 26; DB 2; Length 398;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||||  
DB 263 FVFFA 267

RESULT 73  
H69833  
conserved hypothetical protein yhjI - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: H69833  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin  
ois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecell  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: H69833

A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-401 <KUN>  
A;Cross-references: UNIPROT:O07563; UNIPARC:UPI00000601AF; GB:Z99109; GB:AL009126; NID:  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: yhjI

Query Match 83.9%; Score 26; DB 2; Length 401;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||||  
DB 215 FVFFA 219

RESULT 74  
C95990  
probable sugar uptake ABC transporter permease protein ggub [imported] - Sinorhizobium  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: C95990  
C;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna  
Proc. Natl. Acad. Sci. U.S.A. 98, 9899-9894, 2001  
A;Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing end  
A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: C95990  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-404 <KUR>  
A;Cross-references: UNIPROT:Q92UE4; UNIPARC:UPI00000CB7A2; GB:AL591985; PIDN:CAC49587.1  
A;Experimental source: strain 1021, megaplasmid pSymb  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure  
hebaute, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104

C;Contents: annotation  
C;Genetics:  
A;Gene: ggub; SM520893  
A;Genome: plasmid  
C;Superfamily: 1-arabinose transport system permease arah

Query Match 83.9%; Score 26; DB 2; Length 404;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||||  
DB 223 FVFFA 227

RESULT 75  
CBQFR  
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Rhodospirillum rubrum  
C;Species: Rhodospirillum rubrum  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C;Accession: S12257; A38814  
R;Majewski, C.; Trebst, A.

Mol. Gen. Genet. 224, 373-382, 1990  
A;Title: The pet genes of Rhodospirillum rubrum: cloning and sequencing of the genes for  
A;Reference number: S12255; MUID:91094774; PMID:2176269  
A;Accession: S12257  
A;Molecule type: DNA  
A;Residues: 1-405 <NA1>  
A;Cross-references: UNIPROT:P231134; UNIPARC:UPI0000128ACD; EMBL:X55387; NID:g46382; PIDN  
A;Note: the authors translated the codon AAT for residue 161 as Leu and CTG for residue  
A;Accession: A38914  
A;Molecule type: protein  
A;Residues: 1-26, 'E', <NA2>  
A;Cross-references: UNIPARC:UPI0000171D0F  
C;Genetics:  
A;Gene: petB  
C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol  
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; oxidoreductase  
F;1-405/Product: cytochrome b #status experimental <NA1>  
F;22-354/Domain: cytochrome b homology <CBH>  
F;22-222/Domain: cytochrome b6 homology <CH6>  
F;47-63/Domain: transmembrane #status predicted <TM1>  
F;92-110/Domain: transmembrane #status predicted <TM2>  
F;130-146/Domain: transmembrane #status predicted <TM3>  
F;191-213/Domain: transmembrane #status predicted <TM4>  
F;236-354/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>  
F;244-260/Domain: transmembrane #status predicted <TM5>  
F;303-319/Domain: transmembrane #status predicted <TM6>  
F;338-356/Domain: transmembrane #status predicted <TM7>  
F;368-384/Domain: transmembrane #status predicted <TM8>  
F;94,195/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted  
F;108,209/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 83.9%; Score 26; DB 1; Length 405;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6  
|||  
Db 257 FVFFA 261

Search completed: December 29, 2005, 17:49:11  
Job time : 17.9677 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds  
(without alignments)  
13.656 Million cell updates/sec

Title: US-10-009-122-4

Perfect score: 31

Sequence: 1 KPVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubaa/US03\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	87.1	582	7 US-11-090-439-58	Sequence 58, Appl
2	27	87.1	592	6 US-10-467-657-4888	Sequence 4888, Ap
3	27	87.1	738	7 US-11-147-047-48	Sequence 48, Appl
4	27	87.1	1070	7 US-11-147-047-49	Sequence 49, Appl
5	26	83.9	19	6 US-10-467-657-8712	Sequence 8712, Ap
6	26	83.9	220	6 US-10-467-657-3154	Sequence 3154, Ap
7	26	83.9	299	6 US-10-467-657-2190	Sequence 2190, Ap
8	26	83.9	395	6 US-10-467-657-1950	Sequence 1950, Ap
9	26	83.9	418	6 US-10-467-657-5788	Sequence 5788, Ap
10	25	80.6	19	6 US-10-923-605-5	Sequence 5, Appli
11	25	80.6	19	6 US-10-934-818-5	Sequence 5, Appli
12	25	80.6	40	7 US-11-016-706-36	Sequence 36, Appl
13	25	80.6	40	7 US-11-016-706-12	Sequence 12, Appl
14	25	80.6	42	6 US-10-923-605-1	Sequence 1, Appli
15	25	80.6	42	6 US-10-934-818-1	Sequence 1, Appli
16	25	80.6	42	7 US-11-016-706-37	Sequence 37, Appl
17	25	80.6	43	6 US-10-934-818-6	Sequence 6, Appli
18	25	80.6	43	6 US-10-250-581-1	Sequence 1, Appli
19	25	80.6	43	6 US-10-250-581-1	Sequence 1, Appli
20	25	80.6	184	6 US-10-467-657-7560	Sequence 7560, Ap
21	25	80.6	525	7 US-11-082-389-350	Sequence 350, App
22	25	80.6	770	6 US-10-982-545-15	Sequence 15, Appl
23	25	80.6	770	6 US-10-789-273-38	Sequence 38, Appl
24	24	77.4	194	6 US-10-467-657-3978	Sequence 3978, Ap
25	24	77.4	229	6 US-10-793-626-62	Sequence 62, Appl

Sequence 1860, Ap  
Sequence 4566, Ap  
Sequence 48, Appl  
Sequence 4242, Ap  
Sequence 1120, Ap  
Sequence 1370, Ap  
Sequence 2308, Ap  
Sequence 5610, Ap  
Sequence 7516, Ap  
Sequence 8322, Ap  
Sequence 8286, Ap  
Sequence 2766, Ap  
Sequence 304, App  
Sequence 1034, Ap  
Sequence 4456, Ap  
Sequence 13, Appl  
Sequence 4858, Ap  
Sequence 1096, Ap  
Sequence 186, App  
Sequence 678, App  
Sequence 348, App  
Sequence 3440, Ap  
Sequence 4632, Ap  
Sequence 125, App  
Sequence 917, App  
Sequence 420, App  
Sequence 908, App  
Sequence 760, App  
Sequence 8998, Ap  
Sequence 378, App  
Sequence 850, App  
Sequence 360, App  
Sequence 2026, Ap  
Sequence 286, App  
Sequence 6824, Appl  
Sequence 24, Appl  
Sequence 6110, Ap  
Sequence 7550, Ap  
Sequence 6130, Ap  
Sequence 346, App  
Sequence 65, Appl  
Sequence 4386, Ap  
Sequence 3000, Ap  
Sequence 6248, Ap  
Sequence 1391, Ap  
Sequence 66, Appl  
Sequence 1124, Ap  
Sequence 6144, Ap  
Sequence 1178, Ap  
Sequence 5704, Ap  
Sequence 85, Appl  
Sequence 33, Appl  
Sequence 1, Appli  
Sequence 147, App  
Sequence 124, App  
Sequence 504, App  
Sequence 1379, Ap  
Sequence 6, Appli  
Sequence 2872, Ap  
Sequence 9, Appli  
Sequence 400, App  
Sequence 492, App  
Sequence 490, App  
Sequence 2260, Ap  
Sequence 2026, Ap  
Sequence 7578, Ap  
Sequence 1606, Ap  
Sequence 1676, Ap  
Sequence 599, App  
Sequence 952, App  
Sequence 120, App  
Sequence 604, App



99	22	71.0	528	6	US-10-864-758-7	Sequence 7, Appli	172	21	67.7	652	6	US-10-873-528-26	Sequence 26, Appl
100	22	71.0	541	7	US-11-000-463-238	Sequence 238, App	173	21	67.7	658	6	US-10-873-528-17	Sequence 17, Appl
101	22	71.0	566	6	US-10-467-657-8046	Sequence 8046, Ap	174	21	67.7	676	6	US-10-510-947-1	Sequence 1, Appli
102	22	71.0	578	6	US-11-083-800-2	Sequence 2, Appli	175	21	67.7	677	6	US-10-873-528-155	Sequence 155, App
103	22	71.0	607	7	US-11-080-991-88	Sequence 88, Appl	176	21	67.7	697	6	US-10-485-517-202	Sequence 202, App
104	22	71.0	709	6	US-10-131-826A-202	Sequence 202, App	177	21	67.7	756	6	US-10-467-657-8694	Sequence 8694, Ap
105	22	71.0	786	6	US-10-467-962B-103	Sequence 103, App	178	21	67.7	801	6	US-10-793-626-2020	Sequence 2020, Ap
106	22	71.0	790	6	US-10-131-826A-204	Sequence 204, App	179	21	67.7	837	7	US-11-094-519A-43	Sequence 43, Appl
107	22	71.0	943	6	US-10-821-234-1012	Sequence 1012, Ap	180	21	67.7	845	7	US-11-094-519A-42	Sequence 42, Appl
108	22	71.0	1062	6	US-10-821-234-1079	Sequence 1079, Ap	181	21	67.7	1052	6	US-10-467-657-3392	Sequence 3392, Ap
109	22	71.0	1070	6	US-11-000-463-721	Sequence 721, App	182	21	67.7	1076	6	US-10-467-657-5708	Sequence 5708, Ap
110	22	71.0	1194	7	US-11-000-463-249	Sequence 249, App	183	21	67.7	1170	7	US-11-080-026-2	Sequence 2, Appli
111	21	67.7	5	7	US-11-098-674-1	Sequence 1, Appli	184	21	67.7	1170	7	US-11-107-028-4	Sequence 4, Appli
112	21	67.7	39	6	US-10-467-657-4630	Sequence 4630, Ap	185	21	67.7	1751	7	US-11-103-957-45	Sequence 45, Appl
113	21	67.7	40	6	US-10-467-657-4616	Sequence 4616, Ap	186	20	64.5	16	7	US-11-089-764-65	Sequence 65, Appl
114	21	67.7	43	6	US-10-467-657-8642	Sequence 8642, Ap	187	20	64.5	16	7	US-11-089-764-66	Sequence 66, Appl
115	21	67.7	47	6	US-10-467-657-5436	Sequence 5436, Ap	188	20	64.5	23	7	US-11-085-812-16	Sequence 16, Appl
116	21	67.7	55	6	US-10-485-517-387	Sequence 387, App	189	20	64.5	28	6	US-10-250-581-14	Sequence 14, Appl
117	21	67.7	57	7	US-11-000-463-770	Sequence 770, App	190	20	64.5	28	6	US-10-250-581-17	Sequence 17, Appl
118	21	67.7	63	7	US-11-000-463-353	Sequence 353, App	191	20	64.5	28	6	US-10-250-581-14	Sequence 14, Appl
119	21	67.7	63	7	US-11-000-463-825	Sequence 825, App	192	20	64.5	28	6	US-10-250-581-17	Sequence 17, Appl
120	21	67.7	72	6	US-10-467-657-5578	Sequence 5578, Ap	193	20	64.5	40	6	US-10-250-581-15	Sequence 15, Appl
121	21	67.7	72	7	US-11-000-463-298	Sequence 298, App	194	20	64.5	40	6	US-10-250-581-18	Sequence 18, Appl
122	21	67.7	75	6	US-10-467-657-8472	Sequence 8472, Ap	195	20	64.5	40	6	US-10-250-581-15	Sequence 15, Appl
123	21	67.7	79	7	US-11-123-896-134	Sequence 134, App	196	20	64.5	40	6	US-10-250-581-18	Sequence 18, Appl
124	21	67.7	90	6	US-10-467-657-4374	Sequence 4374, Ap	197	20	64.5	42	6	US-10-250-581-16	Sequence 16, Appl
125	21	67.7	91	6	US-10-821-234-1238	Sequence 1238, Ap	198	20	64.5	42	6	US-10-250-581-16	Sequence 16, Appl
126	21	67.7	94	6	US-10-467-657-4730	Sequence 4730, Ap	199	20	64.5	42	6	US-10-250-581-19	Sequence 19, Appl
127	21	67.7	102	6	US-10-467-657-5604	Sequence 5604, Ap	200	20	64.5	42	6	US-10-250-581-19	Sequence 19, Appl
128	21	67.7	113	6	US-10-793-626-1848	Sequence 1848, Ap	201	20	64.5	44	6	US-10-467-657-1118	Sequence 1118, Ap
129	21	67.7	120	6	US-10-793-626-2376	Sequence 2376, Ap	202	20	64.5	45	6	US-10-467-657-8968	Sequence 8968, Ap
130	21	67.7	140	6	US-10-982-145-66	Sequence 66, Appl	203	20	64.5	50	6	US-10-467-657-7892	Sequence 7892, Ap
131	21	67.7	141	6	US-10-982-145-67	Sequence 67, Appl	204	20	64.5	54	6	US-10-467-657-2264	Sequence 2264, Ap
132	21	67.7	164	6	US-10-467-657-1450	Sequence 1450, Ap	205	20	64.5	54	6	US-10-467-657-4378	Sequence 4378, Ap
133	21	67.7	168	6	US-10-927-641-69	Sequence 69, Appl	206	20	64.5	56	6	US-10-467-657-1050	Sequence 1050, Ap
134	21	67.7	182	6	US-10-793-626-724	Sequence 724, App	207	20	64.5	66	6	US-10-467-657-766	Sequence 766, App
135	21	67.7	182	6	US-10-467-657-8302	Sequence 8302, Ap	208	20	64.5	79	7	US-11-080-991-10	Sequence 10, Appl
136	21	67.7	183	7	US-11-069-642-125	Sequence 125, App	209	20	64.5	92	6	US-10-467-657-5352	Sequence 5352, Ap
137	21	67.7	198	6	US-10-467-657-5440	Sequence 5440, Ap	210	20	64.5	105	6	US-10-467-657-9209	Sequence 9209, Ap
138	21	67.7	220	6	US-10-793-626-1822	Sequence 1822, Ap	211	20	64.5	115	6	US-10-793-626-1554	Sequence 1554, Ap
139	21	67.7	227	6	US-10-793-626-2396	Sequence 2396, Ap	212	20	64.5	120	6	US-10-467-657-6982	Sequence 6982, Ap
140	21	67.7	227	6	US-10-793-626-2362	Sequence 2643, Ap	213	20	64.5	120	6	US-10-467-657-7938	Sequence 7938, Ap
141	21	67.7	233	6	US-10-467-657-8268	Sequence 8268, Ap	214	20	64.5	123	6	US-10-821-234-988	Sequence 988, App
142	21	67.7	235	7	US-11-188-473-2	Sequence 2, Appli	215	20	64.5	123	6	US-10-467-657-6378	Sequence 6378, Ap
143	21	67.7	246	7	US-11-092-140-111	Sequence 111, App	216	20	64.5	127	7	US-11-106-796-10	Sequence 10, Appl
144	21	67.7	247	7	US-11-103-957-69	Sequence 69, Appl	217	20	64.5	129	6	US-10-501-039-8	Sequence 8, Appli
145	21	67.7	248	7	US-11-076-164-9	Sequence 9, Appli	218	20	64.5	135	6	US-10-793-626-2284	Sequence 2284, Ap
146	21	67.7	269	6	US-10-467-657-330	Sequence 330, App	219	20	64.5	138	6	US-10-793-626-1254	Sequence 1254, Ap
147	21	67.7	286	6	US-10-793-626-2192	Sequence 2192, Ap	220	20	64.5	150	6	US-10-793-626-2324	Sequence 2324, Ap
148	21	67.7	294	7	US-11-055-822-480	Sequence 480, App	221	20	64.5	154	7	US-11-082-389-424	Sequence 424, App
149	21	67.7	294	7	US-11-055-822-3884	Sequence 880, App	222	20	64.5	155	6	US-10-467-657-2420	Sequence 2420, Ap
150	21	67.7	298	6	US-10-454-437-384	Sequence 384, App	223	20	64.5	160	7	US-11-009-939-44	Sequence 44, Appl
151	21	67.7	298	7	US-11-055-822-478	Sequence 478, App	224	20	64.5	166	6	US-10-821-234-1293	Sequence 1293, Ap
152	21	67.7	298	7	US-11-055-822-878	Sequence 878, App	225	20	64.5	166	6	US-10-878-556A-20	Sequence 20, Appl
153	21	67.7	301	6	US-10-793-626-206	Sequence 206, App	226	20	64.5	174	6	US-10-793-626-1520	Sequence 1520, Ap
154	21	67.7	355	6	US-10-467-657-7996	Sequence 7996, Ap	227	20	64.5	183	6	US-11-100-183-27	Sequence 27, Appl
155	21	67.7	400	6	US-10-793-626-1056	Sequence 1056, Ap	228	20	64.5	188	7	US-10-467-657-6906	Sequence 6906, Ap
156	21	67.7	403	7	US-11-109-156-29	Sequence 29, Appl	229	20	64.5	190	6	US-10-467-657-3436	Sequence 3436, Ap
157	21	67.7	407	6	US-10-821-234-1389	Sequence 1389, Ap	230	20	64.5	193	6	US-10-793-626-1340	Sequence 1340, Ap
158	21	67.7	419	7	US-11-084-624-18	Sequence 18, Appl	231	20	64.5	196	6	US-10-131-826A-168	Sequence 168, App
159	21	67.7	452	6	US-10-793-626-3092	Sequence 3092, Ap	232	20	64.5	196	6	US-10-793-626-2584	Sequence 2584, Ap
160	21	67.7	464	6	US-10-689-742-164	Sequence 164, App	233	20	64.5	201	5	US-09-940-308-5	Sequence 5, Appli
161	21	67.7	490	7	US-11-074-176-316	Sequence 316, App	234	20	64.5	211	6	US-10-821-234-1372	Sequence 1372, Ap
162	21	67.7	495	7	US-11-074-176-60	Sequence 60, Appl	235	20	64.5	211	6	US-10-467-657-6932	Sequence 6932, Ap
163	21	67.7	502	6	US-10-821-234-1554	Sequence 1554, Ap	236	20	64.5	215	6	US-10-131-826A-4	Sequence 4, Appli
164	21	67.7	514	6	US-10-467-657-2664	Sequence 2664, Ap	237	20	64.5	215	6	US-10-131-826A-488	Sequence 488, App
165	21	67.7	514	7	US-11-103-037-3	Sequence 3, Appli	238	20	64.5	215	7	US-11-080-991-112	Sequence 112, App
166	21	67.7	515	6	US-10-630-203-6	Sequence 6, Appli	239	20	64.5	221	6	US-10-793-626-1392	Sequence 1392, Ap
167	21	67.7	521	6	US-10-793-626-532	Sequence 532, App	240	20	64.5	221	6	US-10-793-626-2420	Sequence 2420, Ap
168	21	67.7	526	6	US-10-606-302-5	Sequence 5, Appli	241	20	64.5	228	6	US-10-793-626-360	Sequence 360, App
169	21	67.7	526	6	US-10-606-302-7	Sequence 7, Appli	242	20	64.5	228	6	US-10-793-626-488	Sequence 488, App
170	21	67.7	528	6	US-10-793-626-1930	Sequence 1930, Ap	243	20	64.5	228	6	US-10-467-657-568	Sequence 568, App
171	21	67.7	537	6	US-10-467-657-6958	Sequence 6958, Ap	244	20	64.5	228	6	US-10-467-657-4838	Sequence 4838, Ap

245	20	64.5	233	6	US-10-821-234-1322	Sequence 1322, Ap
246	20	64.5	234	6	US-10-793-626-192	Sequence 192, App
247	20	64.5	235	6	US-10-467-657-7884	Sequence 7884, Ap
248	20	64.5	263	6	US-10-510-386-234	Sequence 234, App
249	20	64.5	275	4	US-11-110-977-4	Sequence 4, Appli
250	20	64.5	276	6	US-11-112-882-86	Sequence 86, Appli
251	20	64.5	277	6	US-10-454-437-8	Sequence 8, Appli
252	20	64.5	277	7	US-11-055-822-608	Sequence 608, App
253	20	64.5	281	6	US-10-821-234-1080	Sequence 1080, Ap
254	20	64.5	288	6	US-10-467-657-1272	Sequence 1272, Ap
255	20	64.5	291	7	US-11-102-883-22	Sequence 22, Appl
256	20	64.5	292	7	US-11-102-883-22	Sequence 24, Appl
257	20	64.5	294	6	US-10-467-657-7686	Sequence 7686, Ap
258	20	64.5	294	6	US-11-112-882-85	Sequence 85, Appl
259	20	64.5	295	7	US-11-091-100-2	Sequence 2, Appli
260	20	64.5	298	7	US-11-085-812-4	Sequence 3, Appli
261	20	64.5	304	7	US-11-112-882-3	Sequence 3, Appli
262	20	64.5	306	6	US-10-467-657-7222	Sequence 7222, Ap
263	20	64.5	311	6	US-10-793-626-2450	Sequence 2450, Ap
264	20	64.5	319	6	US-10-131-826A-134	Sequence 134, App
265	20	64.5	321	6	US-10-467-657-2504	Sequence 2504, Ap
266	20	64.5	323	6	US-10-467-657-556	Sequence 556, App
267	20	64.5	324	6	US-10-793-626-1282	Sequence 1282, Ap
268	20	64.5	324	6	US-10-467-657-7692	Sequence 7692, Ap
269	20	64.5	324	6	US-10-467-657-8440	Sequence 8440, Ap
270	20	64.5	325	6	US-09-940-308-8	Sequence 8, Appli
271	20	64.5	325	6	US-10-454-437-142	Sequence 142, App
272	20	64.5	330	7	US-11-085-812-2	Sequence 2, Appli
273	20	64.5	335	6	US-10-467-657-3818	Sequence 3818, Ap
274	20	64.5	337	6	US-10-875-716-2	Sequence 2, Appli
275	20	64.5	338	6	US-10-467-657-136	Sequence 136, App
276	20	64.5	338	6	US-10-467-657-6798	Sequence 6798, Ap
277	20	64.5	338	6	US-10-878-556A-19	Sequence 19, Appl
278	20	64.5	344	6	US-10-131-826A-376	Sequence 376, App
279	20	64.5	347	6	US-10-467-657-2014	Sequence 2014, Ap
280	20	64.5	350	6	US-10-485-517-288	Sequence 288, App
281	20	64.5	350	7	US-11-095-624-2	Sequence 2, Appli
282	20	64.5	350	7	US-11-095-624-3	Sequence 3, Appli
283	20	64.5	350	7	US-11-095-624-4	Sequence 4, Appli
284	20	64.5	351	7	US-11-095-624-5	Sequence 5, Appli
285	20	64.5	353	7	US-11-060-023-2	Sequence 2, Appli
286	20	64.5	353	7	US-11-060-023-4	Sequence 4, Appli
287	20	64.5	353	7	US-11-060-023-6	Sequence 6, Appli
288	20	64.5	353	7	US-11-060-023-8	Sequence 8, Appli
289	20	64.5	353	7	US-11-060-023-12	Sequence 12, Appl
290	20	64.5	353	7	US-11-060-023-14	Sequence 14, Appl
291	20	64.5	353	7	US-11-060-023-15	Sequence 15, Appl
292	20	64.5	353	7	US-10-460-023-16	Sequence 16, Appl
293	20	64.5	355	6	US-10-454-437-102	Sequence 102, App
294	20	64.5	356	7	US-11-055-822-972	Sequence 972, App
295	20	64.5	356	7	US-11-055-822-1052	Sequence 1052, App
296	20	64.5	359	7	US-11-060-023-11	Sequence 11, Appl
297	20	64.5	359	7	US-11-060-023-13	Sequence 13, Appl
298	20	64.5	360	7	US-11-060-023-17	Sequence 17, Appl
299	20	64.5	378	7	US-11-080-091-3	Sequence 3, Appli
300						

## ALIGNMENTS

```

RESULT 1
US-11-090-439-58
; Sequence 58, Application US/11090439
; Publication No. US20050266442A1
; GENERAL INFORMATION:
; APPLICANT: Squillace, Rachel
; APPLICANT: Weiner, Michael P.
; TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
; TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
; FILE REFERENCES: 24318-502
; CURRENT APPLICATION NUMBER: US/11/090,439
; CURRENT FILING DATE: 2005-03-25

```

```

1 PRIOR APPLICATION NUMBER: 60/556,344
2
3 PRIOR FILING DATE: 2004-03-25
4
5 NUMBER OF SEQ ID NOS: 62
6
7 SOFTWARE: PatentIn Ver. 2.1
8
9 SEQ ID NO 58
10
11 LENGTH: 582
12
13 TYPE: PRT
14
15 ORGANISM: Homo sapiens
16
17 US-11-090-439-58

```

Query Match 87.1%; Score 27; DB 7; Length 582;  
Best Local Similarity 100.0%; Pred.No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels

Qy 1 KFVFF 5  
Db 378 KFVFF 382

```

RESULT 2
US-10-467-657-4888
; Sequence 4888, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCES:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 4888
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4888

```

Query Match 87.1%; Score 27; DB 6; Length 592;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 5: Conservative 0; Mismatches 0; Indels

Qy 1 KFVF 5  
557 KFVF 561

```

RESULT 3
US-11-147-047-48
; Sequence 48, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rivzi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874

```

```

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-48

```

```

Query Match      87.1%; Score 27; DB 7; Length 738;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVFVF 5
Db      184 KVFVF 188

```

```

RESULT 4
US-11-147-047-49
; Sequence 49, Application US/11147047
; Publication No. US20050260668A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-49

```

```

Query Match      87.1%; Score 27; DB 7; Length 1070;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVFVF 5
Db      244 KVFVF 248

```

```

RESULT 5
US-10-467-657-8712
; Sequence 8712, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia

```

```

; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8712
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8712

```

```

Query Match      83.9%; Score 26; DB 6; Length 19;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVFVF 5
Db      15 KVFVF 19

```

```

RESULT 6
US-10-467-657-3154
; Sequence 3154, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3154
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3154

```

```

Query Match      83.9%; Score 26; DB 6; Length 220;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 FVFVF 6
Db      204 FVFVF 208

```

```

RESULT 7
US-10-467-657-2190
; Sequence 2190, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8

```

; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2190  
; LENGTH: 299  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2190

Query Match 83.9%; Score 26; DB 6; Length 299;  
Best Local Similarity 80.0%; Pred. No. 64;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5  
Db 12 KFIFP 16

RESULT 8  
US-10-467-657-1950  
; Sequence 1950, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 1950  
; LENGTH: 395  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1950

Query Match 83.9%; Score 26; DB 6; Length 395;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6  
Db 120 FVFFA 124

RESULT 9  
US-10-467-657-5788  
; Sequence 5788, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 5788  
; LENGTH: 418  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-5788

Query Match 83.9%; Score 26; DB 6; Length 418;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6  
Db 337 FVFFA 341

RESULT 10  
US-10-923-605-5  
; Sequence 5, Application US/10923605  
; Publication No. US20050249727A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004740US  
; CURRENT APPLICATION NUMBER: US/10/923,605  
; CURRENT FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: US/09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-10-923-605-5

Query Match 80.6%; Score 25; DB 6; Length 19;  
Best Local Similarity 83.3%; Pred. No. 8;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KFVFFA 6  
Db 4 KLVFFA 9

RESULT 11  
US-10-934-818-5  
; Sequence 5, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue

```
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match      80.6%; Score 25; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      | | | | |
Db      4 KLVFFA 9

RESULT 12
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36
```

```
Query Match      80.6%; Score 25; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      | | | | |
Db      16 KLVFFA 21

RESULT 13
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elmova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; FILE REFERENCE: PTO-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match      80.6%; Score 25; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      | | | | |
Db      16 KLVFFA 21

RESULT 14
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match      80.6%; Score 25; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
      | | | | |
Db      16 KLVFFA 21

RESULT 15
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match      80.6%; Score 25; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 KVFVFA 6  
|  
Db 16 KLVFFA 21

## RESULT 16

US-11-016-706-37  
; Sequence 37, Application US/11016706  
; Publication No. US20050244334A1  
; GENERAL INFORMATION:  
; APPLICANT: CASTILLO, GERARDO  
; APPLICANT: LAKE, THOMAS P.  
; APPLICANT: NGUYEN, BETH P.  
; APPLICANT: SANDERS, VIRGINIA J.  
; APPLICANT: SNOW, ALAN D.  
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS  
; FILE REFERENCE: PROTO.F03C13  
; CURRENT APPLICATION NUMBER: US/11/016,706  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 09/962,955  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 37  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-016-706-37

Query Match 80.6%; Score 25; DB 7; Length 42;  
Best Local Similarity 83.3%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
|  
Db 16 KLVFFA 21

## RESULT 17

US-10-934-818-6  
; Sequence 6, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide  
US-10-934-818-6

Query Match 80.6%; Score 25; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
|  
Db 16 KLVFFA 21

## RESULT 18

US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 80.6%; Score 25; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
|  
Db 16 KLVFFA 21

## RESULT 19

US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 80.6%; Score 25; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6  
|  
Db 16 KLVFFA 21

## RESULT 20

US-10-467-657-7560  
; Sequence 7560, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11

```
; PRIOR APPLICATION NUMBER: CB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7560
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7560
```

```
Query Match      80.6%; Score 25; DB 6; Length 184;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KPVFFA 6
      |||||
DB      91 KVFVLA 96
```

```
RESULT 21
US-11-082-389-350
; Sequence 350, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 350
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-350
```

```
Query Match      80.6%; Score 25; DB 7; Length 525;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVFFA 6
      |:|:|
DB      230 KVFVFA 235
```

```
RESULT 22
```

```
US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
```

```
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3 (42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3 (40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF (59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF (57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF (50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; US-10-982-545-15

Query Match      80.6%; Score 25; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 687 KLVFFA 692

RESULT 23
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basl, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-789-273-38

Query Match      80.6%; Score 25; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 687 KLVFFA 692

RESULT 24
US-10-467-657-3978
; Sequence 3978, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3978
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-3978

Query Match      77.4%; Score 24; DB 6; Length 194;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 13 RPAPFA 18

RESULT 25
US-10-793-626-62
; Sequence 62, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-10-793-626-62

Query Match      77.4%; Score 24; DB 6; Length 229;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFF 5
Db 59 KVFVF 63

RESULT 26
US-10-793-626-1860
; Sequence 1860, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
```



```

; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1860
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1860

Query Match      77.4%; Score 24; DB 6; Length 443;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
Db      168 KVVFF 172

RESULT 27
US-10-467-657-4566
; Sequence 4566, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4566
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4566

Query Match      77.4%; Score 24; DB 6; Length 533;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      165 KVVFFA 170

RESULT 28
US-11-080-991-48
; Sequence 48, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Velby, Pette Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 657

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-48

Query Match      77.4%; Score 24; DB 7; Length 657;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
Db      90 KVVFF 94

RESULT 29
US-10-467-657-4242
; Sequence 4242, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4242
; LENGTH: 916
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4242

Query Match      77.4%; Score 24; DB 6; Length 916;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      655 KVVFFA 660

RESULT 30
US-10-821-234-1120
; Sequence 1120, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1120
; LENGTH: 4384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1120

Query Match      77.4%; Score 24; DB 6; Length 4384;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
Qy      1 KFVFFA 6
Db      1320 KFVFFA 1325

RESULT 31
US-10-467-657-1370
; Sequence 1370, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1370
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1370

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFFA 6
Db      23 FVFFS 27

RESULT 32
US-10-467-657-2308
; Sequence 2308, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2308
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2308

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFFA 6
Db      23 FVFFS 27

RESULT 33
US-10-467-657-5610
; Sequence 5610, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5610
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5610

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFFA 6
Db      23 FVFFS 27

RESULT 34
US-10-467-657-7516
; Sequence 7516, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7516
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7516

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFFA 6
Db      23 FVFFS 27

RESULT 35
US-10-467-657-8322
; Sequence 8322, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
```

```
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8322
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8322
```

```
Query Match          74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 FVFFA 6
Db      23 FVFFS 27
```

```
RESULT 36
US-10-467-657-4324
; Sequence 4324, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4324
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4324
```

```
Query Match          74.2%; Score 23; DB 6; Length 54;
Best Local Similarity 80.0%; Pred. No. 53;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 FVFFA 6
Db      44 FVFFS 48
```

```
RESULT 37
US-10-467-657-8286
; Sequence 8286, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
```

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8286
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8286
```

```
Query Match          74.2%; Score 23; DB 6; Length 56;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 FVFFA 6
Db      30 FVFFS 34
```

```
RESULT 38
US-10-793-626-2766
; Sequence 2766, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2766
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2766
```

```
Query Match          74.2%; Score 23; DB 6; Length 126;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 FVFFA 6
Db      10 VVFFA 14
```

```
RESULT 39
US-10-793-626-304
; Sequence 304, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 304
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-304
```

```
Query Match          74.2%; Score 23; DB 6; Length 209;
```

Best Local Similarity 60.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 2; Mismatches 0;

Qy 1 KVFVF 5  
Db 145 RFIFV 149

## RESULT 40

US-10-793-626-1034  
; Sequence 1034, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1034  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1034

Query Match 74.2%; Score 23; DB 6; Length 234;  
Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6  
Db 124 FMFFA 128

## RESULT 41

US-10-467-657-4456  
; Sequence 4456, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 4456  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-4456

Query Match 74.2%; Score 23; DB 6; Length 288;  
Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 61 KFAFF 65

## RESULT 42

US-10-613-744-13  
; Sequence 13, Application US/10613744  
; Publication No. US20050272093A1  
; GENERAL INFORMATION:  
; APPLICANT: MacKinnon, Rodrick  
; APPLICANT: The Rockefeller University  
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With  
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation  
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof  
; FILE REFERENCE: 018512-002901US  
; CURRENT APPLICATION NUMBER: US/10/613,744  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: US/09/275,252  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: US 09/045,529  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: US 09/054,347  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307  
; PRIOR FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-613-744-13

Query Match 74.2%; Score 23; DB 6; Length 391;  
Best Local Similarity 60.0%; Pred. No. 3.3e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5  
Db 61 RFIFV 65

## RESULT 43

US-10-467-657-4858  
; Sequence 4858, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 4858  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-4858

Query Match 74.2%; Score 23; DB 6; Length 410;  
Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6  
Db 207 FLFFA 211

## RESULT 44

US-11-055-822-1096

```

; Sequence 1096, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1096
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1096

Query Match          74.2%; Score 23; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
Db      329 FVFFA 333

RESULT 45
US-11-113-424-186
; Sequence 186, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358

```

```

; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 186
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-11-113-424-186

Query Match          74.2%; Score 23; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
Db      399 FVFFA 403

RESULT 46
US-10-467-657-678
; Sequence 678, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 678
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-678

Query Match          74.2%; Score 23; DB 6; Length 449;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
Db      395 FVFFA 399

RESULT 47
US-11-082-389-348
; Sequence 348, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389

```

```

; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 348
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-348

```

```

Query Match      74.2%; Score 23; DB 7; Length 534;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KPVFF 5
Db      239 KFIFY 243

```

```

RESULT 48
US-10-467-657-3440
; Sequence 3440, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3440
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3440

```

```

Query Match      74.2%; Score 23; DB 6; Length 633;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 KPVFF 5
Db      367 KPAPP 371

```

```

RESULT 49
US-10-467-657-4632

```

```

; Sequence 4632, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4632
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4632

```

```

Query Match      74.2%; Score 23; DB 6; Length 633;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 KPVFF 5
Db      367 KPAPP 371

```

```

RESULT 50
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

```

```

Query Match      74.2%; Score 23; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 KPVFF 6
Db      531 KAVFFA 536

```

```

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 908
; LENGTH: 1012
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-908

Query Match      74.2%; Score 23; DB 6; Length 1012;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
        |:|
Db      988 FLFFA 992

RESULT 54
US-10-793-626-760
; Sequence 760, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 760
; LENGTH: 2323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-760

Query Match      74.2%; Score 23; DB 6; Length 2323;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
        |:|
Db      1210 FMFFA 1214

RESULT 55
US-10-467-657-8998
; Sequence 8998, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8998

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-917

Query Match      74.2%; Score 23; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPVFFA 6
        |:|
Db      579 KAVFFA 584

RESULT 52
US-10-793-626-420
; Sequence 420, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 420
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-420

Query Match      74.2%; Score 23; DB 6; Length 766;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
        |:|
Db      357 FMFFA 361

RESULT 53
US-10-995-561-908
; Sequence 908, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
```

; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8998

Query Match 71.0%; Score 22; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5  
Db 7 FVFF 10

## RESULT 56

US-11-000-463-378  
; Sequence 378, Application US/11000463  
; Publication No. US20050266423A1  
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenchua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Qian, Xiaohong B.  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhou, Ping  
; APPLICANT: Cao, Yi-Cheng  
; APPLICANT: Dmanac, Radoje T.

; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

; FILE REFERENCE: 785CIP4CN  
; CURRENT APPLICATION NUMBER: US/11/000.463  
; CURRENT FILING DATE: 2004-11-29

; PRIOR APPLICATION NUMBER: 10/291,265  
; PRIOR FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: PCT/US01/02623

; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: 09/922,279

; PRIOR FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 09/617,746

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 09/631,451

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: 09/633,870

; PRIOR FILING DATE: 2000-09-15

; NUMBER OF SEQ ID NOS: 944

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 378

; LENGTH: 72

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-000-463-378

Query Match 71.0%; Score 22; DB 7; Length 72;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5  
Db 8 FVFF 11

## RESULT 57

US-11-000-463-850

; Sequence 850, Application US/11000463  
; Publication No. US20050266423A1  
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom

; APPLICANT: Liu, Chenchua

; APPLICANT: Asundi, Vinod

; APPLICANT: Chen, Rui-hong  
; APPLICANT: Qian, Xiaohong B.  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhou, Ping  
; APPLICANT: Cao, Yi-Cheng  
; APPLICANT: Dmanac, Radoje T.

; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

; FILE REFERENCE: 785CIP4CN

; CURRENT APPLICATION NUMBER: US/11/000.463

; CURRENT FILING DATE: 2004-11-29

; PRIOR APPLICATION NUMBER: 10/291,265

; PRIOR FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: PCT/US01/02623

; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: 09/922,279

; PRIOR FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 09/617,746

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 09/631,451

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: 09/633,870

; PRIOR FILING DATE: 2000-09-15

; NUMBER OF SEQ ID NOS: 944

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 850

; LENGTH: 72

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-000-463-850

Query Match 71.0%; Score 22; DB 7; Length 72;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5  
Db 8 FVFF 11

## RESULT 58

US-10-467-657-360

; Sequence 360, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: Seqwin99, version 1.04

; SEQ ID NO 360

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-360

Query Match 71.0%; Score 22; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5  
Db 8 FVFF 11



```
Db          32 FVFF 35

RESULT 59
US-10-467-657-2026
; Sequence 2026, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2026
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2026

Query Match          71.0%; Score 22; DB 6; Length 79;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
   :|||
Db 10 QPIFF 14

RESULT 60
US-10-485-517-286
; Sequence 286, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WQ
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-286

Query Match          71.0%; Score 22; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
   ||||
Db 83 FVFF 86

RESULT 61
US-10-467-657-6824
; Sequence 6824, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6824
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6824

Query Match          71.0%; Score 22; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
   ||||
Db 62 FVFF 65

RESULT 62
US-11-125-837-24
; Sequence 24, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-24

Query Match          71.0%; Score 22; DB 7; Length 139;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
   |:|||
Db 6 KVVFF 10

RESULT 63
US-10-467-657-6110
; Sequence 6110, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6110  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6110

Query Match 71.0%; Score 22; DB 6; Length 149;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
Db 88 EFFFFA 93

## RESULT 64

US-10-467-657-7550  
; Sequence 7550, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 7550  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-7550

Query Match 71.0%; Score 22; DB 6; Length 149;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
Db 88 EFFFFA 93

## RESULT 65

US-10-467-657-6130  
; Sequence 6130, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 6130  
; LENGTH: 154  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6130

Query Match 71.0%; Score 22; DB 6; Length 154;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVFFA 6  
Db 93 EFFFFA 98

## RESULT 66

US-10-485-517-346  
; Sequence 346, Application US/10485517  
; Publication No. US20050256299A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Sheffield  
; APPLICANT: Biosynexus Incorporated  
; APPLICANT: Foster, Simon  
; APPLICANT: Mond, James  
; TITLE OF INVENTION: Antigenic Polypeptides  
; FILE REFERENCE: F100629WC  
; CURRENT APPLICATION NUMBER: US/10/485,517  
; CURRENT FILING DATE: 2004-02-02  
; PRIOR APPLICATION NUMBER: GB 0118825.9  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: GB 0200349.9  
; PRIOR FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 424  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 346  
; LENGTH: 180  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-485-517-346

Query Match 71.0%; Score 22; DB 6; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5  
Db 134 FVFF 137

## RESULT 67

US-10-980-388-65  
; Sequence 65, Application US/10980388  
; Publication No. US20050255490A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogell, Gabriel  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Hiebsch, Ronald R.  
; APPLICANT: Lind, Peter  
; APPLICANT: Kaytes, Paul S.  
; APPLICANT: Huff, Valerie  
; APPLICANT: Huff, Rita M.  
; APPLICANT: Wood, Linda S.  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl  
; FILE REFERENCE: 00325.US1  
; CURRENT APPLICATION NUMBER: US/10/980,388  
; CURRENT FILING DATE: 2004-11-02  
; PRIOR APPLICATION NUMBER: US/09/791,932  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/184,305  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,304  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,303

```

; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-65

Query Match          71.0%; Score 22; DB 6; Length 187;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 179 RYVFFA 184

RESULT 68
US-10-467-657-4386
; Sequence 4386, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4386
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4386

Query Match          71.0%; Score 22; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 72 FVFF 75

RESULT 69
US-10-467-657-3000
; Sequence 3000, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

```

```

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3000
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3000

Query Match          71.0%; Score 22; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 143 FVFF 146

RESULT 70
US-10-467-657-6248
; Sequence 6248, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6248
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6248

Query Match          71.0%; Score 22; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 218 FVFF 221

RESULT 71
US-11-054-515-1391
; Sequence 1391, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14

```

```
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1391
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1391

Query Match          71.0%; Score 22; DB 7; Length 240;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
Db      56 RFVYVA 61

RESULT 72
US-11-074-176-66
; Sequence 66, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Ascarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-66

Query Match          71.0%; Score 22; DB 7; Length 241;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
Db      229 KVFVFA 234

RESULT 73
US-10-793-626-1124
; Sequence 1124, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1124
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1124

Query Match          71.0%; Score 22; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFF 5
Db      65 FVFF 68

RESULT 74
US-10-467-657-6144
; Sequence 6144, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6144

Query Match          71.0%; Score 22; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFF 5
Db      197 FVFF 200

RESULT 75
US-10-467-657-1178
; Sequence 1178, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
```

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1178
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1178
```

```
Query Match      71.0%; Score 22; DB 6; Length 268;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 FVFFA 6
        |   |
Db      25 FAFFA 29
```

```
Search completed: December 29, 2005, 18:50:15
Job time : 4.29032 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds  
(without alignments)  
54.137 Million cell updates/sec

Title: US-10-009-122-9  
Perfect score: 29  
Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	186	1	G119_ORYSA
2	29	100.0	186	2	P3414_ORYSA
3	29	100.0	231	2	Q8C6Y8_MOUSE
4	29	100.0	372	2	Q6D7U3_ERWCT
5	29	100.0	373	2	Q7M9N5_WOLSU
6	29	100.0	387	2	Q9K110_BACCE
7	29	100.0	387	2	Q4MT39_BACCE
8	29	100.0	387	2	Q3DD4_BACCE
9	29	100.0	387	2	Q6HKU6_BACCH
10	29	100.0	387	2	Q73AP3_BACCL
11	29	100.0	387	2	Q81SK9_BACAN
12	29	100.0	410	2	Q8C5T3_MOUSE
13	29	100.0	442	2	Q9PHV5_CAMJE
14	29	100.0	703	2	Q5HYE1_HUMAN
15	29	100.0	721	2	Q6AG25_LEIXX
16	29	100.0	925	2	Q95786_HUMAN
17	29	100.0	925	2	Q5VY71_HUMAN
18	29	100.0	926	2	Q6Q899_MOUSE
19	29	100.0	940	2	Q9GLV6_PIG
20	29	100.0	1144	1	N0S2_MOUSE
21	29	100.0	1144	2	Q5SXT3_MOUSE
22	29	100.0	1145	2	Q8R410_MOUSE
23	29	100.0	1145	2	Q6P6A0_MOUSE
24	28	96.6	164	2	Q73N39_TREDE
25	28	96.6	203	2	Q6AKS9_DESPS
26	28	96.6	380	2	Q67225_AQUAE
27	28	96.6	387	2	Q81FH5_BACCR
28	28	96.6	399	2	Q5WPU9_LUTLO
29	28	96.6	450	2	Q4TRF8_9SPHN
30	28	96.6	464	2	Q4S4T5_TETNG
31	28	96.6	606	2	Q91VU5_MOUSE

32	28	96.6	623	2	Q4WBU2_ASFPU
33	28	96.6	630	2	Q5K7E5_CRYNE
34	28	96.6	663	2	Q6RUU2_MOUSE
35	28	96.6	690	2	Q831B2_TROW8
36	28	96.6	698	2	Q83GW3_TROWT
37	28	96.6	760	2	Q55HW1_CRYNE
38	28	96.6	1265	2	Q6ZQ91_MOUSE
39	28	96.6	1412	2	Q5E3M1_CHICK
40	28	96.6	1655	2	Q4Q5Q4_LEIMA
41	27	93.1	88	2	Q4LBQ8_SODGL
42	27	93.1	183	2	Q9RQ09_BACTN
43	27	93.1	315	2	Q61C67_CABER
44	27	93.1	362	2	Q4HSJ7_CAMUP
45	27	93.1	382	2	Q9V7J0_DROME
46	27	93.1	410	2	Q6L2B4_PICHO
47	27	93.1	447	2	Q59243_PYRHO
48	27	93.1	556	2	Q95S93_DROME
49	27	93.1	556	2	Q9V7I9_DROME
50	27	93.1	785	2	Q9GQ82_DROME
51	27	93.1	1384	2	Q68X27_CHLRE
52	27	93.1	1408	2	Q7QBF0_ANOGR
53	27	93.1	1443	2	Q9VPR0_DROME
54	27	93.1	1458	2	Q5BI64_DROME
55	27	93.1	1503	2	Q7KTZ4_DROME
56	27	93.1	1676	2	Q8A6R7_BACTN
57	26	89.7	33	2	Q9UC33_HUMAN
58	26	89.7	42	2	Q56JJ6_GRAGR
59	26	89.7	42	2	Q56JJ7_TURTR
60	26	89.7	42	2	Q7M088_CAVPO
61	26	89.7	52	2	Q8WZ99_HUMAN
62	26	89.7	55	2	Q82VG8_NITEU
63	26	89.7	57	1	A4_URSHA
64	26	89.7	58	1	A4_CANFA
65	26	89.7	58	1	A4_RABIT
66	26	89.7	58	1	A4_SHEEP
67	26	89.7	59	1	A4_BOVIN
68	26	89.7	79	2	Q5WJL8_BACSK
69	26	89.7	79	2	Q35463_CRIGR
70	26	89.7	81	1	MOAD_ECOLI
71	26	89.7	81	2	Q9APP7_9BACT
72	26	89.7	81	2	Q57RF2_SALCH
73	26	89.7	81	2	Q65TTO_MANSCH
74	26	89.7	81	2	Q7NGP4_PHOLL
75	26	89.7	81	2	Q8D977_VIBVU
76	26	89.7	81	2	Q9KT78_VIBCH
77	26	89.7	81	2	Q83S38_SHIFL
78	26	89.7	81	2	Q7MM72_VIBVU
79	26	89.7	81	2	Q8X807_ECO57
80	26	89.7	81	2	Q5PGA0_SALPA
81	26	89.7	83	2	Q8Z886_SALTI
82	26	89.7	83	2	Q8ZQO0_SALTY
83	26	89.7	85	2	Q87MY3_VIBPA
84	26	89.7	109	2	Q6YVX4_ORYSA
85	26	89.7	113	2	Q8JH58_CHESE
86	26	89.7	137	2	Q7UPR1_RHOBA
87	26	89.7	141	2	Q5LGT9_BACFR
88	26	89.7	141	2	Q64XP1_BACFR
89	26	89.7	143	2	Q8EMC6_OCEIH
90	26	89.7	152	2	Q8STZ9_ARATH
91	26	89.7	163	2	Q5PGG6_ANAMM
92	26	89.7	193	2	Q980V9_SULSO
93	26	89.7	195	2	Q7N3A0_PHOLL
94	26	89.7	207	1	HIS2_CAMJE
95	26	89.7	207	2	Q4HDT2_CAMCO
96	26	89.7	207	2	Q5HSI7_CAMJR
97	26	89.7	218	2	Q8BPV5_MOUSE
98	26	89.7	221	2	Q6AMY5_DESPS
99	26	89.7	229	2	Q8VY56_ARATH
100	26	89.7	231	2	Q9SV79_ARATH
101	26	89.7	252	2	Q73M22_TREDE
102	26	89.7	264	2	Q9FGJ8_ARATH
103	26	89.7	265	2	Q4SV83_TETNG
104	26	89.7	293	1	Y844_ARCFU

Q4WBU2	aspergillus
Q5K7E5	cryptococcus
Q6RUU2	mus musculus
Q831B2	tropheryma
Q83GW3	trichomyces
Q55HW1	cryptococcus
Q6ZQ91	mus musculus
Q5F3M1	gallus gall
Q4Q5Q4	leishmania
Q4LBQ8	sodalis glo
Q9RQ09	bacteroides
Q61C67	caenorhabdi
Q4HSJ7	campylobact
Q9V7J0	drosophila
Q6L2B4	microphilus
Q59243	pyrococcus
Q95S93	drosophila
Q9V7I9	drosophila
Q9GQ82	drosophila
Q68X27	chlamydomon
Q7QBF0	anopheles 9
Q9VPR0	drosophila
Q5BI64	drosophila
Q7KTZ4	drosophila
Q8A6R7	bacteroides
Q9UC33	homo sapien
Q56JJ6	grampus gri
Q56JJ7	tursiops tr
Q7M088	cavia porce
Q8WZ99	homo sapien
Q82VG8	nitrosomona
Q29149	u alzheimer
Q28280	c alzheimer
Q28748	o alzheimer
Q28757	o alzheimer
Q28053	b alzheimer
Q5WJL8	bacillus cl
Q35463	cricketulus
Q30748	escherichia
Q9APP7	uncultured
Q57RF2	salmonella
Q65TTO	mannheimia
Q7NGP4	photorhabdu
Q8D977	vibrio vuln
Q9KT78	vibrio chol
Q83S38	shigella fl
Q7MM72	vibrio vuln
Q8X807	escherichia
Q5PGA0	salmonella
Q8Z886	salmonella
Q8ZQO0	salmonella
Q87MY3	vibrio para
Q6YVX4	oryza sativ
Q8JH58	chelydra se
Q7UPR1	rhodopirell
Q5LGT9	bacteroides
Q64XP1	bacteroides
Q8EMC6	oceanobacil
Q8STZ9	arabidopsis
Q5PGG6	anaplasma m
Q980V9	sulfolobus
Q7N3A0	photorhabdu
Q9PM71	campylobact
Q4HDT2	campylobact
Q5HSI7	campylobact
Q8BPV5	mus musculu
Q6AMY5	desulfotale
Q8VY56	arabidopsis
Q9SV79	arabidopsis
Q73M22	treponema d
Q9FGJ8	arabidopsis
Q4SV83	tetradodon n
Y844	archaeoglob

105	26	89.7	294	2	Q97XW2	SULSO	Q97XW2	sulfolobus	178	26	89.7	751	2	Q6RH28	CANFA	Q6Rh28	canis famil
106	26	89.7	294	2	Q62HR5	BURMA	Q62hr5	burkholderi	179	26	89.7	751	2	Q56JK5	CANFA	Q56jk5	canis famil
107	26	89.7	300	2	Q9XU61	CAECL	Q9xu61	caenorhabdi	180	26	89.7	751	2	Q4R4R8	MACFA	Q4r4r8	macaca faec
108	26	89.7	314	2	Q7S8K9	NEUCR	Q7s8k9	neurospora	181	26	89.7	751	2	Q9DGJ7	CHICK	Q9dgj7	gallus gall
109	26	89.7	330	2	Q9PGI8	XYLFA	Q9pgi8	xyella fas	182	26	89.7	754	2	Q4RYJ3	TETNG	Q4ryj3	tetradodon n
110	26	89.7	339	1	MURG	THEMA	Q9wy74	thermotoga	183	26	89.7	759	2	Q4S0J4	TETNG	Q4s0j4	tetradodon n
111	26	89.7	349	2	Q9XU59	CABEL	Q9xu59	caenorhabdi	184	26	89.7	770	1	A4	CAVFO	Q60J4	c amyloid b
112	26	89.7	352	2	Q87EP8	XYLFT	Q8xg76	simmondsia	185	26	89.7	770	1	A4	HUMAN	P05067	h amyloid b
113	26	89.7	352	2	Q87EP8	XYLFT	Q87ep8	xyella fas	186	26	89.7	770	1	A4	MACFA	P53601	m amyloid b
114	26	89.7	357	2	Q8U460	PYRFU	Q8u460	pyrococcus	187	26	89.7	770	1	A4	MOUSE	P12023	m amyloid b
115	26	89.7	357	2	Q8U4U8	BRARE	Q8uu18	brachydanio	188	26	89.7	770	1	A4	MOUSE	P53601	m amyloid b
116	26	89.7	366	2	Q8EPL1	XANAC	Q8ep11	xanthomonas	189	26	89.7	770	1	A4	PATR	P79307	s amyloid b
117	26	89.7	370	2	Q6S5J1	MANSU	Q6smj1	xanthomelia	190	26	89.7	770	1	A4	RAT	P08592	r amyloid b
118	26	89.7	374	2	Q7MAT1	WOLSU	Q7mat1	wolinella s	191	26	89.7	770	1	A4	RAT	P08592	r amyloid b
119	26	89.7	384	2	Q8BPC7	MOUSE	Q8bpc7	mus musculus	192	26	89.7	770	2	Q56JK6	CANFA	Q56jk6	canis famil
120	26	89.7	391	2	Q4N5U7	THEPA	Q4n5u7	theileria p	193	26	89.7	770	2	Q53ZT3	MOUSE	Q53zt3	mus musculus
121	26	89.7	395	2	Q9S5W9	9DIPT	Q9s5w9	phlebotomus	194	26	89.7	770	2	Q547B7	RAT	Q547b7	rattus norv
122	26	89.7	403	2	Q5L117	GROKA	Q5l117	geobacillus	195	26	89.7	780	1	A4	TETFL	Q73683	tetradodon f
123	26	89.7	404	2	Q4UY55	XANCP	Q4uy55	xanthomonas	196	26	89.7	817	2	Q6QQP9	VIBVU	Q6qqp9	vibrio vuln
124	26	89.7	428	2	Q8P597	XANCP	Q8p597	xanthomonas	197	26	89.7	817	2	Q87FQ8	VIBVU	Q87fq8	vibrio para
125	26	89.7	428	2	Q9M1Q8	ARATH	Q9m1q8	arabidopsis	198	26	89.7	817	2	Q8D4P2	VIBVU	Q8d4p2	vibrio vuln
126	26	89.7	443	2	Q4HHQ1	CAMCO	Q4hhq1	campylobact	199	26	89.7	817	2	Q9KNF1	VIBCH	Q9knf1	vibrio chol
127	26	89.7	461	2	Q89329	9POTV	Q89329	zucchini ye	200	26	89.7	840	2	Q7MG92	VIBVU	Q7mg92	vibrio vuln
128	26	89.7	467	2	Q4L319	STAHJ	Q4l319	staphylococ	201	26	89.7	939	2	Q6CET0	YARLI	Q6cet0	yarrowia li
129	26	89.7	469	2	Q7Y318	PLACH	Q7y318	placodium	202	26	89.7	955	2	Q80RZ2	9POTV	Q80rz2	calla lily
130	26	89.7	470	2	Q7Y318	9POTV	Q7y318	zucchini ye	203	26	89.7	962	2	Q4NTK2	9DELT	Q4ntk2	anaeromyxob
131	26	89.7	472	2	Q8UUS0	BRARE	Q8uus0	brachydanio	204	26	89.7	1016	2	Q05912	9POTV	Q05912	zucchini ye
132	26	89.7	477	1	YPUM	RHOCA	P26176	rhodobacter	205	26	89.7	1056	2	Q8FKH6	CANGA	Q8fkh6	candida gla
133	26	89.7	488	2	Q52NV6	9POTV	Q52nv6	zucchini ye	206	26	89.7	1083	2	Q81311	PLAF7	Q81311	plasmodium
134	26	89.7	490	2	Q7Y312	9POTV	Q7y312	zucchini ye	207	26	89.7	1497	2	Q95YH6	DROME	Q95yh6	drosophila
135	26	89.7	490	2	Q7Y312	9POTV	Q7y312	zucchini ye	208	26	89.7	1571	2	Q95YH7	DROME	Q95yh7	drosophila
136	26	89.7	493	2	Q5K4D4	9POTV	Q5k4d4	soybean mos	209	26	89.7	1571	2	Q8MS04	DROME	Q8maq4	drosophila
137	26	89.7	493	2	Q5K4D5	9POTV	Q5k4d5	soybean mos	210	26	89.7	1612	2	Q9VE37	DROME	Q9ve37	drosophila
138	26	89.7	496	2	Q5K4D0	9POTV	Q5k4d0	daheen mos	211	26	89.7	1916	2	Q8QK4	9POTV	Q8qk4	zucchini ye
139	26	89.7	508	2	Q5GV55	XANOR	Q5gv55	xanthomonas	212	26	89.7	3080	1	POLG	ZYMVC	P18479	z genome po
140	26	89.7	520	2	Q9K207	CHLPN	Q9k207	chlamydia p	213	26	89.7	3080	2	Q6WN47	9POTV	Q6wn47	zucchini ye
141	26	89.7	534	2	Q93296	CHICK	Q93296	gallus gall	214	26	89.7	3080	2	Q6WN48	9POTV	Q6wn48	zucchini ye
142	26	89.7	554	2	Q7P7T7	FUSNV	Q7p7t7	fusobacteri	215	26	89.7	3080	2	Q6WN49	9POTV	Q6wn49	zucchini ye
143	26	89.7	569	2	Q9PVL1	CHICK	Q9pvl1	gallus gall	216	26	89.7	3080	2	Q6Y2U7	9POTV	Q6y2u7	zucchini ye
144	26	89.7	594	2	Q9JSK0	CHLPN	Q9jsk0	chlamydia p	217	26	89.7	3080	2	Q7Y908	9POTV	Q7y908	zucchini ye
145	26	89.7	603	2	Q9X1Q8	THEMA	Q9x1q8	thermotoga	218	26	89.7	3080	2	Q7Y914	9POTV	Q7y914	zucchini ye
146	26	89.7	609	2	Q6CFJ3	YARLI	Q6cfj3	yarrowia li	219	26	89.7	3083	1	POLG	ZYMVS	Q36979	z genome po
147	26	89.7	612	2	Q919E7	BRARE	Q919e7	brachydanio	220	26	89.7	3105	2	Q70XR2	9POTV	Q70xr2	soybean mos
148	26	89.7	613	2	Q8HML1	9TELE	Q8hml1	hiodon alos	221	25	86.2	40	2	Q91FF3	IRV6	Q91ff3	chilo iride
149	26	89.7	614	2	Q94YP6	9TELE	Q94yp6	osteoglossu	222	25	86.2	66	2	Q728F0	DRSVH	Q728f0	desulfovibr
150	26	89.7	615	2	Q50Z85	ENTHI	Q50z85	entamoeba h	223	25	86.2	74	1	Y131	MYCGE	P47377	mycoplasma
151	26	89.7	617	2	Q929B2	CHLPN	Q929b2	chlamydia p	224	25	86.2	81	2	Q6D3D0	ERWCT	Q6d3d0	erwinia car
152	26	89.7	617	2	Q8RDN8	FUSNN	Q8rdn8	fusobacteri	225	25	86.2	89	2	Q83VF2	LACLC	Q83vf2	lactococcus
153	26	89.7	624	2	Q7SD58	NEUCR	Q7sd58	neurospora	226	25	86.2	104	2	Q5LXX2	STR11	Q5lxx2	streptococ
154	26	89.7	638	2	Q5B2V4	EMENI	Q5b2v4	aspergillus	227	25	86.2	104	2	Q5M2H4	STR12	Q5m2h4	streptococ
155	26	89.7	670	2	Q8KGX2	RHIL0	Q8kgx2	rhizobium l	228	25	86.2	105	2	Q64CV5	9ARCH	Q64cv5	uncultured
156	26	89.7	678	2	Q7Z2T1	BRARE	Q7z2t1	brachydanio	229	25	86.2	107	2	Q59MNI	CANAL	Q59mni	candida alb
157	26	89.7	682	2	Q64DY0	9ARCH	Q64dy0	uncultured	230	25	86.2	107	2	Q8E222	STRAS	Q8e222	streptococ
158	26	89.7	693	2	Q98SG0	XENLA	Q98sg0	xenopus lae	231	25	86.2	107	2	Q8E7H9	STRAS	Q8e7h9	streptococ
159	26	89.7	695	2	Q648X4	9ARCH	Q648x4	uncultured	232	25	86.2	109	2	Q9X292	THEMA	Q9x292	thermotoga
160	26	89.7	695	2	Q8R477	PONPY	Q8r477	pongo pygma	233	25	86.2	122	2	Q4Y0Z7	PLACH	Q4y0z7	plasmodium
161	26	89.7	695	2	Q6RH29	CANFA	Q6rh29	canis famil	234	25	86.2	124	2	Q61N30	CAEBR	Q61n30	caenorhabdi
162	26	89.7	695	2	Q56JK3	CANFA	Q56jk3	canis famil	235	25	86.2	125	2	Q6U9U2	9CAUD	Q6u9u2	bacterioph
163	26	89.7	695	2	Q6GR78	MOUSE	Q6gr78	mus musculus	236	25	86.2	125	2	Q56F01	9CAUD	Q56f01	aeromonas p
164	26	89.7	695	2	Q9DGJ8	CHICK	Q9dgj8	gallus gall	237	25	86.2	128	2	Q6LGS9	PHOPR	Q6lgs9	photobacter
165	26	89.7	695	2	Q98SF9	XENLA	Q98sf9	xenopus lae	238	25	86.2	136	2	Q18208	CAEBL	Q18208	caenorhabdi
166	26	89.7	714	2	Q7XQX0	XENLA	Q7xqx0	xenopus lae	239	25	86.2	141	2	Q8U3A1	PYRFU	Q8u3a1	pyrococcus
167	26	89.7	714	2	Q56JK4	CANFA	Q56jk4	canis famil	240	25	86.2	143	2	Q91Y69	MESAU	Q91y69	mesocricetu
168	26	89.7	733	2	Q6P6Q5	RAT	Q6p6q5	rattus norv	241	25	86.2	145	2	Q5USA9	9PEZI	Q5usa9	monacrosop
169	26	89.7	737	1	A4	FUGRU	Q93279	fugu rubrip	242	25	86.2	146	2	Q9V0B4	PYRAB	Q9v0b4	pyrococcus
170	26	89.7	738	2	Q6NUZ1	BRARE	Q6nuz1	brachydanio	243	25	86.2	148	2	Q17202	CAEBL	Q17202	caenorhabdi
171	26	89.7	738	2	Q90W28	BRARE	Q90w28	brachydanio	244	25	86.2	156	2	Q8DN20	STR6	Q8dn20	streptococ
172	26	89.7	747	2	Q91963	9PIPI	Q91963	xenopus. ap	245	25	86.2	157	2	Q97N92	STRPN	Q97n92	streptococ
173	26	89.7	749	2	Q56JK2	STECO	Q56jk2	stenella co	246	25	86.2	157	2	Q8XNL2	CIOPR	Q8xnl2	clostridium
174	26	89.7	749	2	Q6NRR1	XENLA	Q6nrr1	xenopus lae	247	25	86.2	159	2	Q58626	PYRHO	Q58626	pyrococcus
175	26	89.7	750	2	Q6DJB5	XENTR	Q6djb5	xenopus tro	248	25	86.2	161	2	Q32197	9LILI	Q32197	eichhornia
176	26	89.7	751	1	A4	SARSC	Q95241	s amyloid b	249	25	86.2	162	2	Q9N284	BOVIN	Q9n284	bos taurus
177	26	89.7	751	2	Q6GSC0	HUMAN	Q6gsc0	homo sapient	250	25	86.2	163	2	Q32164	9LILI	Q32164	eichhornia

251 25 86.2 163 2 Q32179 9LILI  
 252 25 86.2 163 2 Q32190 9LILI  
 253 25 86.2 163 2 Q32201 9LILI  
 254 25 86.2 163 2 Q32202 9LILI  
 255 25 86.2 163 2 Q32210 9LILI  
 256 25 86.2 163 2 Q32390 9LILI  
 257 25 86.2 163 2 Q32419 9LILI  
 258 25 86.2 163 2 Q32424 9LILI  
 259 25 86.2 163 2 Q32430 9LILI  
 260 25 86.2 163 2 Q32441 9LILI  
 261 25 86.2 163 2 Q32556 9LILI  
 262 25 86.2 163 2 Q32579 9LILI  
 263 25 86.2 163 2 Q32648 9LILI  
 264 25 86.2 163 2 Q32802 FONCO  
 265 25 86.2 163 2 Q32892 9LILI  
 266 25 86.2 163 2 Q32915 9LILI  
 267 25 86.2 164 2 Q32915 BACAN  
 268 25 86.2 165 2 Q37011 PONCO  
 269 25 86.2 172 2 Q53PK3 ORYSA  
 270 25 86.2 180 2 Q5NLQ4 2YMMO  
 271 25 86.2 188 2 Q8W2G3 ORYSA  
 272 25 86.2 188 2 Q7VR37 CANBF  
 273 25 86.2 188 2 Q67835 AQUAE  
 274 25 86.2 190 2 Q92WB8 RHIME  
 275 25 86.2 194 2 Q97G46 CLOAB  
 276 25 86.2 196 2 Q6HV89 BACAN  
 277 25 86.2 197 2 Q4U6V3 9VIRU  
 278 25 86.2 197 2 Q7VR77 CANBF  
 279 25 86.2 198 2 Q46025 CORDI  
 280 25 86.2 198 2 Q847W0 VIBPA  
 281 25 86.2 198 2 Q8NGT3 CORDI  
 282 25 86.2 198 2 Q87I68 VIBPA  
 283 25 86.2 199 2 Q7MFJ3 VIBVY  
 284 25 86.2 200 1 COAE LISIN  
 285 25 86.2 200 2 Q73L44 TREDE  
 286 25 86.2 202 2 Q7P578 FUSNV  
 287 25 86.2 202 2 Q8RE19 FUSNN  
 288 25 86.2 208 2 Q5QBU5 9ACTO  
 289 25 86.2 210 2 Q8T312 DROME  
 290 25 86.2 217 2 Q84019 PSECL  
 291 25 86.2 218 2 Q5CYB3 CRYPV  
 292 25 86.2 218 2 Q5CIV9 CRYHO  
 293 25 86.2 220 2 Q5ZIT4 PEMVM  
 294 25 86.2 228 2 Q51V22 MAGGR  
 295 25 86.2 229 2 Q70Z41 9VIRU  
 296 25 86.2 229 2 Q7TD31 9VIRU  
 297 25 86.2 229 2 Q7TD37 9VIRU  
 298 25 86.2 230 2 Q7RDM9 PLAYO  
 299 25 86.2 231 2 Q637W5 BACCZ  
 300 25 86.2 232 2 Q84601 CHLTR

## ALIGNMENTS

RESULT 1  
 GL19 ORYSA  
 ID GL19 ORYSA STANDARD; PRT; 186 AA.

AC P29835;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE 19 kDa globulin precursor (Alpha-globulin).

OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 NCBI\_TaxID=4530;

RA Shorrosh B.S., Wen L., Zen K.C., Huang J.K., Pan J.S., Hermodson M.A.,  
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
 RC STRAIN=cv. Japonica / Nipponbare; TISSUE=Endosperm;  
 RX MEDLINE=92119226; PubMed=1731968;

RA Tanaka K., Muthukrishnan S., Reeck G.R.;  
 RT "A novel cereal storage protein: molecular genetics of the 19 kDa  
 RL Globulin of rice."; Plant Mol. Biol. 18:151-154 (1992).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE OF 5-186.  
 RC STRAIN=cv. Japonica / Lemont; TISSUE=Endosperm;  
 RX MEDLINE=93277591; PubMed=8503935;  
 RA Krishnan H.B., Puppek S.G.;  
 RT "Nucleotide sequence of an abundant rice seed globulin: homology with  
 RL the high molecular weight glutelins of wheat, rye and tritcale."; Biochem. Biophys. Res. Commun. 193:460-466(1993).  
 CC -1- FUNCTION: Seed storage protein.  
 CC -1- SIMILARITY: Belongs to the 2S seed storage albumins family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC ENBL; X63990; CAA45400.1; -; mRNA.  
 DR EMBL; L12252; AAA72362.1; ALT\_INIT; mRNA.  
 DR PIR; S20024; WNRZ19.  
 DR HSSP; P24565; LPNB.  
 DR Gramene; P29835; -.

DR InterPro; IPR003612; AAI.  
 DR InterPro; IPR001419; Glutenin.  
 DR PANTHER; PTHR14054; Glutenin; 1.  
 DR Pfam; PF00234; Tryp alpha amyl; 1.

DR PRINTS; PR00210; GLUTENIN.  
 DR SMART; SM00499; AAI; 1.  
 DR Direct protein sequencing; Seed storage protein; Signal;  
 KW Storage protein.

FT SIGNAL 1 22 Potential.  
 FT CHAIN 23 186 19 kDa globulin.  
 SQ SEQUENCE 186 AA; 21050 MW; 9E09BA74CB0B6810 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 Db 4 KVVFFA 9

RESULT 2  
 P93414 ORYSA  
 ID P93414 ORYSA PRELIMINARY; PRT; 186 AA.

AC P93414;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE 26 kDa globulin (Alpha-globulin).  
 GN Names=P0010D04.16; Synonyms=Q01057\_B02.5;  
 OS Oryza sativa (Japonica cultivar-group);  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.

NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Endosperm;  
 RX MEDLINE=96235139; PubMed=8666249; DOI=10.1016/0378-1119(95)00887-X;  
 RA Nakase M., Hotta H., Adachi T., Aoki N., Nakamura R., Masumura T.,  
 RA Tanaka K., Matsuda T.;

RT "Cloning of the rice seed alpha-globulin-encoding gene: sequence  
 RL similarity of the 5'-flanking region to those of the genes encoding  
 RL wheat high molecular-weight glutenin and barley D hordein."; Gene 170:223-226(1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.



RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,  
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,  
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,  
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,  
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,  
RA Wu H.-P., Shaw J.-F.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,  
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,  
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,  
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,  
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,  
RA Wu H.-P., Shaw J.-F.,  
RT "Oryza sativa BAC FJ1057 B02 genomic sequence."  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; D50643; BAA09308.1; -; Genomic DNA.  
DR EMBL; AC130605; AAT44292.1; -; Genomic DNA.  
DR EMBL; AC113332; AAT93857.1; -; Genomic DNA.  
DR PIR; JC4784; JC4784.  
DR HSP; P24565; LPNB.  
DR Gramene; P93414; -.  
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.  
DR InterPro; IPR003612; AAI.  
DR InterPro; IPR001419; Glutinin.  
DR Pfam; PF00234; Tryp\_alpha\_aml1; 1.  
DR PRINTS; PR00210; GLUTENIN.  
DR SMART; SM00499; AAI; 1.  
SQ SEQUENCE 186 AA; 21055 MW; AE2B8F1107C8BC94 CRC64;  
Query Match 100.0%; Score 29; DB 2; Length 186;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
DB 4 KVVFFA 9  
|||||  
RESULT 3  
Q8C6Y8 MOUSE PRELIMINARY; PRT; 231 AA.  
AC Q8C6Y8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched  
DE library, clone:D830015B12 product:hypothetical DEAD/DEAH box helicase  
DE containing protein, full insert sequence. (Fragment).  
GN Name=Ddx58;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eumetazoa; Euarchoontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.,  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Niehi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuoka H.A., Ashburner T., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gusninch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer."  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayateu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK052871; BAC35183.1; -; mRNA.  
DR MGI; MGI:2442858; Ddx58.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004386; F:helicase activity; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR InterPro; IPR011545; DEAD/DEAH\_N.  
DR Pfam; PF00270; DEAD; 1.  
DR SMART; SM00487; DEXDC; 1.  
FT NON\_TER 231 231  
SQ SEQUENCE 231 AA; 25524 MW; 1D191607390D7FBB CRC64;  
Query Match 100.0%; Score 29; DB 2; Length 231;

```
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 1 KWVFFA 6
Db 145 KWVFFA 150

RESULT 4
Q6D7U3 ERWCT PRELIMINARY; PRT; 372 AA.
AC Q6D7U3;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Hydrogenase isoenzymes formation protein.
GN Name=hypD; OrderedLocusNames=ECAL1232;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCBI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holleva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin N., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
factors."
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG74142.1; -, Genomic_DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR TIGRFS; PIRSF005622; Hydrn mat_hypD; 1.
DR TIGRFAMS; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 372 AA; 41130 MW; A001A18AC015B620 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KWVFFA 6
Db 139 KWVFFA 144

RESULT 5
Q7M9N5 WOLSU PRELIMINARY; PRT; 373 AA.
AC Q7M9N5;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE HYDROGENASE PROTEIN.
GN Name=HYPD; OrderedLocusNames=WS0793;
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSMZ 1740;
RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Grosse R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer P., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
```

```
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
DR EMBL; BX571659; CAE09906.1; -, Genomic_DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR TIGRFS; PIRSF005622; Hydrn mat_hypD; 1.
DR TIGRFAMS; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 41793 MW; 3B7815EDB25790A6 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KWVFFA 6
Db 138 KWVFFA 143

RESULT 6
Q9KI10 BACCE PRELIMINARY; PRT; 387 AA.
ID Q9KI10 BACCE PRELIMINARY;
AC Q9KI10;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE GerN.
GN Name=gerN;
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1396;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC10876;
RX MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;
RA Thackray P.D., Behravan J., Southworth T.W., Moir A.;
RT "GerN, an antiporter homologue important in germination of Bacillus
cereus endospores."
RL J. Bacteriol. 183:476-482(2001).
DR EMBL; AF246294; AAF91326.1; -, Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMS; TIGR00932; 2a37; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41093 MW; 40DE45B71B715D01 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KWVFFA 6
Db 184 KWVFFA 189

RESULT 7
Q4MT39 BACCE PRELIMINARY; PRT; 387 AA.
ID Q4MT39 BACCE PRELIMINARY;
AC Q4MT39;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Na+/H+ antiporter.
GN ORFNames=BCE_G9241.1647;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
```

```

OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241; DOI=10.1073/pnas.0402414101;
RX Hoffmaster A.R., Ravel J., Raske D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Rillstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAEK01000008; FAL15336.1; -, Genomic DNA.
SQ SEQUENCE 387 AA; 41122 MW; 15CC136E79B12C38 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
DB 184 KVFFFA 189

RESULT 8
Q63DD4 BACCZ
ID Q63DD4 BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18770.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
DB 184 KVFFFA 189

RESULT 9
Q63DD4 BACCZ
ID Q63DD4 BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18770.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
DB 184 KVFFFA 189

```

```

Q6HKU6 BACHK
ID Q6HKU6 BACHK PRELIMINARY; PRT; 387 AA.
AC Q6HKU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN; OrderedLocuNames=BT9727_1493;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017355; AAT63168.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41076 MW; DFFECAD90985F951 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
DB 184 KVFFFA 189

RESULT 10
Q73AP3 BACCI
ID Q73AP3 BACCI PRELIMINARY; PRT; 387 AA.
AC Q73AP3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Germination protein gerN.
GN OrderedLocuNames=BCE1729;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:14960714; DOI=10.1093/nar/gkh258;
RA Raske D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017269; AAS40658.1; -, Genomic DNA.
DR TIGR; BCE1729; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.

```

DR InterPro; IPR004771; K\_eff.  
 DR InterPro; IPR006153; Na\_H\_Porter.  
 DR Pfam; PF00999; Na\_H\_Exchange; 1.  
 DR TIGRFAMs; TIGR00932; 2a37; 1.  
 KW Complete proteome; Transmembrane; Transport.  
 SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FEB3A3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;  
 Best Local Similarity 100.0%; Pred. NO. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 DB 184 KVVFFA 189

## RESULT 11

Q81SK9 BACAN  
 ID Q81SK9 BACAN PRELIMINARY; PRT; 387 AA.  
 AC Q81SK9; Q610J3; Q6KUP8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Germination protein genN.  
 DE OrderedLocustNames=BAL639, BAS1521, GBAAL639;  
 OS Bacillus anthracis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 NCBI\_TaxID=1392;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Ames / isolate Porton;  
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;  
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,  
 RA Nelson K.E., Tetelin H., Fouts D.E., Bisen J.A., Gill S.R.,  
 RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,  
 RA Kolony J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,  
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,  
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,  
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,  
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;  
 RT "The genome sequence of Bacillus anthracis Ames and comparison to  
 RT closely related bacteria."  
 RL Nature 423:81-86(2003).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Ames / isolate 0581;  
 RA Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,  
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,  
 RA Fraser C.M.;  
 RT "Bacillus anthracis comparative genomics."  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Stearns;  
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
 RA Richardson P., Rubin E., Rice H.;  
 RT "Complete genome sequence of Bacillus anthracis Sterne."  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE017029; AAP25572.1; -; Genomic DNA.  
 DR EMBL; AE017334; AAT30749.1; -; Genomic DNA.  
 DR EMBL; AE017225; AAT53839.1; -; Genomic DNA.  
 DR TIGR; BA1639; -;  
 DR TIGR; GBAAL639; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0008324; F:cation transporter activity; IEA.  
 DR GO; GO:0015299; F:solute-hydrogen antiporter activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR GO; GO:0006885; P:regulation of pH; IEA.

DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR004771; K\_eff.  
 DR InterPro; IPR006153; Na\_H\_Porter.  
 DR Pfam; PF00999; Na\_H\_Exchange; 1.  
 DR TIGRFAMs; TIGR00932; 2a37; 1.  
 KW Complete proteome; Transmembrane; Transport.  
 SQ SEQUENCE 387 AA; 40932 MW; D59F6A08A283BCA3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;  
 Best Local Similarity 100.0%; Pred. NO. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 DB 184 KVVFFA 189

## RESULT 12

Q8C5I3 MOUSE  
 ID Q8C5I3 MOUSE PRELIMINARY; PRT; 410 AA.  
 AC Q8C5I3;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length  
 DE enriched library, clone:6430573D20 product:hypothetical DEAD/DEAH box  
 DE helicase containing protein, full insert sequence.  
 GN Names=DDX58;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning."  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
 RX MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Offido T., Furuno M., Aono H., Baldarelli R., Bash G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohteki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [4]

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki R., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi P., Takaku-Akai H., Tanaka Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AK078287; BAC37205.1; -; mRNA.
DR Ensembl; ENSMUSG0000040296; Mus musculus.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDC; 1.
KW Helicase, Hypothetical protein, Nuclear protein.
SQ SEQUENCE 410 AA; 46841 MW; ECC9E3D2D28C5FE0 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 293 KVVFFA 298

RESULT 13
Q9PHV5 CAMJE PRELIMINARY; PRT; 442 AA.
AC Q9PHV5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative integral membrane protein.
GN OrderedLocustNames=Cj0560;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBL_TaxID=197;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagers K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139075; CAB75196.1; -; Genomic_DNA.
DR PIR; H81402; H81402.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:antipporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; P:multidrug transport; IEA.
DR InterPro; IPR002114; HPr_Serp_S.
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; MatE; 1.
DR TIGRFAMs; TIGR00797; matE; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 442 AA; 49452 MW; 38EA04E7AB1A8F3E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 313 KVVFFA 318

RESULT 14
QSHYEL HUMAN PRELIMINARY; PRT; 703 AA.
AC QSHYEL;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFP686N19181 (fragment).
GN Name=DKFP686N19181;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBL_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin endothel;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Newes H.W., Weil B., Amd C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX647917; CA146068.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Hypothetical protein.
FT NON_TER 703
SQ SEQUENCE 703 AA; 80308 MW; 3CF7500F4F955586 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 703;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KVVFPA 6
Db 247 KVVFPA 252

RESULT 15
Q6AG25 LEIXX
ID Q6AG25 LEIXX PRELIMINARY; PRT; 721 AA.
AC Q6AG25;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ATP-dependent RNA helicase.
GN OrderedLocusNames=Lxx07490;
OS Leifsonia xyl (subsp. xyl).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.P., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F. Jr., Carrier H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Secubal J.C.;
RA "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyl subsp. xyl."
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AE016822; AAY88670.1; -; Genomic_DNA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome; DNA-binding; Helicase; Hydrolase.
SQ SEQUENCE 721 AA; 78960 MW; 73F5D2A8435BADE3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 564 KVVFPA 569

RESULT 16
O95786 HUMAN
ID O95786 HUMAN PRELIMINARY; PRT; 925 AA.
AC O95786;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Name=DDX58; Synonym=RII-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Sun Y.W.;
"RIG-I, a human homolog gene of RNA helicase, is induced by retinoic
acid during the differentiation of acute promyelocytic leukemia
cell.";
Thesis (1997), Shanghai Institute of Hematology, Rui-Jin Hospital,
Shanghai Second Medical University.
RL NUCLEOTIDE SEQUENCE.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Yi-Wu S.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038963; AAD19826.1; -; mRNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR HGNC; HGNC:19102; DDX58.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase.
SQ SEQUENCE 925 AA; 106613 MW; 5922B4F3DD0F00D4 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 925;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 292 KVVFPA 297

RESULT 17
Q5VYTI HUMAN
ID Q5VYTI HUMAN PRELIMINARY; PRT; 925 AA.
AC Q5VYTI;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE OTTHUMP00000021185.
GN Name=RP11-334P12.2; ORFNames=RP11-334P12.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sehra H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL353671; CAH71251.1; -; Genomic_DNA.
DR EMBL; AL161783; CAH72600.1; -; Genomic_DNA.
DR EMBL; AL161783; CAH71251.1; JOINED; Genomic_DNA.
DR EMBL; AL353671; CAH72600.1; JOINED; Genomic_DNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.

```

```

DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase; Hydrolase; Nuclear protein.
SQ SEQUENCE 925 AA; 106600 MW; BF0D501C395BAE25 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 925;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |||||
Db 292 KVVFFA 297

RESULT 18
Q60899 MOUSE
ID Q60899_MOUSE PRELIMINARY; PRT; 926 AA.
AC Q60899;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DEAD/H box polypeptide RIG-I.
GN Name=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wei J., Gu J.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY553221; G559532.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR006935; ResIII.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF04851; ResIII; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
SQ SEQUENCE 926 AA; 105877 MW; 632462010107698E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 926;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |||||
Db 293 KVVFFA 298

RESULT 19
Q9GLV6 PIG
ID Q9GLV6_PIG PRELIMINARY; PRT; 940 AA.
AC Q9GLV6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Name=RHIV-1;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhang X., Wang C., Schook L.B., Hawken R.J., Rutherford M.S.;
RX MEDLINE=20261798; PubMed=10799277; DOI=10.1006/mpat.1999.0349;
RN [5]

RT "An RNA helicase, RHIV -1, induced by porcine reproductive and
RT respiratory syndrome virus (PRRSV) is mapped on porcine chromosome
RT 10q13.";
RL Microb. Pathog. 28:267-278(2000).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF181119; AAG09428.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase; Hydrolase; Nuclear protein; Repeat.
SQ SEQUENCE 940 AA; 107584 MW; 118CA910B0AF7821 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |||||
Db 290 KVVFFA 295

RESULT 20
NOS2_MOUSE
ID NOS2_MOUSE STANDARD; PRT; 1144 AA.
AC P29477; O70515; O70516;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (iNOS) (Macrophage NOS) (MAC-NOS).
GN Name=Nos2; Synonyms=Inos1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92229444; PubMed=1373522;
RA Xie Q.-W., Cho H.J., Calaycay J., Munford R.A., Swiderek K.M.,
RA Lee I.D., Ding A., Iroso F., Nathan C.;
RT "Cloning and characterization of inducible nitric oxide synthase from
RT mouse macrophages.";
RL Science 256:225-228(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92357701; PubMed=1379716;
RA Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;
RT "Cloned and expressed macrophage nitric oxide synthase contrasts with
RT the brain enzyme.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92210618; PubMed=1372907;
RA Lyons C.R., Orloff G.J., Cunningham J.M.;
RT "Molecular cloning and functional expression of an inducible nitric
RT oxide synthase from a murine macrophage cell line.";
RL J. Biol. Chem. 267:6370-6374(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96088781; PubMed=7503239;
RA Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;
RT "Role of NF-kappa B in the regulation of inducible nitric oxide
RT synthase in an MTAL cell line";
RL Am. J. Physiol. 269:F718-F729(1995).
RN [5]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-211; LEU-967 AND PHE-968.

```



RC STRAIN-B10.S/J, BALB/cBYJ, DBA/2J, NOD/LtJ, and SJL/J; TISSUE-Spleen;  
RX MEDLINE=99370037; PubMed=10438970;  
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,  
RA Blankenhorn E.P.;  
RT "Sequence polymorphisms in the chemokines Sclav (TCA-3), Scya2  
RT (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are  
RT candidates for eae7, a locus controlling susceptibility to monophasic  
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";  
RL J. Immunol. 163:2262-2266(1999).  
RN [6]  
RN EFFECT OF ASPIRIN.  
RC TISSUE=Macrophage;  
RX MEDLINE=95372392; PubMed=7544010;  
RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,  
RA Waisemann G., Abramson S.B.;  
RT "The mode of action of aspirin-like drugs: effect on inducible nitric  
RT oxide synthase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).  
RN [7]  
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.  
RX MEDLINE=97477482; PubMed=9334294; DOI=10.1126/science.278.5337.425;  
RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,  
RA Stuehr D.J., Tainer J.A.;  
RT "The structure of nitric oxide synthase oxygenase domain and inhibitor  
RT complexes.";  
RL Science 278:425-431(1997).  
RN [8]  
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.  
RX MEDLINE=98182450; PubMed=9516116; DOI=10.1126/science.279.5359.2121;  
RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,  
RA Tainer J.A.;  
RT "Structure of nitric oxide synthase oxygenase dimer with pterin and  
RT substrate.";  
RL Science 279:2121-2126(1998).  
RN [9]  
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.  
RX MEDLINE=20031637; PubMed=10562538; DOI=10.1093/emboj/18.22.6271;  
RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,  
RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;  
RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin  
RT hook and pterin-binding segment in dimerization and  
RT tetrahydropterin interaction.";  
RL EMBO J. 18:6260-6270(1999).  
RN [10]  
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.  
RX MEDLINE=20031638; PubMed=10562539; DOI=10.1093/emboj/18.22.6271;  
RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,  
RA Tainer J.A., Stuehr D.J., Getzoff E.D.;  
RT "N-terminal domain swapping and metal ion binding in nitric oxide  
RT synthase dimerization.";  
RL EMBO J. 18:6271-6281(1999).  
RN [11]  
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.  
RX MEDLINE=20233702; PubMed=10769116; DOI=10.1021/bi992409a;  
RA Crane B.R., Arvai A.S., Ghosh S., Getzoff E.D., Stuehr D.J.,  
RA Tainer J.A.;  
RT "Structures of the N(omega)-hydroxy-L-arginine complex of inducible  
RT nitric oxide synthase oxygenase dimer with active and inactive  
RT pterins.";  
RL Biochemistry 39:4608-4621(2000).  
RN [12]  
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF TRP-457 MUTANTS.  
RX MEDLINE=21526413; PubMed=11669619; DOI=10.1021/bi011183k;  
RA Aoyagi M., Arvai A.S., Ghosh S., Stuehr D.J., Tainer J.A.,  
RA Getzoff E.D.;  
RT "Structures of tetrahydropterin binding-site mutants of inducible  
RT nitric oxide synthase oxygenase dimer and implicated roles of  
RT Trp457.";  
RL Biochemistry 40:12826-12832(2001).  
RN [13]  
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.  
RX MEDLINE=22325496; PubMed=12437348; DOI=10.1021/bi026313j;  
RA Rosenfeld R.J., Garcin E.D., Panda K., Andersson G., Aberg A.,  
RA Wallace A.V., Morris G.M., Olson A.J., Stuehr D.J., Tainer J.A.,  
RA Getzoff E.D.;  
RT "Conformational changes in nitric oxide synthases induced by  
RT chlorazone and nitroindazoles: crystallographic and computational  
RT analyses of inhibitor potency.";  
RL Biochemistry 41:13915-13925(2002).  
RN [14]  
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 77-495.  
RX MEDLINE=2251717; PubMed=12464241; DOI=10.1016/S0003-9861(02)00555-6;  
RA Fedorov R., Ghosh D.K., Schluchting I.;  
RT "Crystal structures of cyanide complexes of p450cam and the oxygenase  
RT domain of inducible nitric oxide synthase - structural models of the  
RT short-lived oxygen complexes.";  
RL Arch. Biochem. Biophys. 409:25-31(2003).  
CC -I- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule  
CC with diverse functions throughout the body. In macrophages, NO  
CC mediates tumoricidal and bactericidal actions.  
CC -I- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline +  
CC nitric oxide + n NADP(+).  
CC -I- COFACTOR: Heme.  
CC -I- COFACTOR: FAD. Binds 1 mole of FAD.  
CC -I- COFACTOR: FMN. Binds 1 mole of FMN.  
CC -I- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric  
CC form of the enzyme.  
CC -I- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin  
CC inhibits expression and function of this enzyme and effects may be  
CC exerted at the level of translational/posttranslational  
CC modification and directly on the catalytic activity.  
CC -I- SUBUNIT: Homodimer. Binds SLC9A3R1 (By similarity).  
CC -I- TISSUE SPECIFICITY: Macrophages.  
CC -I- INDUCTION: By treatment with endotoxins or cytokines.  
CC -I- SIMILARITY: Belongs to the NOS family.  
CC -I- SIMILARITY: Contains 1 flavodoxin-like domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; M87039; AAA39315.1; -; mRNA.  
CC EMBL; M92649; -; NOT ANNOTATED CDS; mRNA.  
CC EMBL; M84373; AAA39834.1; -; mRNA.  
CC EMBL; U43428; AAC52356.1; -; mRNA.  
CC EMBL; AF065919; AAC17914.1; -; mRNA.  
CC EMBL; AF065920; AAC17915.1; -; mRNA.  
CC EMBL; AF065921; AAC17916.2; -; mRNA.  
CC EMBL; AF065922; AAC17917.2; -; mRNA.  
CC EMBL; AF065923; AAC17918.2; -; mRNA.  
CC PIR; A43271; A43271.  
CC DR PDB; 1DD7; X-ray; A=114-498.  
CC DR PDB; 1DF1; X-ray; A/B=77-499.  
CC DR PDB; 1DWV; X-ray; A/B=77-496.  
CC DR PDB; 1DWX; X-ray; A/B=77-496.  
CC DR PDB; 1DXX; X-ray; A/B=77-496.  
CC DR PDB; 1JWJ; X-ray; A/B=66-498.  
CC DR PDB; 1JWK; X-ray; A/B=66-498.  
CC DR PDB; 1MB8; X-ray; A/B=65-498.  
CC DR PDB; 1MBE; X-ray; A/B=65-498.  
CC DR PDB; 1MBH; X-ray; A/B=65-498.  
CC DR PDB; 1MB1; X-ray; A/B=65-498.  
CC DR PDB; 1M9T; X-ray; A/B=65-498.  
CC DR PDB; 1N2N; X-ray; A/B=77-495.  
CC DR PDB; 1NOC; X-ray; A=115-498.  
CC DR PDB; 1NOD; X-ray; A/B=77-499.  
CC DR PDB; 1NOS; X-ray; @=115-498.  
CC DR PDB; 1QOM; X-ray; A/B=65-498.  
CC DR PDB; 1QW4; X-ray; A/B=77-495.  
CC DR PDB; 1QW5; X-ray; A/B=77-495.  
CC DR PDB; 1R35; X-ray; A/B=66-498.  
CC DR PDB; 1VAE; X-ray; A/B=77-495.  
CC DR PDB; 2BRJ; X-ray; A=77-498.  
CC DR PDB; 2NOD; X-ray; A/B=77-499.



```
DR PDB; 2NOS; X-ray; @=115-498.
DR PDB; 3NOD; X-ray; A/B=77-499.
DR IntAct; P29477; -.
DR Ensembl; ENSMUSG0000020826; Mus musculus.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; TAS.
DR GO; GO:0020037; F:heme binding; NAS.
DR GO; GO:0020037; F:heme binding; NAS.

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 21
Q5SXT3_MOUSE PRELIMINARY; PRT; 1144 AA.
AC Q5SXT3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Nitric oxide synthase 2, inducible, macrophage (Inducible nitric oxide
synthase).
GN Names=Nos2; ORFNames=RP23-341J22.2-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Coxe F., Lebacher B., Rique H., Leopold O., Boutin J.A.,
RA Galizzi J.-P.;
RT "Genomic structure of the murine inducible nitric oxide synthase (i-
NOS) gene."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL592185; CA125275.1; -; Genomic DNA.
DR EMBL; AF427516; AAL24076.1; -; Genomic DNA.
SQ SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 22
Q8R410_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q8R410;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Names=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

PDB; 2NOS; X-ray; @=115-498.
PDB; 3NOD; X-ray; A/B=77-499.
IntAct; P29477; -.
Ensembl; ENSMUSG0000020826; Mus musculus.
MGI; MGI:97361; Nos2.
GO; GO:0030863; C:cortical cytoskeleton; IDA.
GO; GO:0005829; C:cytosol; TAS.
GO; GO:0048471; C:perinuclear region; IDA.
GO; GO:0005516; F:calmodulin binding; TAS.
GO; GO:0020037; F:heme binding; NAS.
GO; GO:0020037; F:heme binding; NAS.

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 23
Q6P6A0_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q6P6A0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nos2 protein.
GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
```

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., LeGevan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
SQ SEQUENCE 1145 AA; 130671 MW; C26E09F536923295 CRC64;  
PRT; 164 AA.  
RESULT 24  
ID Q73N39 TREDE PRELIMINARY; PRT; 164 AA.  
AC Q73N39;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Membrane protein, putative.  
GN OrderedLocusNames=TDE1317;  
OS Treponema denticola.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
OX NCBI\_TaxID=158;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RA Strausberg R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC062378; AHA62378.1; -; mRNA.  
DR HSSP; P29477; 1JWK.  
DR MGI; MGI:97361; Nos2.  
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.  
DR GO; GO:0048471; C:perinuclear region; IDA.  
DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0042803; F:protein homodimerization activity; IDA.  
DR GO; GO:0042742; P:defense response to bacteria; IMP.  
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.  
DR GO; GO:0001666; P:response to hypoxia; IDA.  
DR GO; GO:0006801; P:superoxide metabolism; IMP.  
DR InterPro; IPR003097; FAD binding.  
DR InterPro; IPR001094; Flavodoxin like.  
DR InterPro; IPR008254; Flavodoxin synth.  
DR InterPro; IPR001709; PPN\_Cyt\_redctse.  
DR InterPro; IPR012144; NOS.  
DR InterPro; IPR004030; NO synthase.  
DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
DR Pfam; PF00667; FAD binding 1; 1.  
DR Pfam; PF00258; Flavodoxin 1; 1.  
DR Pfam; PF00175; NAD binding 1; 1.  
DR Pfam; PF02898; NO synthase 1; 1.  
DR PIRSP; PIRSF000333; NOS; 1.  
DR PRINTS; PR00369; FLAVODOXIN.  
DR PRINTS; PR00371; FPNCR.  
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.  
DR PROSITE; PS60001; NOS, UNKNOWN 1.  
SQ SEQUENCE 1145 AA; 130671 MW; C26E09F536923295 CRC64;  
PRT; 164 AA.  
Query Match 100.0%; Score 29; DB 2; Length 1145;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
DB 515 KVVFFA 520  
PRT; 164 AA.  
RESULT 24  
ID Q73N39 TREDE PRELIMINARY; PRT; 164 AA.  
AC Q73N39;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Membrane protein, putative.  
GN OrderedLocusNames=TDE1317;  
OS Treponema denticola.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
OX NCBI\_TaxID=158;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 35405 / DSM 14222;  
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;  
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,  
RA Sedghari R., Davidsen T.M., DeBoy R.T., Fouts D.E., Hatt D.H.,  
RA Salengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,  
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,  
RA Gebregeorgis E., Geer K., Teagave G., Malek J.A., Ayodeji B.,  
RA Shatman S., McLeod M.P., Smajd D., Howell J.K., Pal S., Amin A.,  
RA Vashisth P., McNeill T.Z., Xiang D., Sodergren E., Baca E.,  
RA Wainstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;  
RT "Comparison of the genome of the oral pathogen Treponema denticola  
RT with other spirochete genomes";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).  
DR EMBL; AR017250; AAS11834.1; -; Genomic\_DNA.  
DR TIGR; TDE1317; -.  
KW Complete proteome.  
SQ SEQUENCE 164 AA; 18968 MW; 27E92778DDA9117C CRC64;  
PRT; 203 AA.  
Query Match 96.6%; Score 28; DB 2; Length 164;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
DB 50 KVVFFA 55  
PRT; 203 AA.  
RESULT 25  
Q6AKE9 DESPS  
ID Q6AKE9 DESPS PRELIMINARY; PRT; 203 AA.  
AC Q6AKE9;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Related to McbG protein.  
GN OrderedLocusNames=DP2447;  
OS Desulfotalea psychrophila.  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;  
OC Desulfobulbaceae; Desulfotalea.  
OX NCBI\_TaxID=84980;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=LSV54 / DSM 12343;  
RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;  
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,  
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,  
RA Teeling H., Leuschner W.D., Gloeckner P.-O., Lupas A.N., Amann R.,  
RA Klenk H.-P.;  
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium  
RT from permanently cold Arctic sediments.";  
RL Environ. Microbiol. 6:887-902 (2004).  
DR EMBL; CR522870; CAG37176.1; -; Genomic\_DNA.  
DR InterPro; IPR001646; 5peptide repeat.  
DR Pfam; PF00805; Pentapeptide; 3.  
KW Complete proteome.  
SQ SEQUENCE 203 AA; 23270 MW; 2EA1CD022861292D CRC64;  
PRT; 380 AA.  
Query Match 96.6%; Score 28; DB 2; Length 203;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
DB 52 KVVFFA 57  
PRT; 380 AA.  
RESULT 26  
O67225 AQUAE  
ID O67225 AQUAE PRELIMINARY; PRT; 380 AA.  
AC O67225;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

DE Hydrogenase expression/formation protein HypD.
GN Name=hypD; OrderedLocNames=AQ_1157;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AS000726; AAC07185.1; -; Genomic_DNA.
DR PIR; F70399; F70399.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrgn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 141 KVIFFA 146

RESULT 27
Q81FH5_BACCR PRELIMINARY; PRT; 387 AA.
ID Q81FH5;
AC Q81FH5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Na+/H+ antiporter Napa (inosine-dependent germination).
GN OrderedLocNames=BC1612;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Fusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017003; AAP08591.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; C:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; Keff.
DR InterPro; IPR006153; Na/H porter.
DR Pfam; PF00999; Na/H Exchanger; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41037 MW; 907C03B6BA150B4A CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DE Hydrogenase expression/formation protein HypD.
GN Name=hypD; OrderedLocNames=AQ_1157;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AS000726; AAC07185.1; -; Genomic_DNA.
DR PIR; F70399; F70399.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrgn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 141 KVIFFA 146

RESULT 27
Q81FH5_BACCR PRELIMINARY; PRT; 387 AA.
ID Q81FH5;
AC Q81FH5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Na+/H+ antiporter Napa (inosine-dependent germination).
GN OrderedLocNames=BC1612;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Fusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017003; AAP08591.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; C:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; Keff.
DR InterPro; IPR006153; Na/H porter.
DR Pfam; PF00999; Na/H Exchanger; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41037 MW; 907C03B6BA150B4A CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 184 KIVFFA 189

RESULT 28
Q5WPU9_LUTLO PRELIMINARY; PRT; 399 AA.
ID Q5WPU9;
AC Q5WPU9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 43.2 kDa salivary protein.
GN ORFNames=LJM11_Clu9;
OS Lutzomyia longipalpis (Sand fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
OC Psychodidae; Lutzomyia; Lutzomyia.
OX NCBI_TaxID=7200;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Salivary gland;
RX PubMed=15371479; DOI=10.1242/jeb.01185;
RA Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
RT "Identification of the most abundant secreted proteins from the
RT salivary glands of the sand fly Lutzomyia longipalpis, vector of
RT Leishmania chagasi.";
RL J. Exp. Biol. 207:3717-3729(2004).
DR EMBL; AY445935; AAS05318.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
SQ SEQUENCE 399 AA; 45277 MW; F4E19F115794AAE8 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 399;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 305 KVIFFA 310

RESULT 29
Q4TRF8_9SPHN PRELIMINARY; PRT; 450 AA.
ID Q4TRF8;
AC Q4TRF8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Membrane protein.
GN ORFNames=ELI0568;
OS Erythrobacter litoralis HTCC2594.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=314225;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC2594;
RA Giannoni S.J., Cho J.-C., Ferreira S., Johnson J., Kravitz S.,
RA Halpern A., Remington K., Beeson K., Tran B., Rogers V.-H.,
RA Friedman R., Venter J.C.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAG0100001; EAL76762.1; -; Genomic DNA.
SQ SEQUENCE 450 AA; 50280 MW; 077F448E75ADF977 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KVVFPA 6
Db 116 KIVFFA 121

RESULT 30
Q4S4T5_TETNG
ID Q4S4T5_TETNG PRELIMINARY; PRT; 464 AA.
AC Q4S4T5;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 2 SCAF14738, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0024047001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Telostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Doseat C., Segurens B.,
RA David C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014738; CAG04347.1; -; Genomic_DNA.
FT NON_TER 464 464
SQ SEQUENCE 464 AA; 53213 MW; 0F9FF01DB193CE5C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 464;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 304 KIVFFA 309

RESULT 31
Q91VU5_MOUSE
ID Q91VU5_MOUSE PRELIMINARY; PRT; 606 AA.
AC Q91VU5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Wtcd2 protein.
GN Name=Af661311; Synonyms=Wtcd2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

```

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RX NIH MGC Project;
RG Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009019; AA09019.1; -; mRNA.
DR Ensembl; ENSMUSG0000024169; Mus musculus.
DR MGI; MGI:2146906; A1661311.
DR GO; GO:0005488; Fibrinogen; IEA.
DR InterPro; IPR011990; TPR-like helical.
SQ SEQUENCE 606 AA; 70992 MW; 4BB6057E07ADA16C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 606;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 376 KIVFFA 381

RESULT 32
Q4WB22_ASPPU
ID Q4WB22_ASPPU PRELIMINARY; PRT; 623 AA.
AC Q4WB22;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Afug06810;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=AF293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins K., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Gobie A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Kaller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kmagai T., Lafon A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penalba M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,

```

RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,  
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,  
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,  
RA Takeuchi M., Tekala J., Turner G., Vazquez de Aldana C.R., Weidman J.,  
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,  
RA Machida M., Hall N., Barrell B., Denning D.W.,  
RA "Genomic sequence of the pathogenic and allergenic filamentous fungus  
RT Aspergillus fumigatus.";  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAH01000013; EAL85442.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 623 AA; 72379 MW; 08795F0DEF6C18E2 CRC64;  
  
Query Match 96.6%; Score 28; DB 2; Length 623;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
Db 96 KVIFFA 101  
||:||||  
  
RESULT 33  
Q5K7E5 CRYNE PRELIMINARY; PRT; 630 AA.  
AC Q5K7E5;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=CN00130;  
OS Cryptococcus neoformans var. neoformans JEC21.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
OX NCBI\_TaxID=214684;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JEC21;  
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,  
RA Van Aken S., Fraser C.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=JEC21;  
RX PubMed=15653466; DOI=10.1126/science.1103773;  
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,  
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,  
RA Kwon-Chung K.J., Lengler K.B., Maiti R., Marra M.A., Marra R.E.,  
RA Mathewson C.A., Mitchell T.G., Perlea M., Riggs F.R., Salzberg S.L.,  
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,  
RA Fraser C.M., Hyman R.W.;  
RL "The genome of the basidiomycetous yeast and human pathogen  
RT Cryptococcus neoformans.";  
RT Science 307:1321-1324(2005).  
RL EMBL; AS017356; AAW47004.1; -; Genomic\_DNA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0046872; F:metal ion binding; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR InterPro; IPR007219; Fungal trans.  
DR InterPro; IPR001138; Fungal\_Trcrpt\_N.  
DR Pfam; PF04082; Fungal\_trans; 1.

DR Pfam; PF00172; Zn\_c1us; 1.  
DR PRINTS; PR00054; FUNGALZNCYS.  
DR SMART; SMO0066; GAL4; 1.  
DR PROSITE; PS00463; ZN2\_CV6\_FUNGAL\_1; 1.  
DR PROSITE; PS00463; ZN2\_CV6\_FUNGAL\_2; 1.  
KW Complete proteome; DNA-binding; Hypothetical protein; Metal-binding;  
KW Nuclear protein; Transcription; Transcription regulation; Zinc.  
SQ SEQUENCE 630 AA; 68912 MW; 730A7C02A87D6B3B CRC64;  
  
Query Match 96.6%; Score 28; DB 2; Length 630;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
Db 572 KVIFFA 577  
||:||||  
  
RESULT 34  
Q6RUU2 MOUSE PRELIMINARY; PRT; 663 AA.  
AC Q6RUU2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Brathwaite M., Waelitz P., Dudekula D., Nagaraja R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY491413; AAS21643.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 663 AA; 77192 MW; CEB02E3EBD356F1C CRC64;  
  
Query Match 96.6%; Score 28; DB 2; Length 663;  
Best Local Similarity 83.3%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
Db 433 KIVFFA 438  
||:||||  
  
RESULT 35  
Q83IB2 TROMS PRELIMINARY; PRT; 690 AA.  
ID Q83IB2 TROMS PRELIMINARY;  
AC Q83IB2;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative helicase regulator.  
GN OrderedLocNames=TW130;  
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Micrococcineae; Cellulomonadaceae; Tropheryma.  
OX NCBI\_TaxID=218496;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22495039; PubMed=12606174; DOI=10.1016/S0140-6736(03)12597-4;  
RA Bentley S.D., Maitwald M., Murphy L.D., Pallen M.J., Yeats C.A.,  
RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,  
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,  
RA Barrell B.G., Parkhill J., Rellman D.A.;  
RL "Sequencing and analysis of the genome of the Whipple's disease  
RT bacterium Tropheryma whipplei.";  
RL Lancet 361:637-644(2003).  
DR EMBL; BX251410; CAD66810.1; -; Genomic\_DNA.

DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004386; F:Helicase activity; IEA.  
 DR InterPro; IPR011545; DEAD/DEAH\_N.  
 DR InterPro; IPR001650; Helicase\_C.  
 DR InterPro; IPR00330; SNF2\_N.  
 DR Pfam; PF00271; Helicase\_C; 1.  
 DR Pfam; PF00176; SNF2\_N; 1.  
 DR SMART; SM00487; DEXDC; 1.  
 DR SMART; SM00490; HELICc; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 690 AA; 76266 MW; CD3633B948669E32 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 690;  
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 526 KIVFFA 531

## RESULT 36

Q83GW3 TROWT PRELIMINARY; PRT; 698 AA.  
 AC Q83GW3;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE DNA helicase  
 GN OrderedLocustNames=TW1118;  
 OS Tropheryma whipplei (strain Twist) (Whipple's bacillus).  
 OC Bacteria; Actinobacteria; Actinobacteriales;  
 OC Micrococciaceae; Cellulomonadaceae; Tropheryma.  
 OX NCBI\_TaxID=203267;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Twist;  
 RX MEDLINE=22784088; PubMed=12902375;  
 RA Raoult D., Ogata H., Audic S., Robert C., Suhre K., Drancourt M.,  
 RA Claverie J.-M.;  
 RT "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a  
 RT reduced genome.";  
 RL Genome Res. 13:1800-1809(2003).  
 DR EMBL; AE016850; AAO44215.1; -; Genomic\_DNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004386; F:Helicase activity; IEA.  
 DR InterPro; IPR011545; DEAD/DEAH\_N.  
 DR InterPro; IPR001650; Helicase\_C.  
 DR InterPro; IPR00330; SNF2\_N.  
 DR Pfam; PF00271; Helicase\_C; 1.  
 DR Pfam; PF00176; SNF2\_N; 1.  
 DR SMART; SM00487; DEXDC; 1.  
 DR SMART; SM00490; HELICc; 1.  
 KW Complete proteome; Helicase.  
 SQ SEQUENCE 698 AA; 77193 MW; 6D104BF533CDDE72 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 698;  
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 534 KIVFFA 539

## RESULT 37

Q55HW1 CRYNE PRELIMINARY; PRT; 760 AA.  
 ID Q55HW1;  
 AC Q55HW1;  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=CNEN0110;  
 OS Cryptococcus neoformans var. neoformans B-3501A.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=283643;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B-3501A;  
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
 RA Wickes B.L., Fu J., Davis R.W.;  
 RT "Cryptococcus neoformans serotype D sequencing."  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAEY01000066; EAL17182.1; -; Genomic\_DNA.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;  
 KW Transcription; Transcription regulation; Zinc.  
 SQ SEQUENCE 760 AA; 84062 MW; 735C53C64A854619 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 760;  
 Best Local Similarity 83.3%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 702 KIVFFA 707

## RESULT 38

Q6ZQ91 MOUSE PRELIMINARY; PRT; 1265 AA.  
 AC Q6ZQ91;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE MKIAA0590 protein (fragment).  
 GN Name=MKIAA0590;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX PubMed=14621295;  
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,  
 RA Suga Y., Nagase T., Ohara O., Koga H.;  
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:  
 RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous  
 RT cDNAs identified by screening of terminal sequences of cDNA clones  
 RT randomly sampled from size-fractionated libraries.";  
 RL DNA Res. 10:167-180(2003).  
 DR EMBL; AK129167; BAC97977.1; -; mRNA.  
 DR NON TER 1  
 FT SEQUENCE 1265 AA; 143403 MW; C9C157ABE80FF928 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1265;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 1081 KIVFFA 1086

```
RESULT 39
Q5F3M1 CHICK
ID Q5F3M1 CHICK PRELIMINARY; PRT; 1412 AA.
AC Q5F3M1
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.13m2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Biagodateski A., Kostovska D., Koter M.,
RA Flachy J., Carninci P., Hayashizaki Y., Buerstede J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT genefunction analysis."
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851629; CAH65263.1; -; mRNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE 1412 AA; 158448 MW; FA005085B274747 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1412;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 1225 KIVFFA 1230

RESULT 40
Q4Q5Q4 LEIMA
ID Q4Q5Q4 LEIMA PRELIMINARY; PRT; 1655 AA.
AC Q4Q5Q4;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Lmjf32.0310;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivans A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren F., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CT005269; CAJ08491.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1655 AA; 181249 MW; 2B5317E9ED469A55 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1655;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 1397 KIVFFA 1402
```

```
RESULT 41
Q4LBQ8 SODGL
ID Q4LBQ8 SODGL PRELIMINARY; PRT; 88 AA.
AC Q4LBQ8;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chey protein.
GN Name=chey;
OS Sodalis glossinidius.
OC Plasmid pSG4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PLASMID=pSG4;
RA Darby A.C., Lagnel J., Matthew C.Z., Bourtzis K., Maudlin I.,
RA Welburn S.C.;
RT "Extrachromosomal DNA of the symbiont Sodalis glossinidius."
RL J. Bacteriol. 187:5003-5007(2005).
DR EMBL; AJ868439; CAI59440.1; -; Genomic_DNA.
DR EMBL; AJ868438; CAI59427.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 88 AA; 10177 MW; F4168F2A56B8D0AC CRC64;

Query Match 93.1%; Score 27; DB 2; Length 88;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 42 KIIFPA 47

RESULT 42
Q9RQ09 BACTN
ID Q9RQ09 BACTN PRELIMINARY; PRT; 183 AA.
AC Q9RQ09; Q7C422;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE RNA polymerase sigma factor SigZ-like protein (RNA polymerase ECF-type
DE sigma factor).
GN Name=sigZ; OrderedLocusNames=BT1278;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482;
RX MEDLINE=93980805; PubMed=10449780; DOI=10.1073/pnas.96.17.9833;
RA Hooper L.V., Xu J., Falk P.G., Midtvedt T., Gordon J.I.;
RT "A molecular sensor that allows a gut commensal to control its
RT nutrient foundation in a competitive ecosystem."
RL Proc. Natl. Acad. Sci. U.S.A. 96:9833-9838(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; AF137263; AAF01488.1; -; Genomic_DNA.
DR EMBL; AE016931; AAO76385.1; -; Genomic_DNA.
DR GO; GO:0016987; P:sigma factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007627; Sigma70_r2.
```



DR InterPro; IPR011991; Wing\_hlx\_DNA\_bd.  
DR Pfam; PF04542; Sigma70\_r2; 1.  
KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;  
KW Nucleotidyltransferase; Sigma factor; Transcription;  
KW Transcription regulation; Transferase.  
SQ SEQUENCE 193 AA; 22042 MW; 6B24DABC99BEC643 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 183;  
Best Local Similarity 66.7%; Pred. No. 3.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6  
|::|||  
Db 172 KLIFFA 177

## RESULT 43

Q61C67\_CABER  
ID Q61C67\_CABER PRELIMINARY; PRT; 315 AA.  
AC Q61C67;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein CBG13055 (Fragment).  
GN Name=CBG13055;  
OS Caenorhabditis briggsae.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodexinae; Caenorhabditis.  
OX NCBI\_TaxID=6238;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RG The C.briggsae Sequencing Consortium;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CAAC0100061; CA267532.1; -; Genomic DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7cm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODPSN  
DR PROSITE; PS0262; G\_PROTEIN\_RSECP\_F1\_2; 1.  
KW G-protein coupled receptor; Hypothetical protein; Receptor;  
KW Transducer; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 315  
SQ SEQUENCE 315 AA; 35855 MW; 579B59DD01874512 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 315;  
Best Local Similarity 66.7%; Pred. No. 5.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6  
|::|||  
Db 117 KLIFFA 122

## RESULT 44

Q4HSJ7\_CAMUP  
ID Q4HSJ7\_CAMUP PRELIMINARY; PRT; 362 AA.  
AC Q4HSJ7;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hydrogenase expression/formation protein HypD.  
GN Name=hypD; ORFNames=CUP0294;  
OS Campylobacter upsaliensis RM3195.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Campylobacteraceae; Campylobacter.  
OX NCBI\_TaxID=306264;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RC STRAIN=RM3195;  
RA Fouts D.E., Mongodin E.P., Mandrell R.E., Miller W.G., Raeko D.A.,  
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,  
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,  
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,  
RA Nelson K.E.;  
RT "Major structural and novel potential virulence mechanisms from the  
RT genomes of multiple Campylobacter species."  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAFJ01000002; EAL53713.1; -; Genomic DNA.  
SQ SEQUENCE 362 AA; 40365 MW; 15B0A8B12D60CAED CRC64;

Query Match 93.1%; Score 27; DB 2; Length 362;  
Best Local Similarity 66.7%; Pred. No. 6.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6  
|::|||  
Db 132 KLIFFA 137

## RESULT 45

Q9V7J0\_DROME  
ID Q9V7J0\_DROME PRELIMINARY; PRT; 382 AA.  
AC Q9V7J0; Q9GQ81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE C84421-PB, isoform B (Aspartyl beta-hydroxylase variant 2).  
GN Name=Asph; ORFNames=C84421;  
OS Drosophila melanogaster (fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RX Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RX Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RX George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RX Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RX Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RX Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RX Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RX Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RX Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RX Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RX Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RX Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RX de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RX Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RX Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
RX Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RX Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RX Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RX Hoeltin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RX Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RX Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RX Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RX Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RX Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RX Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RX Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclbb J.M.M.,  
RX Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RX Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RX Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RX Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RX Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RX Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,



Cy 1 KVVFFA 6  
Db 53 KIIFFA 58

RESULT 46  
Q6L2B4\_PICTO  
ID ID Q6L2B4\_PICTO PRELIMINARY; PRT; 410 AA.  
AC Q6L2B4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Lipopolysaccharide N-acetylglucosaminyltransferase.  
GN OrderedLocusNames=PTO0303;  
OS Picrophilus torridus.  
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;  
OC Microphlilaceae; Picrophilus.  
OX NCBI\_TaxID=82076;  
[1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DSM 9790 / ATCC 700027;  
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;  
RA Fueterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,  
RS Schnepers B., Dock C., Antranikian G., Liebl W.;  
RT "Genome sequence of Picrophilus torridus and its implications for life  
around pH 0.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).  
DR EMBL; AR017261; RAT42888.1; -; Genomic.DNA.  
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . . ; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.  
DR InterPro; IPR001296; Glyco\_trans\_1.  
DR Pfam; PF00534; Glycos\_transf\_1; I.  
KW Complete proteome; Glycosyltransferase; Transferase.  
SQ SEQUENCE 410 AA; 48120 MW; C192F0152E6E5B90 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 410;  
Best Local Similarity 66.7%; Pred. No. 6.8e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps

Cy 1 KVVFFA 6  
Db 235 KIIFFA 240

RESULT 47  
O59243\_PYRHO  
ID O59243\_PYRHO PRELIMINARY; PRT; 447 AA.  
AC O59243;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein PH1606.  
GN OrderedLocusNames=PHI606;  
OS Pyrococcus horikoshii.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=53953;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=OT3;  
RX MEDLINE=98344137; PubMed=9679194;  
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,,  
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
RA Masuchi Y., Shizuya H., Kikuchi H.;  
RT "Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";  
RL DNA Res. 5:55-76(1998).  
DR EMBL; BA000001; BAA30718.1; -; Genomic\_DNA.  
DR FIR; F71039; F71039.  
DR GO; GO:0016020; C:membrane; IEA.

DR GO: GO:0005355; P:Glucose transporter activity; IEA.  
 DR GO: GO:0006810; P:transport; IEA.  
 DR InterPro; IPRO00803; Gluc Transporter.  
 DR PRINTS; PR00172; GLUCTRNSPORT.  
 KW complete proteome; Hypothetical protein.  
 SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 447;  
 Best Local Similarity 66.7%; Pred. No. 7.3e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVPFFA 6  
 Db 207 KIIFFA 212  
 |:|:|:|

RESULT 48  
 Q95893 DROME PRELIMINARY; PRT; 556 AA.  
 AC Q95893  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE GM05229p.  
 GN Name=Aeph; ORFNames=CG8421;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY060905; AAL28453.1; -; mRNA.  
 DR FlyBase; FBgn0034075; Aeph.  
 DR FlyBase; FBgn0034075; CG8421.  
 SQ SEQUENCE 556 AA; 63089 MW; 95D82EAC57D11F88 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 556;  
 Best Local Similarity 66.7%; Pred. No. 8.9e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVPFFA 6  
 Db 53 KIIFFA 58  
 |:|:|:|

RESULT 49  
 Q9V719 DROME PRELIMINARY; PRT; 556 AA.  
 AC Q9V719  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CG8421-PD, isoform D (CG8421-pe, isoform e).  
 GN Name=Aeph; ORFNames=CG8421;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M.E., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RN Science 287:2185-2195(2000).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
 RT melanogaster euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=22426070; PubMed=12537573;  
 RA Kaminiker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the Drosophila melanogaster euchromatin:  
 RT a genomics perspective.";  
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=22426069; PubMed=12537572;  
 RA Milera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradscky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Berkeley Drosophila Genome Project;  
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,

RA Yu C., Rubin G.;  
 RT "Drosophila melanogaster release 4 sequence.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RG FlyBase;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- INTERACTION:  
 CC O46085;EG:63B12.5;NbExp=1;IntAct=EBI-123244, EBI-151469;  
 DR EMBL; AE003808; AAF58064.2; -; Genomic\_DNA.  
 DR IntAct; Q9V719; -;  
 DR Ensembl; CG8421; Drosophila melanogaster.  
 DR FlyBase; FBgn0034075; Asph.  
 DR FlyBase; FBgn0034075; CG8421.  
 SQ SEQUENCE 556 AA; 63144 MW; B420980CBD6C357A CRC64;

Query Match 93.1%; Score 27; DB 2; Length 556;  
 Best Local Similarity 66.7%; Pred. No. 8.9e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6 PRT; 785 AA.  
 Db 53 KLIFFA 58

RESULT 50  
 Q9GQ82 DROME PRELIMINARY;  
 ID Q9GQ82; PRT; 785 AA.  
 AC Q9GQ82;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Aspartyl beta-hydroxylase variant 1 (CG8421-PA, isoform A).  
 GN Name=Asph; ORFNames=CG8421;  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;  
 RA Dinchuk J.E., Huber R., Burn T.C., Huber R., Ho S.P., Link J.,  
 RA O'Neil K.T., Pocht R.J., Scully M.S., Hollis J.M., Hollis G.F.,  
 RA Friedman P.A.;  
 RA "Aspartyl beta-hydroxylase (Asph) and an evolutionarily conserved  
 RT isoform of Asph missing the catalytic domain share exons with  
 RT junctin.";  
 RL J. Biol. Chem. 275:39543-39554 (2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Duzan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostali M., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195 (2000).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
 RT melanogaster euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the Drosophila melanogaster euchromatin:  
 RT a genomics perspective.";  
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Berkeley Drosophila Genome Project;  
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,  
 RA Yu C., Rubin G.;  
 RT "Drosophila melanogaster release 4 sequence.";  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RG FlyBase;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF289493; AAG40806.1; -; mRNA.  
 DR EMBL; AE003808; AAM70947.1; -; Genomic\_DNA.  
 DR Ensembl; CG8421; Drosophila melanogaster.  
 DR FlyBase; FBgn0034075; Asph.  
 DR FlyBase; FBgn0034075; CG8421.  
 DR GO; GO:000176; C:integral to endoplasmic reticulum membrane; IEA.  
 DR GO; GO:001502; C:integral to membrane; IEA.  
 DR GO; GO:0005486; F:peptide-aspartate beta-dioxygenase activity; IEA.  
 DR GO; GO:0004597; F:peptide-aspartate beta-dioxygenase activity; IEA.  
 DR GO; GO:0018193; P:peptidyl-amino acid modification; IEA.

DR InterPro; IPR007803; Asp Arg Hydrex.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR001440; TPR.  
 DR InterPro; IPR011990; TPR-like helical.  
 DR Pfam; PF05118; Asp Arg Hydrex; 1.  
 DR PROSITE; PS50293; TPR\_REGION; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
 SQ SEQUENCE 785 AA; 89843 MW; 30ABDFCD8836F7F1 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 785;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:|:|  
 Db 53 KIIFFA 58

## RESULT 51

Q68K27 CHLRE  
 ID Q68K27 CHLRE PRELIMINARY; PRT; 1394 AA.  
 AC Q68K27;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Intracellular transport particle protein 140.  
 GN Name=IFT140;  
 OS Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;  
 OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.  
 OK NCBI\_TaxID=3055;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

Walker B.L., Hou Y., Dentler W.L., Witman G.B., Pazour G.J.;  
 "Intracellular transport protein IFT140.";  
 Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY686103; AAT95430.1; -; mRNA.  
 DR GO; GO:0019861; C:flagellum; IEA.  
 DR InterPro; IPR002885; PPR.  
 DR Pfam; PF00400; WD40; 2.  
 DR SMART; SM00320; WD40; 5.  
 DR TIGRFAMs; TIGR00756; PPR; 2.  
 DR PROSITE; PS50082; WD\_REPEATS\_2; 1.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 KW Flagellum.  
 SQ SEQUENCE 1394 AA; 154603 MW; 5D3E70C8440DABCD CRC64;

Query Match 93.1%; Score 27; DB 2; Length 1384;  
 Best Local Similarity 66.7%; Pred. NO. 2e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:|:|  
 Db 1154 KIIFFA 1159

## RESULT 52

Q7QEF0 ANOGA  
 ID Q7QEF0 ANOGA PRELIMINARY; PRT; 1408 AA.  
 AC Q7QEF0;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE ENSANGP0000001545 (Fragment).  
 GN ORFNames=ENSANGG00000001308;  
 OS Anopheles gambiae str. PEST.  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;  
 OC Anophelinae; Anopheles.  
 OK NCBI\_TaxID=180454;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PEST;  
 RG The Anopheles gambiae Sequence Committee;  
 RT "Anopheles gambiae re-annotation.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PEST;  
 RG The Anopheles gambiae Sequence Committee;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAAB01008847; EAA06855.1; -; Genomic\_DNA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR011990; TPR-like\_helical.  
 DR InterPro; IPR001680; WD40.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 FT NON TER 1408 1408  
 SQ SEQUENCE 1408 AA; 157382 MW; FF63317DAB976DB2 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 1408;  
 Best Local Similarity 66.7%; Pred. No. 2e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:|:|  
 Db 1212 KIIFFA 1217

## RESULT 53

Q9VPRO DROME  
 ID Q9VPRO DROME PRELIMINARY; PRT; 1443 AA.  
 AC Q9VPRO;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE CG11938-PA; isoform A.  
 GN Names=Ose93; ORFNames=CG11838;  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OK NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Anantides P.G., Scherzer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko K., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Furi V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong Y., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Celnik S.E., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA Patel S., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
RT *melanogaster* euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celnik S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RN NUCLEOTIDE SEQUENCE.  
RG Berkeley *Drosophila* Genome Project;  
RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacieb J., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence.";  
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RN NUCLEOTIDE SEQUENCE.  
RG FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; A8003589; AAF51483.1; -; Genomic\_DNA.  
DR FlyBase; Fgn0031262; Ose93.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR011990; TPR-like\_helical.  
DR InterPro; IPR001680; WD40.  
DR SMART; SM00320; WD40; 3.  
DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
KW Repeat.  
SQ SEQUENCE 1443 AA; 161316 MW; A8C5997678040B88 CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 1443;  
Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|::|||

Db 1204 KIIFFA 1209  
RESULT 54  
Q5BI64 DROME PRELIMINARY; PRT; 1458 AA.  
AC Q5BI64;  
DT 10-MAY-2005 (TReMBLrel. 30, Created)  
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)  
DE LPI4662p.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; *Drosophila*.  
OX NCBI\_TaxID=7227;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=Berkeley;  
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacieb J.,  
RA Park S., Wan K., Yu C., Rubin G.M., Celnik S.;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; E021360; AAX33508.1; -; mRNA.  
DR InterPro; IPR011990; TPR-like\_helical.  
DR InterPro; IPR001680; WD40.  
DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN 1.  
DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
KW Repeat.  
SQ SEQUENCE 1458 AA; 163133 MW; 2D704C8970E541EC CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 1458;  
Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|::|||  
Db 1219 KIIFFA 1224  
RESULT 55  
Q7KTZ4 DROME PRELIMINARY; PRT; 1503 AA.  
AC Q7KTZ4;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE CG11838-PB, isoform B.  
GN Name=Ose93; ORFNames=CG11838;  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; *Drosophila*.  
OX NCBI\_TaxID=7227;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherly J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glaeser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun B.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RA "The genome sequence of Drosophila melanogaster";  
RT Science 287:2183-2195 (2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celnikier S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomic perspective";  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Mirra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celnikier S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.B., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RG Berkeley Drosophila Genome Project;  
RA Celnikier S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RG FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB003589; AAS64635.1; -; Genomic DNA.  
DR InterPro; IPR011990; TPR-like\_helical.  
DR InterPro; IPR001680; WD40.  
DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
RW Repeat.

SQ SEQUENCE 1503 AA; 167957 MW; A0DD3F532590486 CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 1503;  
Best Local Similarity 66.7%; Pred. No. 2.2e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
DB 1264 KIIFFA 1269  
RESULT 56  
Q8A6R7 BACTN PRELIMINARY; PRT; 1676 AA.  
ID Q8A6R7; BACTN PRELIMINARY;  
AC Q8A6R7;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Conserved protein, with weak BamHI domain.  
GN Ordered locus names=BT1809;  
OS Bacteroides thetaiotaomicron.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=818;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=VPI-5482 / ATCC 29148;  
RC MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;  
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
RA Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis";  
RL Science 299:2074-2076 (2003).  
RL EMBL; AB016933; AAO76916.1; -; Genomic DNA.  
DR InterPro; IPR002048; EF-hand.  
DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_1.  
RW Complete proteome.  
SQ SEQUENCE 1676 AA; 193673 MW; 28065878C0F6C961 CRC64;  
Query Match 93.1%; Score 27; DB 2; Length 1676;  
Best Local Similarity 66.7%; Pred. No. 2.4e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
DB 1656 KIIFFA 1661  
RESULT 57  
Q9UC33 HUMAN PRELIMINARY; PRT; 33 AA.  
ID Q9UC33; HUMAN PRELIMINARY;  
AC Q9UC33;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Beta-amyloid peptide (Fragment).  
OS Homo sapiens (Human).  
OC Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Euarchopterygii; Primates; Catarrhini; Hominidae;  
OC Mammalia; Eutheria; Euarchontoglires;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;  
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,  
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;  
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from  
RT biological fluids";  
RL Nature 359:325-327 (1992).  
RL HSSP; Q16019; 1BA4.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.



DR PRINTS; PR00204; BETAAMYLOID.  
SQ SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 33;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 16 KLVFFA 21

RESULT 58

Q56JJ6 GRAGR

ID Q56JJ6 GRAGR PRELIMINARY; PRT; 42 AA.

AC Q56JJ6

DT 10-MAY-2005 (Tremblrel. 30, Created)

DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)

DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)

DE Amyloid beta protein (Fragment).

OS Grampus griseus (Risso's dolphin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;

OC Odontoceti; Delphinidae; Grampus.

OX NCBI\_TaxID=83653;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Gallego C., Sarasa M.

RT "The molecular machinery of Alzheimer's disease in the dolphin.";

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY926589; AAX81918.1; -; mRNA.

FT NON\_TER 1

FT NON\_TER 42

SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 16 KLVFFA 21

RESULT 59

Q56JJ7 TURTR

ID Q56JJ7 TURTR PRELIMINARY; PRT; 42 AA.

AC Q56JJ7

DT 10-MAY-2005 (Tremblrel. 30, Created)

DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)

DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)

DE Amyloid beta protein (Fragment).

OS Tursiops truncatus (Atlantic bottle-nosed dolphin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;

OC Odontoceti; Delphinidae; Tursiops.

OX NCBI\_TaxID=9739;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Gallego C., Sarasa M.

RT "The molecular machinery of Alzheimer's disease in the dolphin.";

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY926588; AAX81917.1; -; mRNA.

FT NON\_TER 1

FT NON\_TER 42

SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 16 KLVFFA 21

Db 16 KLVFFA 21

RESULT 60

Q7M088 CAVPO

ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.

AC Q7M088

DT 01-MAR-2004 (Tremblrel. 26, Created)

DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Beta-amyloid protein (Fragment).

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

OC Hystricognathi; Caviidae; Cavia.

OX NCBI\_TaxID=10141;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=93290653; PubMed=7685598;

RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,

RA Kamiya H., Ohno M.

RT "Receptor-mediated specific biological activity of a beta-amyloid

protein fragment for NK-1 substance p receptors.";

RL Biochem. Biophys. Res. Commun. 193:624-630(1993).

DR PIR; PNO512; PNO512.

DR HSP; Q16019; 11YT.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00204; BETAAMYLOID.

FT NON\_TER 1

FT NON\_TER 42

SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 16 KLVFFA 21

RESULT 61

Q8WZ99 HUMAN

ID Q8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.

AC Q8WZ99

DT 01-MAR-2002 (Tremblrel. 20, Created)

DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE Amyloid protein (Fragment).

GN Name=APP;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;

RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,

RA Ninomiya H., Saido TC., Hashimoto T., Iwatsubo T., Nakashima K.;

RT "Novel amyloid precursor protein gene missense mutation (D678N) in

probable familial Alzheimer's disease.";

RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).

DR EMBL; AB066441; BAB71958.2; -; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00204; BETAAMYLOID.

FT NON\_TER 1

```

FT NON TER 52 52
SQ SEQUENCE 52 AA; 5597 MW; 3F08B9E9EC18011AD CRC64;

Query Match 89.7%; Score 26; DB 2; Length 52;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 16 KLVFFA 21

RESULT 62
Q82VGB NITEU
ID Q82VGB NITEU PRELIMINARY; PRT; 55 AA.
AC Q82VGB;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=NE1120;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19718 /IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773 (2003).
DR EMBL; BX321859; CAD85031.1; -; Genomic_DNA.
DR InterPro; IPR009760; DUF1328.
DR Pfam; PF07043; DUF1328; 1.
DR PIRSF; PIRSF036466; UCP036466; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 55 AA; 5845 MW; 4F68395F53BE308C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 55;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 32 KLVFFA 37

RESULT 63
A4_URSWA
ID A4_URSWA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;

MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X56128; CAA39593.1; -; mRNA.
CC PIR; B60045; B60045.
CC HSSP; P08592; INMO.
CC InterPro; IPR008155; A4_APP.
CC InterPro; IPR001255; Beta-APP.
CC PANTHER; PTHR10083:SP6; Beta-APP; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC PRINTS; PR00204; BETAAMYLOID.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Amyloid; Transmembrane.
CC CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >57 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
FT CHAIN <1 33 Extracellular (Potential).
FT TOPO_DOM 34 57 Potential.
FT TRANSMEM 1 1
FT NON_TER 57 57
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;

Query Match 89.7%; Score 26; DB 1; Length 57;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 21 KLVFFA 26

RESULT 64
A4_CANFA
ID A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

```



RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -!- FUNCTION: Functional neuronal receptor which couples to  
 CC intracellular signaling pathway through the GTP-binding protein  
 CC G(O) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; X56125; CAA39590.1; -; mRNA.  
 DR HSSP; P08592; INMJ.  
 DR InterPro; ENSCAFG0000008557; Canis familiaris.  
 DR Ensembl; IPR008155; A4 APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PROSITE; PS00319; A4 EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4 INTRA; PARTIAL.  
 KW Amyloid; Transmembrane.  
 FT CHAIN <1 6  
 FT CHAIN 7 >58 Soluble APP-beta (By similarity).  
 FT CHAIN 7 >58 CTF-alpha (By similarity).  
 FT CHAIN 7 46 Beta-amyloid protein 42 (By similarity).  
 FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).  
 FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).  
 FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).  
 FT CHAIN <1 34 Extracellular (Potential).  
 FT TOPO\_DOM 35 58 Potential.  
 FT TRANSMEM 1 1  
 FT NON\_TER 58 58  
 FT SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;  
 Query Match 89.7%; Score 26; DB 1; Length 58;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |:|:|:|  
 Db 22 KLVFFA 27

RESULT 65  
 A4\_RABIT ID A4\_RABIT STANDARD; PRT; 58 AA.  
 AC Q28748;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-WAY-2005 (Rel. 47, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-  
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);  
 DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase  
 DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal  
 DE fragment 57)] (Fragment).  
 GN Name=APP;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;  
 OC Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC Tissue=Brain;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -!- FUNCTION: Functional neuronal receptor which couples to  
 CC intracellular signaling pathway through the GTP-binding protein  
 CC G(O) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; X56125; CAA39594.1; -; mRNA.  
 DR HSSP; P08592; INMJ.  
 DR InterPro; IPR008155; A4 APP.  
 DR Ensembl; IPR001255; Beta-APP.  
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PROSITE; PS00319; A4 EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4 INTRA; PARTIAL.  
 KW Amyloid; Transmembrane.  
 FT CHAIN <1 5  
 FT CHAIN 6 >58 Soluble APP-beta (By similarity).  
 FT CHAIN 6 47 CTF-alpha (By similarity).  
 FT CHAIN 6 45 Beta-amyloid protein 42 (By similarity).  
 FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).  
 FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).  
 FT TOPO\_DOM <1 33 Extracellular (Potential).  
 FT TRANSMEM 34 57 Potential.  
 FT TOPO\_DOM 58 >58 Cytoplasmic (Potential).  
 FT NON\_TER 1 1  
 FT NON\_TER 58 58  
 FT SEQUENCE 58 AA; 6300 MW; F434209D88BA82D CRC64;  
 Query Match 89.7%; Score 26; DB 1; Length 58;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |:|:|:|  
 Db 21 KLVFFA 26

RESULT 66  
 A4\_SHEEP ID A4\_SHEEP STANDARD; PRT; 58 AA.  
 AC Q28757;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-  
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);  
 DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase  
 DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal  
 DE fragment 57)] (Fragment).  
 GN Name=APP;  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC Tissue=Heart;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).

```
CC CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X56130; CAA39595.1; -; mRNA.
CC HSSP; P08592; INMJ.
CC InterPro; IPR008155; A4 APP.
CC InterPro; IPR001255; Beta-APP.
CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC PRINTS; PR00204; BETAAMYLOID.
CC PROSITE; PS00319; A4 EXTRA; PARTIAL.
CC PROSITE; PS00320; A4 INTRA; PARTIAL.
CC KW Amyloid; Transmembrane.
CC CHAIN <1 5 Soluble APP-beta (By similarity).
CC FT CHAIN 6 >58 CTF-alpha (By similarity).
CC FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
CC FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
CC FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
CC FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
CC FT TOPO_DOM <1 33 Extracellular (Potential).
CC FT TRANSMEM 34 57 Potential.
CC FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
CC FT NON_TER 1 1
CC FT NON_TER 58 58
CC SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 21 KLVFFA 26
|:|:|:|:|

RESULT 67
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain.
RX MEDLINE=9201079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
```

```
CC CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X56124; CAA39589.1; -; mRNA.
CC HSSP; X56126; CAA39591.1; -; mRNA.
CC HSSP; P08592; INMJ.
CC InterPro; IPR008155; A4 APP.
CC InterPro; IPR001255; Beta-APP.
CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC PRINTS; PR00204; BETAAMYLOID.
CC PROSITE; PS00319; A4 EXTRA; PARTIAL.
CC PROSITE; PS00320; A4 INTRA; PARTIAL.
CC KW Amyloid; Transmembrane.
CC CHAIN <1 6 Soluble APP-beta (By similarity).
CC FT CHAIN 7 >59 CTF-alpha (By similarity).
CC FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
CC FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
CC FT CHAIN 47 >59 Gamma-CTF(59) (By similarity).
CC FT CHAIN 49 >59 Gamma-CTF(57) (By similarity).
CC FT TOPO_DOM <1 34 Extracellular (Potential).
CC FT TRANSMEM 35 58 Potential.
CC FT TOPO_DOM 59 >59 Cytoplasmic (Potential).
CC FT NON_TER 1 1
CC FT NON_TER 59 59
CC SQ SEQUENCE 59 AA; 6414 MW; F43469D480A2E12D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 59;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 22 KLVFFA 27
|:|:|:|:|

RESULT 68
ID Q5WJL8 BACSK PRELIMINARY; PRT; 79 AA.
AC Q5WJL8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Molybdopterin converting factor subunit 1 Moab.
GN Name=moab; OrderedLocNames=ABC0898;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=66692;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSM-K16;
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RA "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16."
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006627; BAD63437.1; -; Genomic DNA.
DR GO; GO:0006777; P-Mo-molybdopterin cofactor biosynthesis; IEA.
DR GO; GO:0006790; P-sulfur metabolism; IEA.
DR InterPro; IPR010034; Moab.
DR InterPro; IPR003749; ThisS.
DR TIGRFAMs; TIGR01682; moab; 1.
DR Complete proteome.
KW SEQUENCE 79 AA; 8341 MW; 37F0600DEC90F10A CRC64;
```

Query Match 89.7%; Score 26; DB 2; Length 79;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 ||:||||  
 DB 3 KVLFFA 8

## RESULT 69

035463 CRIGR  
 ID 035463\_CRIGR PRELIMINARY; PRT; 79 AA.  
 AC 035463;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Alzheimer's amyloid beta protein (Fragment).  
 GN Namesbeta APP;  
 OS Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Cricetinae; Cricetulus.  
 OX NCBI\_TaxID=10029;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sambamurti K., Pinnix I., Gandhi S.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RE EMBL; AF030413; AAB86608.1; -; mRNA.  
 DR HSP; P08592; INMJ  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00204; BETRAYLOID.  
 FT NON\_TER 1 79  
 FT NON\_TER 79 79  
 SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 79;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 ||:||||  
 DB 36 KLVFFA 41

## RESULT 70

MOAD\_ECOLI  
 ID MOAD\_ECOLI STANDARD; PRT; 81 AA.  
 AC P30748; P77422;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Molybdopterine converting factor subunit 1 (MPT synthase subunit 1)  
 DE (Molybdopterine synthase subunit 1) (Molybdenum cofactor biosynthesis  
 protein D) (molybdopterine converting factor small subunit).  
 GN Namesmoad; Synonyms=chlA4, chlM; OrderedLocusNames=b0784;  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K12 / MC4100;  
 RX MEDLINE=93368423; PubMed=8361352;  
 RA Rivers S.L., McNaughton E., Blasco F., Giordano G., Boxer D.H.;  
 RT "Molecular genetic analysis of the moa operon of Escherichia coli K-12  
 required for molybdenum cofactor biosynthesis.";  
 RL Mol. Microbiol. 8:1071-1081(1993).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;  
 RA Blattner F.R.; Plunkett G. III; Bloch C.A.; Perna N.T.; Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=K12;  
 RX MEDLINE=97061202; PubMed=8905232;  
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.;  
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 12.7-28.0 min region on the linkage map.";  
 RL DNA Res. 3:137-155(1996).  
 RN [4]  
 RP PROTEIN SEQUENCE OF 1-15, CHARACTERIZATION, AND MASS SPECTROMETRY.  
 RX MEDLINE=93293873; PubMed=8514782;  
 RA Pitterle D.M., Rajagopalan K.V.;  
 RT "The biosynthesis of molybdopterine in Escherichia coli. Purification  
 and characterization of the converting factor.";  
 RL J. Biol. Chem. 268:13499-13505(1993).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS).  
 RX MEDLINE=20577273; PubMed=11135669; DOI=10.1038/83034;  
 RA Rudolph M.J., Wuebbens M.M., Rajagopalan K.V., Schindelin H.;  
 RT "Crystal structure of molybdopterine synthase and its evolutionary  
 relationship to ubiquitin activation.";  
 RL Nat. Struct. Biol. 8:42-46(2001).  
 CC -!- FUNCTION: Converts molybdopterine precursor Z into molybdopterine.  
 CC This requires the incorporation of two sulfur atoms into precursor  
 CC Z to generate a dithiolene group. The sulfur atoms are provided by  
 CC the active form of the small subunit, whose activation involves  
 CC the acquisition of sulfur and the activity of moeB/chlN.  
 CC -!- PATHWAY: Molybdenum cofactor biosynthesis.  
 CC -!- SUBUNIT: Heterodimer of 2 moad subunits and 2 moe subunits.  
 CC -!- INTERACTION: P30749:moeA; NbExp=1; IntAct=EBI-554366, EBI-554376;  
 CC P0A7K2:rpIL; NbExp=1; IntAct=EBI-554366, EBI-543702;  
 CC -!- INDUCTION: By anaerobiosis, repressed by the molybdenum cofactor.  
 CC -!- MASS SPECTROMETRY: MW=8773.6; MW\_ERR=0.2; METHOD=Electrospray;  
 CC RANGE=1-81; NOTE=Ref. 4.  
 CC -!- SIMILARITY: Belongs to the moad family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; X70420; CAA49864.1; -; Genomic DNA.  
 CC EMBL; U00096; AAC73871.1; -; Genomic DNA.  
 CC EMBL; D90716; BAA35442.1; -; Genomic DNA.  
 CC PIR; H64814; H64814.  
 CC PDB; IFM0; X-ray; D=1-81.  
 CC PDB; IFM1; X-ray; D=1-81.  
 CC PDB; IFM2; X-ray; D=1-81.  
 CC PDB; IFM3; X-ray; D=1-81.  
 CC PDB; IFM4; X-ray; D=1-81.  
 CC PDB; IFM5; X-ray; D=1-81.  
 CC PDB; IFM6; X-ray; D=1-81.  
 CC PDB; IFM7; X-ray; D=1-81.  
 CC PDB; IFM8; X-ray; D=1-81.  
 CC PDB; IFM9; X-ray; D=1-81.  
 CC PDB; IFM10; X-ray; D=1-81.  
 CC PDB; IFM11; X-ray; D=1-81.  
 CC PDB; IFM12; X-ray; D=1-81.  
 CC PDB; IFM13; X-ray; D=1-81.  
 CC PDB; IFM14; X-ray; D=1-81.  
 CC PDB; IFM15; X-ray; D=1-81.  
 CC PDB; IFM16; X-ray; D=1-81.  
 CC PDB; IFM17; X-ray; D=1-81.  
 CC PDB; IFM18; X-ray; D=1-81.  
 CC PDB; IFM19; X-ray; D=1-81.  
 CC PDB; IFM20; X-ray; D=1-81.  
 CC PDB; IFM21; X-ray; D=1-81.  
 CC PDB; IFM22; X-ray; D=1-81.  
 CC PDB; IFM23; X-ray; D=1-81.  
 CC PDB; IFM24; X-ray; D=1-81.  
 CC PDB; IFM25; X-ray; D=1-81.  
 CC PDB; IFM26; X-ray; D=1-81.  
 CC PDB; IFM27; X-ray; D=1-81.  
 CC PDB; IFM28; X-ray; D=1-81.  
 CC PDB; IFM29; X-ray; D=1-81.  
 CC PDB; IFM30; X-ray; D=1-81.  
 CC PDB; IFM31; X-ray; D=1-81.  
 CC PDB; IFM32; X-ray; D=1-81.  
 CC PDB; IFM33; X-ray; D=1-81.  
 CC PDB; IFM34; X-ray; D=1-81.  
 CC PDB; IFM35; X-ray; D=1-81.  
 CC PDB; IFM36; X-ray; D=1-81.  
 CC PDB; IFM37; X-ray; D=1-81.  
 CC PDB; IFM38; X-ray; D=1-81.  
 CC PDB; IFM39; X-ray; D=1-81.  
 CC PDB; IFM40; X-ray; D=1-81.  
 CC PDB; IFM41; X-ray; D=1-81.  
 CC PDB; IFM42; X-ray; D=1-81.  
 CC PDB; IFM43; X-ray; D=1-81.  
 CC PDB; IFM44; X-ray; D=1-81.  
 CC PDB; IFM45; X-ray; D=1-81.  
 CC PDB; IFM46; X-ray; D=1-81.  
 CC PDB; IFM47; X-ray; D=1-81.  
 CC PDB; IFM48; X-ray; D=1-81.  
 CC PDB; IFM49; X-ray; D=1-81.  
 CC PDB; IFM50; X-ray; D=1-81.  
 CC PDB; IFM51; X-ray; D=1-81.  
 CC PDB; IFM52; X-ray; D=1-81.  
 CC PDB; IFM53; X-ray; D=1-81.  
 CC PDB; IFM54; X-ray; D=1-81.  
 CC PDB; IFM55; X-ray; D=1-81.  
 CC PDB; IFM56; X-ray; D=1-81.  
 CC PDB; IFM57; X-ray; D=1-81.  
 CC PDB; IFM58; X-ray; D=1-81.  
 CC PDB; IFM59; X-ray; D=1-81.  
 CC PDB; IFM60; X-ray; D=1-81.  
 CC PDB; IFM61; X-ray; D=1-81.  
 CC PDB; IFM62; X-ray; D=1-81.  
 CC PDB; IFM63; X-ray; D=1-81.  
 CC PDB; IFM64; X-ray; D=1-81.  
 CC PDB; IFM65; X-ray; D=1-81.  
 CC PDB; IFM66; X-ray; D=1-81.  
 CC PDB; IFM67; X-ray; D=1-81.  
 CC PDB; IFM68; X-ray; D=1-81.  
 CC PDB; IFM69; X-ray; D=1-81.  
 CC PDB; IFM70; X-ray; D=1-81.  
 CC PDB; IFM71; X-ray; D=1-81.  
 CC PDB; IFM72; X-ray; D=1-81.  
 CC PDB; IFM73; X-ray; D=1-81.  
 CC PDB; IFM74; X-ray; D=1-81.  
 CC PDB; IFM75; X-ray; D=1-81.  
 CC PDB; IFM76; X-ray; D=1-81.  
 CC PDB; IFM77; X-ray; D=1-81.  
 CC PDB; IFM78; X-ray; D=1-81.  
 CC PDB; IFM79; X-ray; D=1-81.  
 CC PDB; IFM80; X-ray; D=1-81.  
 CC PDB; IFM81; X-ray; D=1-81.  
 CC PDB; IFM82; X-ray; D=1-81.  
 CC PDB; IFM83; X-ray; D=1-81.  
 CC PDB; IFM84; X-ray; D=1-81.  
 CC PDB; IFM85; X-ray; D=1-81.  
 CC PDB; IFM86; X-ray; D=1-81.  
 CC PDB; IFM87; X-ray; D=1-81.  
 CC PDB; IFM88; X-ray; D=1-81.  
 CC PDB; IFM89; X-ray; D=1-81.  
 CC PDB; IFM90; X-ray; D=1-81.  
 CC PDB; IFM91; X-ray; D=1-81.  
 CC PDB; IFM92; X-ray; D=1-81.  
 CC PDB; IFM93; X-ray; D=1-81.  
 CC PDB; IFM94; X-ray; D=1-81.  
 CC PDB; IFM95; X-ray; D=1-81.  
 CC PDB; IFM96; X-ray; D=1-81.  
 CC PDB; IFM97; X-ray; D=1-81.  
 CC PDB; IFM98; X-ray; D=1-81.  
 CC PDB; IFM99; X-ray; D=1-81.  
 CC PDB; IFM100; X-ray; D=1-81.  
 CC PDB; IFM101; X-ray; D=1-81.  
 CC PDB; IFM102; X-ray; D=1-81.  
 CC PDB; IFM103; X-ray; D=1-81.  
 CC PDB; IFM104; X-ray; D=1-81.  
 CC PDB; IFM105; X-ray; D=1-81.  
 CC PDB; IFM106; X-ray; D=1-81.  
 CC PDB; IFM107; X-ray; D=1-81.  
 CC PDB; IFM108; X-ray; D=1-81.  
 CC PDB; IFM109; X-ray; D=1-81.  
 CC PDB; IFM110; X-ray; D=1-81.  
 CC PDB; IFM111; X-ray; D=1-81.  
 CC PDB; IFM112; X-ray; D=1-81.  
 CC PDB; IFM113; X-ray; D=1-81.  
 CC PDB; IFM114; X-ray; D=1-81.  
 CC PDB; IFM115; X-ray; D=1-81.  
 CC PDB; IFM116; X-ray; D=1-81.  
 CC PDB; IFM117; X-ray; D=1-81.  
 CC PDB; IFM118; X-ray; D=1-81.  
 CC PDB; IFM119; X-ray; D=1-81.  
 CC PDB; IFM120; X-ray; D=1-81.  
 CC PDB; IFM121; X-ray; D=1-81.  
 CC PDB; IFM122; X-ray; D=1-81.  
 CC PDB; IFM123; X-ray; D=1-81.  
 CC PDB; IFM124; X-ray; D=1-81.  
 CC PDB; IFM125; X-ray; D=1-81.  
 CC PDB; IFM126; X-ray; D=1-81.  
 CC PDB; IFM127; X-ray; D=1-81.  
 CC PDB; IFM128; X-ray; D=1-81.  
 CC PDB; IFM129; X-ray; D=1-81.  
 CC PDB; IFM130; X-ray; D=1-81.  
 CC PDB; IFM131; X-ray; D=1-81.  
 CC PDB; IFM132; X-ray; D=1-81.  
 CC PDB; IFM133; X-ray; D=1-81.  
 CC PDB; IFM134; X-ray; D=1-81.  
 CC PDB; IFM135; X-ray; D=1-81.  
 CC PDB; IFM136; X-ray; D=1-81.  
 CC PDB; IFM137; X-ray; D=1-81.  
 CC PDB; IFM138; X-ray; D=1-81.  
 CC PDB; IFM139; X-ray; D=1-81.  
 CC PDB; IFM140; X-ray; D=1-81.  
 CC PDB; IFM141; X-ray; D=1-81.  
 CC PDB; IFM142; X-ray; D=1-81.  
 CC PDB; IFM143; X-ray; D=1-81.  
 CC PDB; IFM144; X-ray; D=1-81.  
 CC PDB; IFM145; X-ray; D=1-81.  
 CC PDB; IFM146; X-ray; D=1-81.  
 CC PDB; IFM147; X-ray; D=1-81.  
 CC PDB; IFM148; X-ray; D=1-81.  
 CC PDB; IFM149; X-ray; D=1-81.  
 CC PDB; IFM150; X-ray; D=1-81.  
 CC PDB; IFM151; X-ray; D=1-81.  
 CC PDB; IFM152; X-ray; D=1-81.  
 CC PDB; IFM153; X-ray; D=1-81.  
 CC PDB; IFM154; X-ray; D=1-81.  
 CC PDB; IFM155; X-ray; D=1-81.  
 CC PDB; IFM156; X-ray; D=1-81.  
 CC PDB; IFM157; X-ray; D=1-81.  
 CC PDB; IFM158; X-ray; D=1-81.  
 CC PDB; IFM159; X-ray; D=1-81.  
 CC PDB; IFM160; X-ray; D=1-81.  
 CC PDB; IFM161; X-ray; D=1-81.  
 CC PDB; IFM162; X-ray; D=1-81.  
 CC PDB; IFM163; X-ray; D=1-81.  
 CC PDB; IFM164; X-ray; D=1-81.  
 CC PDB; IFM165; X-ray; D=1-81.  
 CC PDB; IFM166; X-ray; D=1-81.  
 CC PDB; IFM167; X-ray; D=1-81.  
 CC PDB; IFM168; X-ray; D=1-81.  
 CC PDB; IFM169; X-ray; D=1-81.  
 CC PDB; IFM170; X-ray; D=1-81.  
 CC PDB; IFM171; X-ray; D=1-81.  
 CC PDB; IFM172; X-ray; D=1-81.  
 CC PDB; IFM173; X-ray; D=1-81.  
 CC PDB; IFM174; X-ray; D=1-81.  
 CC PDB; IFM175; X-ray; D=1-81.  
 CC PDB; IFM176; X-ray; D=1-81.  
 CC PDB; IFM177; X-ray; D=1-81.  
 CC PDB; IFM178; X-ray; D=1-81.  
 CC PDB; IFM179; X-ray; D=1-81.  
 CC PDB; IFM180; X-ray; D=1-81.  
 CC PDB; IFM181; X-ray; D=1-81.  
 CC PDB; IFM182; X-ray; D=1-81.  
 CC PDB; IFM183; X-ray; D=1-81.  
 CC PDB; IFM184; X-ray; D=1-81.  
 CC PDB; IFM185; X-ray; D=1-81.  
 CC PDB; IFM186; X-ray; D=1-81.  
 CC PDB; IFM187; X-ray; D=1-81.  
 CC PDB; IFM188; X-ray; D=1-81.  
 CC PDB; IFM189; X-ray; D=1-81.  
 CC PDB; IFM190; X-ray; D=1-81.  
 CC PDB; IFM191; X-ray; D=1-81.  
 CC PDB; IFM192; X-ray; D=1-81.  
 CC PDB; IFM193; X-ray; D=1-81.  
 CC PDB; IFM194; X-ray; D=1-81.  
 CC PDB; IFM195; X-ray; D=1-81.  
 CC PDB; IFM196; X-ray; D=1-81.  
 CC PDB; IFM197; X-ray; D=1-81.  
 CC PDB; IFM198; X-ray; D=1-81.  
 CC PDB; IFM199; X-ray; D=1-81.  
 CC PDB; IFM200; X-ray; D=1-81.  
 CC PDB; IFM201; X-ray; D=1-81.  
 CC PDB; IFM202; X-ray; D=1-81.  
 CC PDB; IFM203; X-ray; D=1-81.  
 CC PDB; IFM204; X-ray; D=1-81.  
 CC PDB; IFM205; X-ray; D=1-81.  
 CC PDB; IFM206; X-ray; D=1-81.  
 CC PDB; IFM207; X-ray; D=1-81.  
 CC PDB; IFM208; X-ray; D=1-81.  
 CC PDB; IFM209; X-ray; D=1-81.  
 CC PDB; IFM210; X-ray; D=1-81.  
 CC PDB; IFM211; X-ray; D=1-81.  
 CC PDB; IFM212; X-ray; D=1-81.  
 CC PDB; IFM213; X-ray; D=1-81.  
 CC PDB; IFM214; X-ray; D=1-81.  
 CC PDB; IFM215; X-ray; D=1-81.  
 CC PDB; IFM216; X-ray; D=1-81.  
 CC PDB; IFM217; X-ray; D=1-81.  
 CC PDB; IFM218; X-ray; D=1-81.  
 CC PDB; IFM219; X-ray; D=1-81.  
 CC PDB; IFM220; X-ray; D=1-81.  
 CC PDB; IFM221; X-ray; D=1-81.  
 CC PDB; IFM222; X-ray; D=1-81.  
 CC PDB; IFM223; X-ray; D=1-81.  
 CC PDB; IFM224; X-ray; D=1-81.  
 CC PDB; IFM225; X-ray; D=1-81.  
 CC PDB; IFM226; X-ray; D=1-81.  
 CC PDB; IFM227; X-ray; D=1-81.  
 CC PDB; IFM228; X-ray; D=1-81.  
 CC PDB; IFM229; X-ray; D=1-81.  
 CC PDB; IFM230; X-ray; D=1-81.  
 CC PDB; IFM231; X-ray; D=1-81.  
 CC PDB; IFM232; X-ray; D=1-81.  
 CC PDB; IFM233; X-ray; D=1-81.  
 CC PDB; IFM234; X-ray; D=1-81.  
 CC PDB; IFM235; X-ray; D=1-81.  
 CC PDB; IFM236; X-ray; D=1-81.  
 CC PDB; IFM237; X-ray; D=1-81.  
 CC PDB; IFM238; X-ray; D=1-81.  
 CC PDB; IFM239; X-ray; D=1-81.  
 CC PDB; IFM240; X-ray; D=1-81.  
 CC PDB; IFM241; X-ray; D=1-81.  
 CC PDB; IFM242; X-ray; D=1-81.  
 CC PDB; IFM243; X-ray; D=1-81.  
 CC PDB; IFM244; X-ray; D=1-81.  
 CC PDB; IFM245; X-ray; D=1-81.  
 CC PDB; IFM246; X-ray; D=1-81.  
 CC PDB; IFM247; X-ray; D=1-81.  
 CC PDB; IFM248; X-ray; D=1-81.  
 CC PDB; IFM249; X-ray; D=1-81.  
 CC PDB; IFM250; X-ray; D=1-81.  
 CC PDB; IFM251; X-ray; D=1-81.  
 CC PDB; IFM252; X-ray; D=1-81.  
 CC PDB; IFM253; X-ray; D=1-81.  
 CC PDB; IFM254; X-ray; D=1-81.  
 CC PDB; IFM255; X-ray; D=1-81.  
 CC PDB; IFM256; X-ray; D=1-81.  
 CC PDB; IFM257; X-ray; D=1-81.  
 CC PDB; IFM258; X-ray; D=1-81.  
 CC PDB; IFM259; X-ray; D=1-81.  
 CC PDB; IFM260; X-ray; D=1-81.  
 CC PDB; IFM261; X-ray; D=1-81.  
 CC PDB; IFM262; X-ray; D=1-81.  
 CC PDB; IFM263; X-ray; D=1-81.  
 CC PDB; IFM264; X-ray; D=1-81.  
 CC PDB; IFM265; X-ray; D=1-81.  
 CC PDB; IFM266; X-ray; D=1-81.  
 CC PDB; IFM267; X-ray; D=1-81.  
 CC PDB; IFM268; X-ray; D=1-81.  
 CC PDB; IFM269; X-ray; D=1-81.  
 CC PDB; IFM270; X-ray; D=1-81.  
 CC PDB; IFM271; X-ray; D=1-81.  
 CC PDB; IFM272; X-ray; D=1-81.  
 CC PDB; IFM273; X-ray; D=1-81.  
 CC PDB; IFM274; X-ray; D=1-81.  
 CC PDB; IFM275; X-ray; D=1-81.  
 CC PDB; IFM276; X-ray; D=1-81.  
 CC PDB; IFM277; X-ray; D=1-81.  
 CC PDB; IFM278; X-ray; D=1-81.  
 CC PDB; IFM279; X-ray; D=1-81.  
 CC PDB; IFM280; X-ray; D=1-81.  
 CC PDB; IFM281; X-ray; D=1-81.  
 CC PDB; IFM282; X-ray; D=1-81.  
 CC PDB; IFM283; X-ray; D=1-81.  
 CC PDB; IFM284; X-ray; D=1-81.  
 CC PDB; IFM285; X-ray; D=1-81.  
 CC PDB; IFM286; X-ray; D=1-81.  
 CC PDB; IFM287; X-ray; D=1-81.  
 CC PDB; IFM288; X-ray; D=1-81.  
 CC PDB; IFM289; X-ray; D=1-81.  
 CC PDB; IFM290; X-ray; D=1-81.  
 CC PDB; IFM291; X-ray; D=1-81.  
 CC PDB; IFM292; X-ray; D=1-81.  
 CC PDB; IFM293; X-ray; D=1-81.  
 CC PDB; IFM294; X-ray; D=1-81.  
 CC PDB; IFM295; X-ray; D=1-81.  
 CC PDB; IFM296; X-ray; D=1-81.  
 CC PDB; IFM297; X-ray; D=1-81.  
 CC PDB; IFM298; X-ray; D=1-81.  
 CC PDB; IFM299; X-ray; D=1-81.  
 CC PDB; IFM300; X-ray; D=1-81.  
 CC PDB; IFM301; X-ray; D=1-81.  
 CC PDB; IFM302; X-ray; D=1-81.  
 CC PDB; IFM303; X-ray; D=1-81.  
 CC PDB; IFM304; X-ray; D=1-81.  
 CC PDB; IFM305; X-ray; D=1-81.  
 CC PDB; IFM306; X-ray; D=1-81.  
 CC PDB; IFM307; X-ray; D=1-81.  
 CC PDB; IFM308; X-ray; D=1-81.  
 CC PDB; IFM309; X-ray; D=1-81.  
 CC PDB; IFM310; X-ray; D=1-81.  
 CC PDB; IFM311; X-ray; D=1-81.  
 CC PDB; IFM312; X-ray; D=1-81.  
 CC PDB; IFM313; X-ray; D=1-81.  
 CC PDB; IFM314; X-ray; D=1-81.  
 CC PDB; IFM315; X-ray; D=1-81.  
 CC PDB; IFM316; X-ray; D=1-81.  
 CC PDB; IFM317; X-ray; D=1-81.  
 CC PDB; IFM318; X-ray; D=1-81.  
 CC PDB; IFM319; X-ray; D=1-81.  
 CC PDB; IFM320; X-ray; D=1-81.  
 CC PDB; IFM321; X-ray; D=1-81.  
 CC PDB; IFM322; X-ray; D=1-81.  
 CC PDB; IFM323; X-ray; D=1-81.  
 CC PDB; IFM324; X-ray; D=1-81.  
 CC PDB; IFM325; X-ray; D=1-81.  
 CC PDB; IFM326; X-ray; D=1-81.  
 CC PDB; IFM327; X-ray; D=1-81.  
 CC PDB; IFM328; X-ray; D=1-81.  
 CC PDB; IFM329; X-ray; D=1-81.  
 CC PDB; IFM330; X-ray; D=1-81.  
 CC PDB; IFM331; X-ray; D=1-81.  
 CC PDB; IFM332; X-ray; D=1-81.  
 CC PDB; IFM333; X-ray; D=1-81.  
 CC PDB; IFM334; X-ray; D=1-81.  
 CC PDB; IFM335; X-ray; D=1-81.  
 CC PDB; IFM336; X-ray; D=1-81.  
 CC PDB; IFM337; X-ray; D=1-81.  
 CC PDB; IFM338; X-ray; D=1-81.  
 CC PDB; IFM339; X-ray; D=1-81.  
 CC PDB; IFM340; X-ray; D=1-81.  
 CC PDB; IFM341; X-ray; D=1-81.  
 CC PDB; IFM342; X-ray; D=1-81.  
 CC PDB; IFM343; X-ray; D=1-81.  
 CC PDB; IFM344; X-ray; D=1-81.  
 CC PDB; IFM345; X-ray; D=1-81.  
 CC PDB; IFM346; X-ray; D=1-81.  
 CC PDB; IFM347; X-ray; D=1-81.  
 CC PDB; IFM348; X-ray; D=1-81.  
 CC PDB; IFM349; X-ray; D=1-81.  
 CC PDB; IFM350; X-ray; D=1-81.  
 CC PDB; IFM351; X-ray; D=1-81.  
 CC PDB; IFM352; X-ray; D=1-81.  
 CC PDB; IFM353; X-ray; D=1-81.  
 CC PDB; IFM354; X-ray; D=1-81.  
 CC PDB; IFM355; X-ray; D=1-81.  
 CC PDB; IFM356; X-ray; D=1-81.  
 CC PDB; IFM357; X-ray; D=1-81.  
 CC PDB; IFM358; X-ray; D=1-81.  
 CC PDB; IFM359; X-ray; D=1-81.  
 CC PDB; IFM360; X-ray; D=1-81.  
 CC PDB; IFM361; X-ray; D=1-81.  
 CC PDB; IFM362; X-ray; D=1-81.  
 CC PDB; IFM363; X-ray; D=1-81.  
 CC PDB; IFM364; X-ray; D=1-81.  
 CC PDB; IFM365; X-ray; D=1-81.  
 CC PDB; IFM366; X-ray; D=1-81.  
 CC PDB; IFM367; X-ray; D=1-81.  
 CC PDB; IFM368; X-ray; D=1-81.  
 CC PDB; IFM369; X-ray; D=1-81.  
 CC PDB; IFM370; X-ray; D=1-81.  
 CC PDB; IFM371; X-ray; D=1-81.  
 CC PDB; IFM372; X-ray; D=1-81.  
 CC PDB; IFM373; X-ray; D=1-81.  
 CC PDB; IFM374; X-ray; D=1-81.  
 CC PDB; IFM375; X-ray; D=1-81.  
 CC PDB; IFM376; X-ray; D=1-81.  
 CC PDB; IFM377; X-ray; D=1-81.  
 CC PDB; IFM378; X-ray; D=1-81.  
 CC PDB; IFM379; X-ray; D=1-81.  
 CC PDB; IFM380; X-ray; D=1-81.  
 CC PDB; IFM381; X-ray; D=1-81.  
 CC PDB; IFM382; X-ray; D=1-81.  
 CC PDB; IFM383; X-ray; D=1-81.  
 CC PDB; IFM384; X-ray; D=1-81.  
 CC PDB; IFM385; X-ray; D=1-81.  
 CC PDB; IFM386; X-ray; D=1-81.  
 CC PDB; IFM387; X-ray; D=1-81.  
 CC PDB; IFM388; X-ray; D=1-81.  
 CC PDB; IFM389;

Molybdenum cofactor biosynthesis.  
 KW CONFLICT 9 Q -> E (in Ref. 4).  
 FT CONFLICT 45 A -> R (in Ref. 1).  
 FT STRAND 2  
 FT HELIX 8  
 FT STRAND 18  
 FT STRAND 27  
 FT STRAND 28  
 FT TURN 37  
 FT HELIX 40  
 FT TURN 46  
 FT TURN 48  
 FT TURN 52  
 FT TURN 56  
 FT STRAND 58  
 FT TURN 62  
 FT STRAND 65  
 FT TURN 68  
 FT STRAND 71  
 SQ SEQUENCE 81 AA; 8758 MW; 1E0A440520EE82F4 CRC64;  
 Query Match 89.7%; Score 26; DB 1; Length 81;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 ||:||||  
 Db 3 KVLFFA 8

RESULT 71  
 Q9APP7\_9BACT PRELIMINARY; PRT; 81 AA.  
 AC Q9APP7;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative molybdenum cofactor biosynthesis protein D.  
 GN Name=moaD;  
 OS uncultured bacterium pCoshE1.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=143796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20575196; PubMed=11133432; DOI=10.1128/AEM.67.1.89-99.2001;  
 RA Entcheva P., Liebl W., Johann A., Hartsch T., Streit W.R.;  
 RT "Direct cloning from enrichment cultures, a reliable strategy for  
 isolation of complete operons and genes from microbial consortia."  
 RL Appl. Environ. Microbiol. 67:89-99(2001).  
 DR EMBL; AF250774; AAG60573.1; -; Genomic\_DNA.  
 DR HSSP; P30748; 1JW9.  
 DR SRR; Q9APP7; 1-81.  
 DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.  
 DR GO; GO:0006790; P:sulfur metabolism; IEA.  
 DR InterPro; IPR010034; MoaD.  
 DR InterPro; IPR003749; This.  
 DR Pfam; PF02597; This; 1.  
 DR TIGRFAMs; TIGR01682; moaD; 1.  
 SQ SEQUENCE 81 AA; 8739 MW; 21361C1FCA3AA24C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 ||:||||  
 Db 3 KVLFFA 8

RESULT 72  
 Q57RF2\_SALCH PRELIMINARY; PRT; 81 AA.  
 AC Q57RF2;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Molybdopterin biosynthesis protein.  
 GN Name=moaD; OrderedLocusNames=SC0803;  
 OS Salmonella cholerae-suis (Salmonella enterica).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=591;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=SC-B67;  
 RX PubMed=15781495;  
 RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,  
 Wang H.-S., Lee Y.-S.;  
 RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a  
 highly invasive and resistant zoonotic pathogen."  
 RL Nucleic Acids Res. 33:1690-1698(2005).  
 DR EMBL; AS017220; AAX64709.1; -; Genomic\_DNA.  
 DR KW Complete proteome.  
 SQ SEQUENCE 81 AA; 8772 MW; 5821119685621426 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 ||:||||  
 Db 3 KVLFFA 8

RESULT 73  
 Q65TTO\_MANSN PRELIMINARY; PRT; 81 AA.  
 ID Q65TTO\_MANSN PRELIMINARY;  
 AC Q65TTO;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE MoaD protein.  
 GN Name=moaD; OrderedLocusNames=MS1023;  
 OS Mannheimia succiniciproducens (strain MBEL55E).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Mannheimia.  
 OX NCBI\_TaxID=221988;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15378067; DOI=10.1038/nbt1010;  
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,  
 Kim C.H., Jeong H., Hur C.G., Kim J.J.;  
 RT "The genome sequence of the capnophilic rumen bacterium Mannheimia  
 succiniciproducens."  
 RL Nat. Biotechnol. 22:1275-1281(2004).  
 DR EMBL; AE016827; AAC37630.1; -; Genomic DNA.  
 DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.  
 DR GO; GO:0006790; P:sulfur metabolism; IEA.  
 DR InterPro; IPR010034; MoaD.  
 DR InterPro; IPR003749; This.  
 DR Pfam; PF02597; This; 1.  
 DR TIGRFAMs; TIGR01682; moaD; 1.  
 DR KW Complete proteome.  
 SQ SEQUENCE 81 AA; 8617 MW; E529ED840985D661 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 ||:||||  
 Db 3 KVLFFA 8

RESULT 74  
 Q7N6P4\_PHOLL

ID Q7N6P4 PHOLL PRELIMINARY; PRT; 81 AA.  
AC Q7N6P4;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Molybdopterin.  
GN Name=moaD; OrderedLocusNames=plu1501;  
OS Photorhabdus luminescens (subsp. laumondii).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Photorhabdus.  
OX NCBI\_TaxID=141679;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=TT01;  
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;  
RA Duchaud E., Ruenliok C., Frangeul L., Buchrieser C., Givaudan A.,  
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,  
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,  
RA Medigue C., Lanois A., Powell K., Siguiet P., Vincent R., Wingate V.,  
RA Zouline M., Glaeser P., Boemare N., Danchin A., Kunst F.;  
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus  
luminescens.";  
RL Nat. Biotechnol. 21:1307-1313 (2003).  
DR EMBL; BX571864; CAE13794.1; -; Genomic\_DNA.  
DR HSSP; P30748; 1JW9.  
DR PhotoList; plu1501; -.  
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.  
DR GO; GO:0006790; P:sulfur metabolism; IEA.  
DR InterPro; IPR010034; Moad.  
DR InterPro; IPR003749; This.  
DR Pfam; PF02597; This; 1.  
DR TIGRFAMS; TIGR01682; moad; 1.  
KW Complete proteome.  
SQ SEQUENCE 81 AA; 8886 MW; 6646B5932531F136 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
||:||||  
DB 3 KVLFFA 8

RESULT 75  
Q8D897 VIBVU  
ID Q8D897 VIBVU PRELIMINARY; PRT; 81 AA.  
AC Q8D897;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Molybdenum cofactor biosynthesis protein D.  
GN OrderedLocusNames=VVI3085;  
OS Vibrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=672;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CMCP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
RA Choy H.E.;  
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AEO16807; AAO11408.1; -; Genomic\_DNA.  
DR HSSP; P30748; 1JW9.  
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.  
DR GO; GO:0006790; P:sulfur metabolism; IEA.  
DR InterPro; IPR010034; Moad.  
DR InterPro; IPR003749; This.  
DR Pfam; PF02597; This; 1.  
DR TIGRFAMS; TIGR01682; moad; 1.  
KW Complete proteome.

SQ SEQUENCE 81 AA; 8731 MW; 4BE52COABDE06418 CRC64;  
Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
||:||||  
DB 3 KVLFFA 8

Search completed: December 29, 2005, 17:47:26  
Job time : 82.1936 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds  
(without alignments)  
44.518 Million cell updates/sec

Title: US-10-009-122-9  
Perfect score: 29  
Sequence: 1 KVPFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : PIR 80:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	186	1 WMR219	19K globulin precu
2	29	100.0	186	2 JC4784	alpha-globulin pre
3	29	100.0	442	2 H81402	probable integral
4	29	100.0	1144	1 A43271	nitric-oxide synth
5	28	96.6	380	2 F70399	hydrogenase expres
6	27	93.1	447	2 F71039	hypothetical prote
7	26	89.7	33	2 S23094	beta-amyloid prote
8	26	89.7	42	2 PN0512	beta-amyloid prote
9	26	89.7	57	2 A60045	Alzheimer's diseas
10	26	89.7	57	2 F60045	Alzheimer's diseas
11	26	89.7	57	2 D60045	Alzheimer's diseas
12	26	89.7	57	2 G60045	Alzheimer's diseas
13	26	89.7	57	2 G60045	Alzheimer's diseas
14	26	89.7	57	2 B60045	Alzheimer's diseas
15	26	89.7	81	2 F90736	molybdopterin bios
16	26	89.7	81	2 A82251	molybdenum cofacto
17	26	89.7	81	2 G85586	molybdopterin bios
18	26	89.7	81	2 H64814	molybdopterin bios
19	26	89.7	82	2 PQ0438	Alzheimer's diseas
20	26	89.7	83	2 AC0598	molybdopterin conv
21	26	89.7	152	2 T06645	hypothetical prote
22	26	89.7	193	2 B90157	hypothetical prote
23	26	89.7	207	2 B81256	phosphoribosyl-AMP
24	26	89.7	231	2 H85138	hypothetical prote
25	26	89.7	293	2 D69355	hypothetical prote
26	26	89.7	294	2 H90318	glycerol kinase (g
27	26	89.7	300	2 T26245	hypothetical prote
28	26	89.7	330	2 B82822	NADH2 dehydrogenas
29	26	89.7	339	2 B72402	UDP-N-acetylglucos

30	26	89.7	349	2 T26247	hypothetical prote
31	26	89.7	352	2 T48903	wax synthase (impo
32	26	89.7	428	2 T48008	hypothetical prote
33	26	89.7	477	2 B28988	hypothetical prote
34	26	89.7	520	2 A81548	hypothetical prote
35	26	89.7	594	2 F86499	hypothetical prote
36	26	89.7	603	2 F72237	conserved hypotet
37	26	89.7	617	2 A72123	hypothetical prote
38	26	89.7	695	1 A49795	Alzheimer's diseas
39	26	89.7	695	2 A27485	Alzheimer's diseas
40	26	89.7	695	2 S00550	Alzheimer's diseas
41	26	89.7	747	2 JH0773	Alzheimer's diseas
42	26	89.7	770	1 QRHUA4	Alzheimer's diseas
43	26	89.7	817	2 A82511	glycogen phosphory
44	26	89.7	1016	2 S30236	hypothetical prote
45	25	86.2	74	2 E64214	conserved hypotet
46	25	86.2	109	2 B72213	hypothetical prote
47	25	86.2	136	2 T19479	hypothetical prote
48	25	86.2	146	2 E75134	hypothetical prote
49	25	86.2	148	2 T32362	hypothetical prote
50	25	86.2	156	2 H95252	PTS system, IIB co
51	25	86.2	156	2 F98117	hypothetical prote
52	25	86.2	159	2 C71080	hypothetical prote
53	25	86.2	162	2 T13659	NADH2 dehydrogenas
54	25	86.2	162	2 T13656	NADH2 dehydrogenas
55	25	86.2	162	2 T13563	NADH2 dehydrogenas
56	25	86.2	162	2 T13487	NADH2 dehydrogenas
57	25	86.2	164	2 T13562	NADH2 dehydrogenas
58	25	86.2	188	2 G70475	conserved hypotet
59	25	86.2	190	2 A95895	probable permease
60	25	86.2	194	2 B97211	uncharacterized co
61	25	86.2	200	2 AE1632	hypothetical prote
62	25	86.2	232	2 A71495	probable polysacch
63	25	86.2	234	2 T23466	hypothetical prote
64	25	86.2	247	2 T32514	hypothetical prote
65	25	86.2	253	2 D82405	transcription regu
66	25	86.2	255	2 C87434	2-deoxy-D-gluconat
67	25	86.2	257	2 C83982	hypothetical prote
68	25	86.2	261	2 D64166	hypothetical prote
69	25	86.2	277	2 T31855	hypothetical prote
70	25	86.2	286	2 C84857	hypothetical prote
71	25	86.2	295	2 JC4744	NAD-dinitrogen-red
72	25	86.2	295	2 I39751	NAD-dinitrogen-red
73	25	86.2	295	2 C70736	hypothetical prote
74	25	86.2	302	2 A99074	hypothetical prote
75	25	86.2	302	2 B35961	hypothetical 21K p
76	25	86.2	311	2 S73625	methionyl-tRNA for
77	25	86.2	316	2 S61237	capsid protein - b
78	25	86.2	318	2 A75275	methionyl-tRNA for
79	25	86.2	321	2 H71729	hypothetical prote
80	25	86.2	328	2 T11938	NADH2 dehydrogenas
81	25	86.2	330	2 H75505	tryptophanyl-tRNA
82	25	86.2	340	1 MMBE85	cell fusion protei
83	25	86.2	347	2 S35229	hypD' protein - Br
84	25	86.2	352	2 AH2097	sorbitol dehydroge
85	25	86.2	352	2 H97272	histidinol-phospha
86	25	86.2	373	2 AE0847	hydrogenase isoenz
87	25	86.2	373	2 A85922	pleiotrophic effec
88	25	86.2	373	2 A91077	hydrogenase isoenz
89	25	86.2	373	2 S15200	hydrogenase expres
90	25	86.2	379	2 I39743	hydrogenase homolo
91	25	86.2	382	2 G83808	hypothetical prote
92	25	86.2	384	2 H64161	hypothetical prote
93	25	86.2	385	2 S32877	hypD protein - Rhi
94	25	86.2	399	2 G97727	proton/sodium-glut
95	25	86.2	399	2 D71728	conserved hypotet
96	25	86.2	399	2 A82842	probable LPS biosy
97	25	86.2	402	2 E86038	lipid A-core surfa
98	25	86.2	402	2 D91191	tyrosine-tRNA liga
99	25	86.2	405	2 A70146	hypothetical prote
100	25	86.2	455	2 T34366	hypothetical prote
101	25	86.2	469	2 T02325	probable selenium-
102	25	86.2	477	2 T02505	probable beta-alan

103	25	86.2	512	2	T19806	hypothetical prote	176	24	82.8	241	2	G71045	hypothetical prote
104	25	86.2	572	2	H96685	probable AMP-bindi	177	24	82.8	245	2	T49889	zinc finger transac
105	25	86.2	604	1	QXXL5M	NADH2 dehydrogenas	178	24	82.8	246	2	E90309	hypothetical prote
106	25	86.2	620	2	H69382	ABC transporter, A	179	24	82.8	248	2	F71849	amino acid ABC tra
107	25	86.2	646	2	AD3409	ABC transporter AT	180	24	82.8	248	2	C54666	glutamine transpor
108	25	86.2	657	2	G86590	exinuclease ABC su	181	24	82.8	254	2	T28170	hypothetical prote
109	25	86.2	657	2	B72034	exinuclease ABC,	182	24	82.8	256	2	AC1561	conserved hypothet
110	25	86.2	657	2	H90523	exinuclease ABC s	183	24	82.8	262	2	AE1203	conserved hypothet
111	25	86.2	660	1	A28153	gelatinase A (EC 3	184	24	82.8	262	2	D88930	protein R11G11.10
112	25	86.2	662	2	S70365	gelatinase A (EC 3	185	24	82.8	262	2	A81056	conserved hypothet
113	25	86.2	662	2	A42496	gelatinase A (EC 3	186	24	82.8	263	2	C89887	hypothetical prote
114	25	86.2	662	2	S34780	gelatinase A (EC 3	187	24	82.8	269	2	A81820	conserved hypothet
115	25	86.2	663	1	S46492	gelatinase A (EC 3	188	24	82.8	276	2	S05343	NAD ADP-ribosyltra
116	25	86.2	676	2	D81654	exinuclease ABC c	189	24	82.8	278	1	S01065	probable dehydroge
117	25	86.2	681	2	T39814	hypothetical prote	190	24	82.8	281	2	F69400	2-deoxy-D-gluconat
118	25	86.2	774	2	F96639	protein T1F9.8 [im	191	24	82.8	283	2	T20734	hypothetical prote
119	25	86.2	774	2	T34496	hypothetical prote	192	24	82.8	286	2	AI3105	hypothetical prote
120	25	86.2	804	2	G71546	probable DNA gyras	193	24	82.8	287	2	AI2038	carboxyphosphonoe
121	25	86.2	812	2	H87386	hypothetical prote	194	24	82.8	300	2	F83621	hypothetical prote
122	25	86.2	1119	2	A86340	protein F2D10.24 [	195	24	82.8	301	2	C98181	sitC protein (AF12
123	25	86.2	1147	1	I53165	nitric-oxide synth	196	24	82.8	309	2	T35801	probable polyamine
124	25	86.2	1147	1	I58575	nitric-oxide synth	197	24	82.8	311	2	D64240	methionyl-tRNA for
125	25	86.2	1147	1	S38253	nitric-oxide synth	198	24	82.8	315	2	S59779	probable membrane
126	25	86.2	1147	1	S47647	nitric-oxide synth	199	24	82.8	323	2	AC2119	hypothetical prote
127	25	86.2	1147	2	JC5029	nitric-oxide synth	200	24	82.8	325	1	B40358	NADH2 dehydrogenas
128	25	86.2	1147	2	JC5028	nitric-oxide synth	201	24	82.8	330	2	T29640	mitochondrial carr
129	25	86.2	1147	2	JC5027	nitric-oxide synth	202	24	82.8	331	1	DN0BU1	NADH2 dehydrogenas
130	25	86.2	1147	2	S65440	nitric-oxide synth	203	24	82.8	335	2	A72289	oligopeptide ABC t
131	25	86.2	1324	2	T01508	mismatch repair en	204	24	82.8	337	2	AG0963	hypothetical prote
132	25	86.2	2241	2	T02857	conserved hypothet	205	24	82.8	337	2	T48341	hypothetical prote
133	25	86.2	3623	2	T08618	intrinsic factor-B	206	24	82.8	341	2	S73685	hypothetical prote
134	25	86.2	4152	2	T31102	filamentous hemagg	207	24	82.8	342	2	AE2238	methionyl-tRNA for
135	25	86.2	4919	2	T31105	hypothetical prote	208	24	82.8	344	2	E83562	N-acetyl-gamma-glu
136	24	82.8	20	2	JU0030	hypothetical prote	209	24	82.8	345	2	A81837	hypothetical prote
137	24	82.8	20	2	A99091	hypothetical prote	210	24	82.8	352	2	E90175	NADH dehydrogenase
138	24	82.8	62	2	E64530	hypothetical prote	211	24	82.8	352	2	AB3079	transcription regu
139	24	82.8	68	2	C71970	hypothetical prote	212	24	82.8	352	2	G98207	hypothetical prote
140	24	82.8	77	2	AC1381	preprotein translo	213	24	82.8	363	2	S56273	probable membrane
141	24	82.8	91	2	H82370	conserved hypothet	214	24	82.8	379	2	S23443	hypothetical prote
142	24	82.8	95	2	AG0277	probable phage-rel	215	24	82.8	380	2	T39248	hypothetical prote
143	24	82.8	106	2	AG2113	hypothetical prote	216	24	82.8	380	2	F86038	probable LPS biosy
144	24	82.8	108	2	C64516	hypothetical prote	217	24	82.8	380	2	E91191	probable LPS biosy
145	24	82.8	138	2	I47205	Ig heavy chain var	218	24	82.8	382	2	AI1427	efflux proteins ho
146	24	82.8	141	1	B70457	gliding motility p	219	24	82.8	383	2	AF1893	hydrogenase expres
147	24	82.8	141	2	I47177	Ig H-chain - pig {	220	24	82.8	385	2	T31493	hypothetical prote
148	24	82.8	143	1	A44397	cofilin - yeast {S	221	24	82.8	393	2	D86168	hypothetical prote
149	24	82.8	144	2	D72219	conserved hypothet	222	24	82.8	400	2	H99009	hypothetical prote
150	24	82.8	147	2	H82313	hypothetical prote	223	24	82.8	401	2	T44831	probable emulsan r
151	24	82.8	163	2	F86878	hypothetical prote	224	24	82.8	409	2	S29124	membrane glycoprot
152	24	82.8	169	2	AF2630	hypothetical prote	225	24	82.8	415	2	C71467	probable tyrosine
153	24	82.8	171	2	C71244	hypothetical prote	226	24	82.8	416	2	I64039	hypothetical prote
154	24	82.8	174	2	G81349	periplasmic nitrat	227	24	82.8	422	2	E82904	hypothetical prote
155	24	82.8	179	2	AB0652	probable intracell	228	24	82.8	429	2	T28950	hypothetical prote
156	24	82.8	179	2	T45503	hypothetical prote	229	24	82.8	440	1	B29413	ubiquinol-cytochro
157	24	82.8	179	2	S07799	probable membrane	230	24	82.8	442	2	T39683	zuotin-like protei
158	24	82.8	179	2	B90848	probable membrane	231	24	82.8	448	2	A86534	integral membrane
159	24	82.8	179	2	A85706	probable membrane	232	24	82.8	448	2	A72089	integral membrane
160	24	82.8	179	2	S70898	intracellular sept	233	24	82.8	451	2	A81581	ABC transporter, p
161	24	82.8	184	2	AH3581	alkyl hydroperoxid	234	24	82.8	451	2	G71561	probable integral
162	24	82.8	193	2	A82435	conserved hypothet	235	24	82.8	452	2	H84016	hypothetical prote
163	24	82.8	197	2	T22032	hypothetical prote	236	24	82.8	455	2	H9837	conserved hypothet
164	24	82.8	197	2	G83597	conserved hypothet	237	24	82.8	456	2	D95384	protein imported
165	24	82.8	210	2	C97260	probable membrane	238	24	82.8	463	2	S52754	aromatic amino aci
166	24	82.8	210	2	S67140	probable membrane	239	24	82.8	466	2	A95179	hypothetical prote
167	24	82.8	214	2	B84217	hypothetical prote	240	24	82.8	466	2	B97030	LPS glycosyltransf
168	24	82.8	216	2	B88065	protein T16A1.3 [i	241	24	82.8	466	2	H98045	hypothetical prote
169	24	82.8	219	1	A35617	HDLEL receptor ERD2	242	24	82.8	471	2	T41602	hypothetical prote
170	24	82.8	219	2	A75004	hypothetical prote	243	24	82.8	485	2	B84394	argininosuccinate
171	24	82.8	221	2	G72322	glutaredoxin-relat	244	24	82.8	490	2	A35312	potassium channel
172	24	82.8	222	2	T47768	hypothetical prote	245	24	82.8	500	2	B83364	pyoverdine biosynt
173	24	82.8	225	2	A90260	conserved hypothet	246	24	82.8	500	2	F83418	sodium/proton anti
174	24	82.8	238	2	E75169	hypothetical prote	247	24	82.8	503	2	T34694	probable cationic
175	24	82.8	240	2	G70303	cytochrome c - Aqu	248	24	82.8	507	2	F97765	hypothetical prote







A;Cross-references: UNIPROT:O9PHV5; UNIPARC:UPI00000C217E; GB:AL139075; GB:AL1111168; NID  
A;Experimental source: serotype O2, strain NCTC 11168  
C;Genetics:  
A;Gene: CJ0560

Query Match 100.0%; Score 29; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
DB 313 KVVFFA 318

RESULT 4  
A43271  
nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 05-Oct-2004  
C;Accession: A43271; A42166; JN0458; A46186  
R;Xie, Q.; Cho, H.J.; Calavay, J.; Mumford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A.;  
Science 256, 225-228, 1992  
A;Title: Cloning and characterization of inducible nitric oxide synthase from mouse macrophages  
A;Reference number: A43271; MUID:92229444; PMID:1373522  
A;Accession: A43271  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1144 <XIE>  
A;Cross-references: UNIPROT:P29477; UNIPARC:UPI000000D36; GB:M87039; NID:g198406; PIDN:  
R;Lyons, C.R.; Orloff, G.J.; Cunningham, J.M.  
J. Biol. Chem. 267, 6370-6374, 1992  
A;Title: Molecular cloning and functional expression of an inducible nitric oxide synthase  
A;Reference number: A42166; MUID:92210618; PMID:1372907  
A;Accession: A42166  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1144 <LYO>  
A;Cross-references: UNIPARC:UPI000000D36; GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:  
R;Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.  
Biochem. Biophys. Res. Commun. 191, 767-774, 1993  
A;Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxide  
A;Reference number: JN0457; MUID:93221515; PMID:7682072  
A;Accession: JN0458  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-278, F', 280-682, H', 684-937, 939-1144 <NO>  
A;Cross-references: UNIPARC:UPI000017223A  
R;Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992  
A;Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the brain  
A;Reference number: A46186; MUID:92357701; PMID:1379716  
A;Accession: A46186  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-190, V', 192-765, P', 767-843, G', 845-1144 <LOW>  
A;Cross-references: UNIPARC:UPI000017223B; GB:M92649; NID:g200109  
A;Experimental source: BALB/c, RAW 264.7 cells, macrophage  
A;Note: sequence extracted from NCBI backbone (NCBIP:113541)  
C;Genetics:  
A;Gene: NOS  
C;Function:  
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH  
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reductase  
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
F;533-1121/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F;535-671/Domain: flavodoxin homology <FLX>  
F;194/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
DB 514 KVVFFA 519

RESULT 5  
F70399  
hydrogenase expression/formaton protein HypD - Aquifex aeolicus  
C;Species: Aquifex aeolicus  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C;Accession: F70399  
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi  
V.  
Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A;Reference number: A70300; MUID:98196666; PMID:9537320  
A;Accession: F70399  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-380 <AOE>  
A;Cross-references: UNIPROT:O67225; UNIPARC:UPI0000056543; GB:AE000726; NID:g2983612; PI  
A;Experimental source: strain VF5  
C;Genetics:  
A;Gene: hypD  
C;Superfamily: [Nipel]-hydrogenase maturation factor, HypD type

Query Match 96.6%; Score 28; DB 2; Length 380;  
Best Local Similarity 83.3%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
DB 141 KVVFFA 146

RESULT 6  
F71039  
hypothetical protein PH1606 - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 05-Oct-2004  
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch  
DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: F71039  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-447 <KAW>  
A;Cross-references: UNIPROT:O59243; UNIPARC:UPI00000630DE; GB:AP000006; NID:g3236133; P  
A;Experimental source: strain OR3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C;Genetics:  
A;Gene: PH1606  
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1142

Query Match 93.1%; Score 27; DB 2; Length 447;  
Best Local Similarity 66.7%; Pred. No. 91;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
DB 207 KIIFFA 212

RESULT 7  
S23094  
beta-amyloid protein precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
C;Accession: S23094  
R;Kojima, S.; Omori, M.

FEBS Lett. 304, 57-60, 1992

A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
A;Reference number: S23094; MUID:92316198; PMID:1618299  
A;Accession: S23094  
A;Molecule type: protein  
A;Residues: 1-33 <KQ>  
A;Cross-references: UNIPARC:UPI00001777EB  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 89.7%; Score 26; DB 2; Length 33;  
Best Local Similarity 83.3%; Pred. No. 14;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 21 KLVFFA 26

# RESULT 8

PN0512  
beta-amyloid protein - guinea pig (fragment)  
C;Species: Cavia porcellus (guinea pig)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: PN0512  
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.  
Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment  
A;Reference number: PN0512; MUID:93290653; PMID:7685598  
A;Accession: PN0512  
A;Molecule type: protein  
A;Residues: 1-42 <SH>  
A;Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C;Keywords: alternative splicing; amyloid

Query Match 89.7%; Score 26; DB 2; Length 42;  
Best Local Similarity 83.3%; Pred. No. 17;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

# RESULT 9

A60045  
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C;Species: Canis lupus familiaris (dog)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C;Accession: A60045  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A;Reference number: A60045; MUID:92017079; PMID:1656157  
A;Accession: A60045  
A;Molecule type: mRNA  
A;Residues: 1-57 <JOH>  
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56125  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
Best Local Similarity 83.3%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 21 KLVFFA 26

# RESULT 10

F60045  
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C;Accession: F60045  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A;Reference number: A60045; MUID:92017079; PMID:1656157  
A;Accession: F60045  
A;Molecule type: mRNA  
A;Residues: 1-57 <JOH>  
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:gl895; PIDN:CAA39592.1; PID  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
Best Local Similarity 83.3%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 21 KLVFFA 26

# RESULT 11

D60045  
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C;Accession: D60045  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A;Reference number: A60045; MUID:92017079; PMID:1656157  
A;Accession: D60045  
A;Molecule type: mRNA  
A;Residues: 1-57 <JOH>  
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56124  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
Best Local Similarity 83.3%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 21 KLVFFA 26

# RESULT 12

E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C;Species: Ovis sp. (sheep)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C;Accession: E60045  
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A;Reference number: A60045; MUID:92017079; PMID:1656157  
A;Accession: E60045  
A;Molecule type: mRNA  
A;Residues: 1-57 <JOH>  
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56130  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;  
Best Local Similarity 83.3%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 21 KLVFFA 26

C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 KVVFFA 6  
|||  
DB 3 KVLFFA 8

RESULT 16  
A82251  
molybdenum cofactor biosynthesis protein D VC1027 [imported] - Vibrio cholerae  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 16-Aug-2004  
C:Accession: A82251  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson  
R:Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; S  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholera  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: A82251  
A:Status: preliminary  
A:Molecule type: DNA  
A:Molecule type: DNA  
A:Residues: 1-81 <HEI>  
A:Cross-references: UNIPROT:Q9KT78; UNIPARC:UPI00000C3E5B; GB:AE004184; GB:AE00  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC1027  
A:Map position: 1  
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein  
P:81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 KVVFFA 6  
|||  
DB 3 KVLFFA 8

RESULT 17  
G85586  
molybdopterin biosynthesis [imported] - Escherichia coli (strain O157:H7, subs  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
C:Accession: G85586  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: G85586  
A:Status: preliminary  
A:Molecule type: DNA  
A:Molecule type: DNA  
A:Residues: 1-81 <STO>  
A:Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000D09BF; GB:AE005174; NID:gi2  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: moaD  
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 89.7%; Score 26; DB 2; Length 81;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

## RESULT 18

H64814

molybdopterin biosynthesis protein D chain [validated] - Escherichia coli (strain K-12)  
 A;Alternate names: moaD protein; molybdopterin-converting factor 10K chain; molybdopterin C;Species: Escherichia coli  
 C;Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text\_change 05-Oct-2004  
 C;Accession: H64814; S35001; A46585; S31882 #text\_change 05-Oct-2004  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: H64814

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-81 <BLAT>

A;Cross-references: UNIPROT:P30748; UNIPARC:UPI00001116DF; GB:AE000181; GB:U00096; NID:9

A;Experimental source: strain K-12, substrain MGI655

R;Rivers, S.L.; McNairn, E.; Blasco, F.; Giordano, G.; Boxer, D.H.

Mol. Microbiol. 8, 1071-1081, 1993

A;Title: Molecular genetic analysis of the moa operon of Escherichia coli K-12 required

A;Reference number: S34998; MUID:93369423; PMID:8361352

A;Accession: S35001

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-44, 'R', '46-81 <RIV>

A;Cross-references: UNIPARC:UPI000016F2FD; EMBL:X70420; NID:942007; PIDN:CAA49864.1; PID

A;Experimental source: strain K12

R;Pitterle, D.M.; Rajagopalan, K.V.

J. Biol. Chem. 268, 13493-13505, 1993

A;Title: The biosynthesis of molybdopterin in Escherichia coli. Purification and character

A;Reference number: A46585; MUID:93293873; PMID:8514782

A;Accession: A46585

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8, 'G', 10-15 <PIT>

A;Cross-references: UNIPARC:UPI0000178EC3

A;Note: sequence extracted from NCBI backbone (NCBIP:134491)

C;Genetics:

A;Gene: moaD

A;Map position: 17, 7 min

C;Complex: heterodimer with D chain (PIR:S31983) [validated, MUID:93293873]

C;Function:

A;Description: required for the addition of the Mo-binding dithiolene group to a molybdo

C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

C;Keywords: heterodimer; molybdopterin biosynthesis

F;81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match

Best Local Similarity 89.7%; Score 26; DB 2; Length 81;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

||:||||

Db 3 KVLFFA 8

## RESULT 19

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence revision 19-Oct-1995 #text\_change 19-Oct-1995

C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 189, 905-911, 1992

A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor

A;Reference number: PQ0438; MUID:93075180; PMID:1445331

A;Accession: PQ0438

A;Molecule type: DNA

A;Residues: 1-82 <DAV>

A;Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: C60045

A;Molecule type: mRNA

A;Residues: 12-68 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56129

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 89.7%; Score 26; DB 2; Length 82;

Best Local Similarity 83.3%; Pred. No. 32;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

||:||||

Db 32 KLVFFA 37

## RESULT 20

AC0598

molybdopterin converting factor, chain 1 [imported] - Salmonella enterica subsp. enteri

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 16-Aug-2004

C;Accession: AC0598

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar

S.; Moutle, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AC0598

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-83 <PAR>

A;Cross-references: UNIPARC:UPI000005A0EA; GB:AL513382; PIDN:CAD05253.1; PID:gl65020222,

C;Genetics:

A;Gene: STY0839

C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match

Best Local Similarity 89.7%; Score 26; DB 2; Length 83;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

||:||||

Db 5 KVLFFA 10

## RESULT 21

T06645

hypothetical protein T20K18.220 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C;Accession: T06645

R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mc

submitted to the Protein Sequence Database, April 1999

A;Reference number: Z15790

A;Accession: T06645

A;Molecule type: DNA

A;Residues: 1-152 <BEV>

A;Cross-references: UNIPROT:Q9ST29; UNIPARC:UPI00000A0722; EMBL:AL049640; GSPDB:GN000662

A;Experimental source: cultivar Columbia; BAC clone T20K18

C;Genetics:

A;Gene: ATSP:T20K18.220

A;Map position: 4

A;Introns: 87/3; 109/3

C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match

Best Local Similarity 89.7%; Score 26; DB 2; Length 152;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFPA 6							
Db	9	KLVFFA 14							
RESULT 22									
B90157									
hypothetical protein SSO0168 [imported] - Sulfolobus solfataricus									
C:Species: Sulfolobus solfataricus									
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004									
C:Accession: B90157									
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-									
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, E									
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.									
submitted to GenBank, April 2001									
A:Description: Sulfolobus solfataricus complete genome.									
A:Reference number: A99139									
A:Accession: B90157									
A:Molecule type: DNA									
A:Status: preliminary									
A:Residues: 1-193 <KUR>									
A:Cross-references: UNIPROT:Q980V9; UNIPARC:UPI00000641A8; GB:AE006641; NID:g13813299; E									
C:Genetics:									
A:Gene: SSO0168									
Query Match	89.7%;	Score 26;	DB 2;	Length 193;					
Best Local Similarity	83.3%;	Pred. No. 72;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFPA 6							
Db	117	KVFFA 122							
RESULT 23									
B81256									
phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3									
C:Species: Campylobacter jejuni									
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004									
C:Accession: B81256									
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin									
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel									
Nature 403, 665-668, 2000									
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp									
A:Reference number: B81250; MUID:20150912; PMID:10688204									
A:Accession: B81256									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-207 <PAR>									
A:Cross-references: UNIPROT:Q9PM71; UNIPARC:UPI000012C76D; GB:AL1139079; GB:AL1111168; NID									
A:Experimental source: serotype O2, strain NCTC 11168									
C:Genetics:									
A:Gene: hlsI; Cj1604									
C:Superfamily: hlsI bifunctional enzyme; hlsI bifunctional enzyme homology; hlsI protein									
C:Keywords: hydrolase									
Query Match	89.7%;	Score 26;	DB 2;	Length 207;					
Best Local Similarity	83.3%;	Pred. No. 77;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFPA 6							
Db	51	KVFFS 56							
RESULT 24									
B85138									
hypothetical protein AT4g12900 [imported] - Arabidopsis thaliana									
C:Species: Arabidopsis thaliana (mouse-ear cress)									
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004									
C:Accession: B85138									

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin									
Nature 402, 769-777, 1999									
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.									
A:Reference number: A85001; MUID:20083488; PMID:10617198									
A:Accession: B85138									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-231 <STO>									
A:Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI00000A7E0E; GB:NC_001368; NID:g7267992; I									
C:Genetics:									
A:Gene: AT4g12900									
A:Map position: 4									
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100									
Query Match	89.7%;	Score 26;	DB 2;	Length 231;					
Best Local Similarity	83.3%;	Pred. No. 85;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFPA 6							
Db	12	KLVFFA 17							
RESULT 25									
D69355									
hypothetical protein AF0844 - Archaeoglobus fulgidus									
C:Species: Archaeoglobus fulgidus									
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004									
C:Accession: D69355									
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson									
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F									
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.									
Nature 390, 364-370, 1997									
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S									
Smith, H.O.; Woese, C.R.; Venter, J.C.									
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae									
A:Reference number: A69250; MUID:98049343; PMID:9389475									
A:Accession: D69355									
A:Status: preliminary; nucleic acid sequence not shown; translation not shown									
A:Molecule type: DNA									
A:Residues: 1-293 <KLS>									
A:Cross-references: UNIPROT:029414; UNIPARC:UPI0000056F64; GB:AE001046; GB:AE000782; NI									
Query Match	89.7%;	Score 26;	DB 2;	Length 293;					
Best Local Similarity	83.3%;	Pred. No. 1.1e+02;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFPA 6							
Db	140	KVLFFA 145							
RESULT 26									
H90318									
glycerol kinase (glpK-1) [imported] - Sulfolobus solfataricus									
C:Species: Sulfolobus solfataricus									
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004									
C:Accession: H90318									
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan									
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, M									
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.									
submitted to GenBank, April 2001									
A:Description: Sulfolobus solfataricus complete genome.									
A:Reference number: A99139									
A:Accession: H90318									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-294 <KUR>									
A:Cross-references: UNIPROT:Q97XW2; UNIPARC:UPI0000064E6; GB:AE006641; NID:g13814829; I									
C:Genetics:									
A:Gene: glpK-1									
Query Match	89.7%;	Score 26;	DB 2;	Length 294;					

Best Local Similarity 83.3%; Pred. No. 1.1e+02; DB 2; Length 300;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:|:|  
Db 184 KVVFFA 189

## RESULT 27

T26245  
hypothetical protein W06G6.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T26245

R;McMurray, A.  
submitted to the EMBL Data Library, November 1996

A;Accession: T26245

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-300 <WIL>

A;Cross-references: UNIPROT:Q9XU61; UNIPARC:UPI0000061208; EMBL:Z83129; PIDN:CAB05641.1;  
A;Experimental source: clone W06G6

C;Genetics:

A;Gene: CESP:W06G6.6

A;Map position: 5

A;Introns: 171/2; 204/2

Query Match 89.7%; Score 26; DB 2; Length 300;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:|:|  
Db 281 KVVFFA 286

## RESULT 28

B82822  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 [similarity] - *Xylella fastidiosa*

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C;Accession: B82822

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: B82822

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-330 <SIM>

A;Cross-references: UNIPROT:Q9PGI8; UNIPARC:UPI00000C2381; GB:AE003884; GB:AE003849; NID

A;Experimental source: strain 985C

R;Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrez, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facinani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsuchino, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0312

C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-b

C;Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match 89.7%; Score 26; DB 2; Length 330;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:|:|  
Db 275 KVVFFA 280

## RESULT 29

B72402

UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-a

C;Species: *Thermotoga maritima*

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: B72402

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

Garratt, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: B72402

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-339 <ARN>

A;Cross-references: UNIPROT:Q9WY74; UNIPARC:UPI0000012F9EB; GB:AE001707; GB:AE0000512; NI

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM0232

C;Superfamily: murG protein

Query Match 89.7%; Score 26; DB 2; Length 339;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:|:|  
Db 32 KVVFFA 37

## RESULT 30

T26247

hypothetical protein W06G6.8 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T26247

R;McMurray, A.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z20180

A;Accession: T26247

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-349 <WIL>

A;Cross-references: UNIPROT:Q9XU59; UNIPARC:UPI00000061209; EMBL:Z83129; PIDN:CAB05643.1;

A;Experimental source: clone W06G6

C;Genetics:

A;Gene: CESP:W06G6.8

A;Map position: 5

A;Introns: 172/2; 210/3; 247/2

Query Match 89.7%; Score 26; DB 2; Length 349;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:|:|  
Db 324 KVVFFA 329

## RESULT 31

T48903

wax synthase [imported] - *Simmondsia chinensis*

C;Species: *Simmondsia chinensis*

```

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T48903
R:Lardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W.
Plant Physiol. 122, 645-655, 2000
A:Title: Purification of a jojoba embryo wax synthase, cloning of its cDNA and production
A:Reference number: Z25002
A:Accession: T48903
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-352 <LAR>
A:Cross-references: UNIPROT:Q9XGV6; UNIPARC:UPI000000A1C81; EMBL:AF149919; PIDN:AAD38041.

Query Match      89.7%; Score 26; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      135 KLVFFFA 140

RESULT 32
T48008
hypothetical protein T17J13.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C:Accession: T48008
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24482
A:Accession: T48008
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <RIE>
A:Cross-references: UNIPROT:Q9M1Q8; UNIPARC:UPI00000488B7; EMBL:AL1138651
A:Experimental source: cultivar Columbia; BAC clone T17J13
C:Genetics:
A:Map position: 3
A:Introns: 137/3
A:Note: T17J13.120
C:Superfamily: N-hydroxycinnamoyl/benzoyl transferase

Query Match      89.7%; Score 26; DB 2; Length 428;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      271 KLVFFFA 276

RESULT 33
B28988
hypothetical protein F1696 (photosynthetic gene cluster) - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
C:Accession: B28988
R:Youván, D.C.; Bylina, E.J.; Alberti, M.; Begusch, H.; Hearst, J.E.
Cell 37, 949-957, 1984
A:Title: Nucleotide and deduced polypeptide sequences of the photosynthetic reaction-
A:Reference number: A90850; MUID:84259352; PMID:6744416
A:Accession: B28988
A:Molecule type: DNA
A:Residues: 1-477 <YOU>
A:Cross-references: UNIPROT:P26176; UNIPARC:UPI000013BE54; GB:K01183

Query Match      89.7%; Score 26; DB 2; Length 477;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      349 KVLFFFA 354

```

```

RESULT 34
A81548
hypothetical protein CP0705 [imported] - Chlamydophila pneumoniae (strain AR39)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81548
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: A81548
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520 <REA>
A:Cross-references: UNIPROT:Q9K207; UNIPARC:UPI000000CCCE9F; GB:AE002229; GB:AE002161; NT1
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0705

Query Match      89.7%; Score 26; DB 2; Length 520;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      381 RVVFFFA 386

RESULT 35
F86499
hypothetical protein CPj0069 [imported] - Chlamydophila pneumoniae (strain J138)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86499
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: F86499
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-594 <STO>
A:Cross-references: UNIPROT:Q9JSK0; UNIPARC:UPI000000CCCE9F; GB:BA000008; NID:g8978443; PI
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPj0069

Query Match      89.7%; Score 26; DB 2; Length 594;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      455 RVVFFFA 460

RESULT 36
F72237
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: F72237
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: F72237
A>Status: preliminary

```



A;Molecule type: DNA  
A;Residues: 1-603 <ARN>  
A;Cross-references: UNIPROT:Q9X1Q9; UNIPARC:UPI00000C125F; GB:AE001802; GB:AE000512; NID:  
C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
A;Experimental source: strain MSB8  
C;Genetics:  
A;Gene: TM1573

Query Match 89.7%; Score 26; DB 2; Length 603;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 193 KVVFFS 198  
|:|||||

RESULT 37  
A27123  
hypothetical protein CT326 homolog - Chlamydomydia pneumoniae (strain CWL029)  
C;Species: Chlamydomydia pneumoniae, Chlamydia pneumoniae  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
A;Accession: A72123  
R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A;Reference number: A72000; MUID:99206606; PMID:10192388  
A;Accession: A72123  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-617 <ARN>  
A;Cross-references: UNIPROT:Q9Z9B2; UNIPARC:UPI00000C11C1; GB:AE001592; GB:AE001363; NID:  
A;Experimental source: strain CWL029  
C;Genetics:  
A;Gene: CPh069

Query Match 89.7%; Score 26; DB 2; Length 617;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 478 RVVFFA 483  
|:|||||

RESULT 38  
A49795  
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
C;Species: Macaca fascicularis (crab-eating macaque)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: A49795  
R;Podlany, M.B.; Tolan, D.R.; Selkoe, D.J.  
Am. J. Pathol. 138, 1423-1435, 1991  
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a F  
A;Reference number: A49795; MUID:91273117; PMID:1905108  
A;Accession: A49795  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-695 <POD>  
A;Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;Keywords: alternative splicing

Query Match 89.7%; Score 26; DB 1; Length 695;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 612 KLVFFA 617  
|:|||||

RESULT 39  
A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
N;Alternate names: proteinase nexin II  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
A;Experimental source: strain MSB8  
C;Genetics:  
A;Gene: TM1573

Query Match 89.7%; Score 26; DB 2; Length 603;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 193 KVVFFS 198  
|:|||||

RESULT 37  
A27123  
hypothetical protein CT326 homolog - Chlamydomydia pneumoniae (strain CWL029)  
C;Species: Chlamydomydia pneumoniae, Chlamydia pneumoniae  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
A;Accession: A72123  
R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A;Reference number: A72000; MUID:99206606; PMID:10192388  
A;Accession: A72123  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-617 <ARN>  
A;Cross-references: UNIPROT:Q9Z9B2; UNIPARC:UPI00000C11C1; GB:AE001592; GB:AE001363; NID:  
A;Experimental source: strain CWL029  
C;Genetics:  
A;Gene: CPh069

Query Match 89.7%; Score 26; DB 2; Length 617;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 478 RVVFFA 483  
|:|||||

RESULT 38  
A49795  
Alzheimer's disease amyloid beta protein precursor - rat  
N;Alternate names: beta-A4 amyloid protein  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: S00550; A41245; A39820; S46251  
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
EMBO J. 7, 1365-1370, 1988  
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
A;Reference number: S00550; MUID:88312583; PMID:2900758  
A;Accession: S00550  
A;Molecule type: mRNA  
A;Residues: 1-695 <SHI>  
A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2F8; EMBL:X07648; NID:955616; PID:  
R;Schubert, D.; Schroeder, R.; Lacorbiere, M.; Saitoh, T.; Cole, G.  
Science 241, 223-226, 1988  
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
A;Reference number: A41245; MUID:88264430; PMID:2968652  
A;Accession: A41245  
A;Molecule type: protein  
A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
A;Cross-references: UNIPARC:UPI0000177FD  
A;Note: evidence for heparan sulfate attachment  
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.  
FEBS Lett. 349, 109-116, 1994  
A;Title: The beta-A4 amyloid precursor protein binding to copper.  
A;Reference number: S46251; MUID:94320627; PMID:7913895



A;Contents: annotation; copper binding sites  
A;Note: rat peptides were isolated but not sequenced  
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
J. Biol. Chem. 266, 8464-8469, 1991  
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
A;Reference number: A39820; MUID:91217087; PMID:1673681  
A;Accession: A39820  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 18-32 <POR>  
A;Cross-references: UNIPARC:UPI00001777FE  
A;Experimental source: brain  
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor  
C;Superfamily: Alzheimer's disease amyloid; glycoprotein; transmembrane protein  
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 89.7%; Score 26; DB 2; Length 695;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:|||||  
Db 612 KLVFFA 617

RESULT 41

Alzheimer's disease amyloid beta protein precursor - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
R;Okado, H.; Okamoto, H.  
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental  
A;Reference number: JH0773; MUID:93129227; PMID:1282805  
A;Accession: JH0773  
A;Molecule type: mRNA  
A;Residues: 1-747 <OKA>  
A;Cross-references: UNIPARC:UPI0000FC980; GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:  
A;Experimental source: larva  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor  
C;Keywords: alternative splicing; amyloid  
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 89.7%; Score 26; DB 2; Length 747;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:|||||  
Db 664 KLVFFA 669

RESULT 42

ORHUA4  
Alzheimer's disease amyloid beta protein precursor [validated] - human  
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibitor  
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
protein precursor splice form APP(770)  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44  
468; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S23076; S38252; S3  
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey  
Nucleic Acids Res. 17, 517-522, 1989  
A;Title: The PrA4 (695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
A;Reference number: S02260; MUID:89128427; PMID:2783775  
A;Accession: S02260  
A;Molecule type: DNA  
A;Residues: 1-288,'V',365-770 <LEM1>  
A;Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466  
A;Note: alternative splice form APP(695)

R;Lemaire, H.G.  
submitted to the EMBL Data Library, November 1988  
A;Reference number: S05194  
A;Accession: S05194  
A;Molecule type: DNA  
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>  
A;Cross-references: UNIPARC:UPI000016A5FC; EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PII  
A;Note: alternative splice form APP(695)  
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote  
A;Reference number: A32277; MUID:89165870; PMID:2538123  
A;Accession: A32277  
A;Molecule type: DNA  
A;Residues: 1-75 <LAF>  
A;Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:g341202; PIDN:AAAC13  
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit  
A;Reference number: A33260; MUID:89392030; PMID:2675837  
A;Accession: A33260  
A;Molecule type: DNA  
A;Residues: 656-737 <JOH>  
A;Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:g178863; PIDN:AAAS1768.1; PID  
R;Prelili, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
A;Reference number: A35486; MUID:90321244; PMID:2196878  
A;Accession: A35486  
A;Molecule type: DNA  
A;Residues: 672-710 <PRE1>  
A;Cross-references: UNIPARC:UPI0000148176  
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 87, 257-263, 1990  
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.  
A;Reference number: I39451; MUID:90236318; PMID:2110105  
A;Accession: I39452  
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL  
A;Molecule type: DNA  
A;Residues: 1-770 <YOS1>  
A;Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:g178613; PIDN:AAB59502.1; PID  
A;Accession: I39451  
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL  
A;Molecule type: DNA  
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>  
A;Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:g178608; PIDN:AAB59501.1; PID  
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 102, 291-292, 1991  
A;Reference number: A59020; MUID:91340168; PMID:1908403  
A;Contents: annotation; erratum  
A;Note: revised physical map for reference I39451  
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine  
Science 248, 1124-1126, 1990  
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh  
A;Reference number: I39453; MUID:90260663; PMID:2111584  
A;Accession: I39453  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 656-737 <LEV>  
A;Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:g178618; PIDN:AAAS1727.1; PID  
A;Note: a mutation with 693-Gln is presented  
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
Science 254, 97-99, 1991  
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer  
A;Reference number: I59562; MUID:9022553; PMID:1925564  
A;Accession: I59562  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 689-716,'F',718-737 <MUR>  
A;Cross-references: UNIPARC:UPI000011F7EA; GB:S57665; NID:g236720; PIDN:AAB19991.1; PID  
R;Kamino, K.; Orr, H.T.; Payami, H.; Wajsbman, H.; Alonso, M.E.; Pulst, S.M.; Anderson,  
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,

Am. J. Hum. Genet. 51, 998-1014, 1992  
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the  
A;Reference number: A44017; MUID:93035397; PMID:1415269  
A;Accession: A44017  
A;Molecule type: DNA  
A;Residues: 687-692, 'G', 694-718 <KAM1>  
A;Cross-references: UNIPARC:UPI00000117EB; GB:S45135; NID:G257377; PIDN:AAB23645.1; PID:  
A;Experimental source: familial Alzheimer disease family SB  
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)  
A;Accession: B44017  
A;Molecule type: DNA  
A;Residues: 687-718 <KAM2>  
A;Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:G257379; PIDN:AAB23646.1; PID:  
A;Experimental source: familial Alzheimer disease family Lit  
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)  
A;Note: this sequence has a silent mutation  
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
Nature 325, 733-736, 1987  
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
A;Reference number: A03134; MUID:87144572; PMID:2881207  
A;Accession: A03134  
A;Molecule type: mRNA  
A;Residues: 1-288, 'V', 365-770 <KAN>  
A;Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:G  
A;Note: alternative splice form APP(695)  
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a  
A;Reference number: A29030; MUID:87231971; PMID:3035574  
A;Accession: A29030  
A;Molecule type: mRNA  
A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
A;Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:G178539; PIDN:AAA51722.1; PID:  
A;Note: the authors translated the codon GAG for residue 647 as Asp  
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
Science 235, 877-880, 1987  
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
A;Reference number: A47584; MUID:87120328; PMID:3810169  
A;Accession: A47584  
A;Molecule type: mRNA  
A;Residues: 674-756, 'S', 758-770 <GOL>  
A;Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:G178706; PIDN:AAA35540.1; PID:  
A;Experimental source: brain  
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
Science 235, 880-884, 1987  
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
A;Reference number: A47585; MUID:87120329; PMID:2949367  
A;Accession: A47585  
A;Molecule type: mRNA  
A;Residues: 674-703 <TAN1>  
A;Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:G177957; PIDN:AAA51564.1; PID:  
R;Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
EMBO J. 7, 949-957, 1988  
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
A;Reference number: S02638; MUID:88296437; PMID:2900137  
A;Accession: S02638  
A;Molecule type: mRNA  
A;Residues: 672-678 <DYR>  
A;Cross-references: UNIPARC:UPI0000035AB0  
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
Nature 331, 528-530, 1988  
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
A;Reference number: S00707; MUID:88122640; PMID:2893290  
A;Accession: S00707  
A;Molecule type: mRNA  
A;Residues: 286-344, 'I', 365-366 <TAN2>  
A;Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PID:  
A;Experimental source: promyelocytic leukemia cell line HL60  
A;Note: alternative splice form APP(751)  
R;Ponte, P.; Gonzalez-DeHitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da  
Nature 331, 525-527, 1988  
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi  
A;Reference number: S00925; MUID:88122639; PMID:2893289

A;Accession: S00925  
A;Molecule type: mRNA  
A;Residues: 1-344, 'I', 365-770 <PO2>  
A;Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:X00297; NID:G28720; PIDN:CAA  
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
Nature 331, 530-532, 1988  
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito  
A;Reference number: A38949; MUID:88122641; PMID:2893291  
A;Accession: A38949  
A;Molecule type: mRNA  
A;Residues: 287-367 <KIT>  
A;Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:  
A;Experimental source: glioblastoma cell line  
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtoc  
Brain Res. Mol. Brain Res. 4, 121-131, 1988  
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three  
A;Reference number: A30320  
A;Accession: A30320  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 284-288, 'V', 365-770 <VIT1>  
A;Cross-references: UNIPARC:UPI0000174094  
A;Accession: B30320  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 122-288, 'V', 365-770 <VIT2>  
A;Cross-references: UNIPARC:UPI0000174094  
A;Accession: C30320  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 606-770 <VIT3>  
A;Cross-references: UNIPARC:UPI0000174094  
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C  
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b  
A;Reference number: A31087; MUID:88124954; PMID:2893379  
A;Accession: A31087  
A;Molecule type: mRNA  
Query Match 89.7%; Score 26; DB 1; Length 770;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KWVFFA 6  
|:|:|:|  
Db 687 KLVFFA 692  
RESULT 43  
A82511  
glycogen phosphorylase (EC 2.4.1.1) [similarity] - Vibrio cholerae (strain N16961 sero  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 18-Aug-2003  
C;Accession: A82511  
R;Heidelbergt, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,  
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20408833; PMID:10952301  
A;Accession: A82511  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-817 <HRI>  
A;Cross-references: UNIPARC:UPI00000C33C4; GB:AE004345; GB:AE003853; NID:G9657390; PID  
A;Experimental source: serogroup O1, strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VCA0013  
A;Map position: 2  
C;Superfamily: glucan phosphorylase  
C;Keywords: Glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phospho

Qy 1 KVFFA 6  
|::|||

A;Accession: E75134  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-146 <KAW>  
A;Cross-references: UNIPARC:UPI000063351; GB:AJ248285; GB:AL096836; NID:95458067; PIDN:  
A;Experimental source: strain Orsay  
C;Genetics:  
A;Gene: PAB1779  
C;Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 146;  
Best Local Similarity 66.7%; Pred. No. 96;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6  
|||:  
Db 39 KVIFPA 44

RESULT 49  
T32362  
hypothetical protein C08E3.11 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T32362  
R;Miller, N.; Kramer, J.; Keppler, D.  
A;Description: The EMBL Data Library, September 1997  
submitted to the sequence of C. elegans cosmid C08E3.  
A;Reference number: 221155  
A;Accession: T32362  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-148 <MIL>  
A;Cross-references: UNIPROT:O17202; UNIPARC:UPI000076D24; EMBL:AF025457; PIDN:AAB70972.  
A;Experimental source: strain Bristol N2; clone C08E3  
C;Genetics:  
A;Gene: CESP:C08E3.11  
A;Map position: 2  
A;Introns: 66/2

Query Match 86.2%; Score 25; DB 2; Length 148;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVF 5  
|||:  
Db 126 KVVF 130

RESULT 50  
H95252  
PTS system, IIB component [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: H95252  
R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: H95252  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-156 <KUR>  
A;Cross-references: UNIPROT:Q97N92; UNIPARC:UPI000051B4E; GB:AE005672; PIDN:AAK76217.1;  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP2163  
C;Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 86.2%; Score 25; DB 2; Length 156;

Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6  
|||:  
Db 56 KIVFPA 61

RESULT 51  
F98117  
hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)  
C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C;Accession: F98117  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blassczak, L.; Burgett, S.; DeHoff, B.S.;  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;  
Y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A;Reference number: A97872; MUID:21429245; PMID:11544234  
A;Accession: F98117  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-156 <KUR>  
A;Cross-references: UNIPROT:Q8DN20; UNIPARC:UPI00000E3754; GB:AE007317; PIDN:AAL00771.1;  
C;Genetics:  
A;Gene: PTS-EII  
C;Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 86.2%; Score 25; DB 2; Length 156;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6  
|||:  
Db 56 KIVFPA 61

RESULT 52  
C71080  
hypothetical protein PH0907 - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 16-Aug-2004  
C;Accession: C71080  
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch  
DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: C71080  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-159 <KAW>  
A;Cross-references: UNIPARC:UPI0000062F34; GB:AP000004; NID:g3236131; PIDN:BA330001.1;  
A;Experimental source: strain OT3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBan  
C;Genetics:  
A;Gene: PH0907  
C;Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 159;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6  
|||:  
Db 54 KVIFPA 59

RESULT 53  
T13659  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia sagittata chloroplast

C:Species: chloroplast Pontederia sagittata  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13659  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Synt. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13659  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <GRA>  
A:Cross-references: UNIPROT:Q32915; UNIPARC:UPI0000096540; EMBL:U41621; NID:g1174015; P13659  
C:Genetics:  
A:Genome: chloroplast  
A>Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||:  
Db 13 KVIFFS 18

RESULT 54  
T13656  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia rotundifolia chloroplast  
C:Species: chloroplast Pontederia rotundifolia  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13656  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Synt. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13656  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <GRA>  
A:Cross-references: UNIPROT:Q32892; UNIPARC:UPI000008CB4C; EMBL:U41620; NID:g1174011; P13656  
C:Genetics:  
A:Genome: chloroplast  
A>Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||:  
Db 13 KVIFFS 18

RESULT 55  
T13563  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia cordata chloroplast  
C:Species: chloroplast Pontederia cordata  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13563  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Synt. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13563  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <GRA>  
A:Cross-references: UNIPROT:Q32802; UNIPARC:UPI000008F006; EMBL:U41619; NID:g1174003; P13563  
A:Experimental source: var. ovalis

C:Genetics:  
A:Genome: chloroplast  
A>Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||:  
Db 13 KVIFFS 18

RESULT 56  
T13487  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Monochoria vaginalis chloroplast  
C:Species: chloroplast Monochoria vaginalis  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13487  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Synt. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13487  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <GRA>  
A:Cross-references: UNIPROT:Q32648; UNIPARC:UPI00000976P4; EMBL:U41616; NID:g1173991; P13487  
C:Genetics:  
A:Genome: chloroplast  
A>Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||:  
Db 13 KVIFFS 18

RESULT 57  
T13562  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia cordata chloroplast  
C:Species: chloroplast Pontederia cordata  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13562  
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.  
Synt. Biol. 47, 545-567, 1998  
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets  
A:Reference number: Z17600  
A:Accession: T13562  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-164 <GRA>  
A:Cross-references: UNIPROT:Q37011; UNIPARC:UPI000016D3B6; EMBL:U41617; NID:g1173999; P13562  
A:Experimental source: var. cordata  
C:Genetics:  
A:Genome: chloroplast  
A>Note: ndhf  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 164;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||:  
Db 13 KVIFFS 18

Db 13 KVIPP 18

RESULT 58  
G70475  
conserved hypothetical protein aq\_2049 - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: G70475  
V:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: G70475  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-188 <AOF>  
A:Cross-references: UNIPROT:O67835; UNIPARC:UPI000005679F; GB:AE000770; NID:G2984274; PI  
A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: aq\_2049

Query Match 86.2%; Score 25; DB 2; Length 188;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPF 5  
|||||  
79 KVVPF 83

Db 79 KVVPF 83

RESULT 59  
A95895  
probable permease protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: A95895  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1.683-kb pSymB megaplasamid from the N2-fixing endo  
A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: A95895  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-190 <KUR>  
A:Cross-references: UNIPROT:Q92WB8; UNIPARC:UPI00000CB514; GB:AL591985; PIDN:CAC48825.1;  
A:Experimental source: strain 1021, megaplasamid pSymB  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebaute, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Smb20443  
A:Genome: plasmid

Query Match 86.2%; Score 25; DB 2; Length 190;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPFA 6  
|||||  
116 RIVPFA 121

Db 116 RIVPFA 121

RESULT 60  
B97211  
uncharacterized conserved membrane protein CAC2524 [imported] - Clostridium acetobutylic

C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: B97211  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: B97211  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-194 <KUR>  
A:Cross-references: UNIPROT:Q97G46; UNIPARC:UPI00000CA55C; GB:AE001437; PIDN:AAK80477.1  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC2524

Query Match 86.2%; Score 25; DB 2; Length 194;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPFA 6  
|||||  
165 KILPFA 170

Db 165 KILPFA 170

RESULT 61  
AE1632  
hypothetical protein homolog lin1598 [imported] - Listeria innocua (strain Clip11262)  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AE1632  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke  
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dusauguet, O.; Entian, K.D.; Fsihi, H  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlan  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1632  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-200 <GLA>  
A:Cross-references: UNIPROT:Q92BF2; UNIPARC:UPI0000127CE2; GB:AL592022; PIDN:CAC96829.1  
A:Experimental source: strain Clip11262  
C:Genetics:  
A:Gene: lin1598  
C:Superfamily: conserved hypothetical protein YDR196c

Query Match 86.2%; Score 25; DB 2; Length 200;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPF 5  
|||||  
109 KVVPF 113

Db 109 KVVPF 113

RESULT 62  
A71495  
probable polysaccharide transporter - Chlamydia trachomatis (serotype D, strain UM3/Cx)  
C:Species: Chlamydia trachomatis  
C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: A71495  
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell  
Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tr  
A:Reference number: A71570; MUID:99000809; PMID:9784136  
A:Accession: A71495  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-232 <ARN>

A;Cross-References: UNIPROT:O84601; UNIPARC:UPI00000D336C; GB:AE001330; GB:AE001273; NID:DB2405  
 A;Experimental source: serotype D, strain UW-3/Cx  
 C;Gene: exbB  
 C;Superfamily: biopolymer transport protein

Query Match 86.2%; Score 25; DB 2; Length 232;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6  
 |||:  
 Db 21 KVIFPS 26

RESULT 63  
 T23466  
 hypothetical protein K08E4.6 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T23466  
 R;Percy, C.  
 submitted to the EMBL Data Library, December 1995  
 A;Reference number: Z19744  
 A;Accession: T23466  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-234 <WIL>  
 A;Cross-References: UNIPROT:Q21336; UNIPARC:UPI00000765B4; EMBL:Z68316; PIDN:CAA92683.1;  
 A;Experimental source: clone K08E4  
 C;Genetics:  
 A;Gene: CESP:K08E4.6  
 A;Map position: 4  
 A;Introns: 54/3; 154/3

Query Match 86.2%; Score 25; DB 2; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVEF 5  
 |||||  
 Db 109 KVVEF 113

RESULT 64  
 T32514  
 hypothetical protein C44B12.1 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Dec-2004  
 C;Accession: T32514  
 R;Tin-Wollam, A.  
 submitted to the EMBL Data Library, December 1997  
 A;Description: The sequence of C. elegans cosmid C44B12.  
 A;Reference number: Z21183  
 A;Accession: T32514  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-247 <TIN>  
 A;Cross-References: UNIPROT:O44145; UNIPARC:UPI00001793B3; EMBL:AF036692; PIDN:AA888324.  
 A;Experimental source: strain Bristol N2; clone C44B12  
 C;Genetics:  
 A;Gene: CESP:C44B12.1  
 A;Map position: 4  
 A;Introns: 28/3; 82/1; 164/1; 192/1

Query Match 86.2%; Score 25; DB 2; Length 247;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6  
 |||:  
 Db 224 KIVFFS 229

RESULT 65  
 DB2405  
 transcription regulator LuxR family VCA0888 [imported] - Vibrio cholerae (strain N16961)  
 C;Species: Vibrio cholerae  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C;Accession: D82405  
 R;Heidelber, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.;  
 J., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A;Reference number: A82035; MUID:20406833; PMID:10952301  
 A;Accession: D82405  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-253 <HEI>  
 A;Cross-References: UNIPROT:Q9KL60; UNIPARC:UPI00000C36AA; GB:AE004416; GB:AE003853; NID:  
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C;Genetics:  
 A;Gene: VCA0888  
 A;Map position: 2

Query Match 86.2%; Score 25; DB 2; Length 253;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6  
 |||:  
 Db 51 KIVFFS 56

RESULT 66  
 C87434  
 2-deoxy-D-glucuronate 3-dehydrogenase [imported] - Caulobacter crescentus  
 C;Species: Caulobacter crescentus  
 C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 05-Oct-2004  
 C;Accession: C87434  
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A;Title: Complete Genome Sequence of Caulobacter crescentus.  
 A;Reference number: A87249; MUID:21173698; PMID:11259647  
 A;Accession: C87434  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-255 <STO>  
 A;Cross-References: UNIPROT:Q9A872; UNIPARC:UPI00000C73DC; GB:AB005673; NID:G13422867; F:  
 C;Genetics:  
 A;Gene: CC1492  
 C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 86.2%; Score 25; DB 2; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVF 5  
 |||||  
 Db 117 KVVF 121

RESULT 67  
 C83982  
 hypothetical protein BH2659 [imported] - Bacillus halodurans (strain C-125)  
 C;Species: Bacillus halodurans  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C;Accession: C83982  
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A;Reference number: A83650; MUID:20512582; PMID:11056132  
 A;Accession: C83982



A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-257 <STO>  
A;Cross-references: UNIPROT:Q9K9I8; UNIPARC:UPI00000C3F80; GB:AP001516; GB:BA000004; NID:  
C;Genetics:  
A;Gene: BH2659

Query Match 86.2%; Score 25; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5  
| | | | |  
Db 4 KVVFF 8

RESULT 68  
D64166  
hypothetical protein H11086 - Haemophilus influenzae (strain Rd KW20)  
C;Species: Haemophilus influenzae  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: D64166  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A;Accession: D64166  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-261 <TIGR>  
A;Cross-references: UNIPROT:P45030; UNIPARC:UPI00013BFD; GB:U32788; GB:L42023; NID:915  
A;Note: best homolog was a hypothetical protein from Escherichia coli  
C;Superfamily: conserved hypothetical protein H11086

Query Match 86.2%; Score 25; DB 2; Length 261;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6  
| | | | |  
Db 205 KVVFF 210

RESULT 69  
T31855  
hypothetical protein C02E7.12 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C;Accession: T31855  
R;Fulton, B.; Wohldmann, P.  
submitted to the EMBL Data Library, June 1998  
A;Description: The sequence of C. elegans cosmid C02E7.  
A;Reference number: Z21093  
A;Accession: T31855  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-277 <FUL>  
A;Cross-references: UNIPARC:UPI000017B71A; EMBL:AF016446; PIDN:AAC24170.1; GSPDB:GN00023  
A;Experimental source: strain Bristol N2; clone C02E7  
C;Genetics:  
A;Gene: CESP:C02E7.12  
A;Map position: 5  
A;Introns: 45/2; 146/3

Query Match 86.2%; Score 25; DB 2; Length 277;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 6

Db 112 KVVFF 117  
| | | | |

RESULT 70  
C84857  
hypothetical protein At2g42710 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: C84857  
R;Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Status: preliminary  
A;Accession: C84857  
A;Molecule type: DNA  
A;Residues: 1-286 <STO>  
A;Cross-references: UNIPROT:Q9SJ15; UNIPARC:UPI00000A82D6; GB:AE002093; NID:94512681; P:  
C;Genetics:  
A;Gene: At2g42710  
A;Map position: 2  
C;Superfamily: ribosomal protein L1p/L10e

Query Match 86.2%; Score 25; DB 2; Length 286;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6  
| | | | |  
Db 241 KVVFF 246

RESULT 71  
JC4744  
NAD-dinitrogen-reductase ADP-D-ribosyltransferase (EC 2.4.2.37) - rice  
C;Species: Oryza sativa (rice)  
C;Date: 10-May-1996 #sequence\_revision 16-Aug-1996 #text\_change 02-Aug-2002  
C;Accession: JC4744  
R;Inoue, A.; Shigematsu, T.; Hidaka, M.; Masaki, H.; Uozumi, T.  
Gene 170, 101-106, 1996  
A;Title: Cloning, sequencing and transcriptional regulation of the drat and drAG genes  
A;Reference number: JC4744; MUID:96200864; PMID:8621068  
A;Accession: JC4744  
A;Molecule type: DNA  
A;Residues: 1-295 <INO>  
A;Cross-references: UNIPARC:UPI00000BDA45; DBJ:D55631; NID:9862322; PID:9862323  
C;Comment: This enzyme is responsible for the post-translation regulation of nitrogenase  
C;Genetics:  
A;Gene: drat  
C;Superfamily: Azospirillum NAD+-nitrogenase ADP-D-ribosyltransferase  
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 86.2%; Score 25; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5  
| | | | |  
Db 262 KVVFF 266

RESULT 72  
I39751  
NAD-dinitrogen-reductase ADP-D-ribosyltransferase (EC 2.4.2.37) - Azospirillum brasilense  
C;Species: Azospirillum brasilense  
C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I39751  
R;Zhang, Y.; Burris, R.H.; Roberts, G.P.  
J. Bacteriol. 174, 3364-3369, 1992  
A;Title: Cloning, sequencing, mutagenesis, and functional characterization of drat and



A:Reference number: I39751; MUID:92250433; PMID:1577701  
A:Accession: I39751  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-295 <RES>  
A:Cross-references: UNIPROT:Q43903; UNIPARC:UPI0000B0CDE; GB:M87319; NID:g142411; PIDN:  
C:Genetics:  
A:Gene: drat  
C:Superfamily: Azospirillum NAD+-nitrogenase ADP-D-ribosyltransferase  
C:Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 86.2%; Score 25; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
|||  
Db 262 KVVFF 266

## RESULT 73

C70736  
Hypothetical protein RV3406 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: C70736  
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A: Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A: Reference number: A70500; MUID:98295987; PMID:9634230

A: Accession: C70736  
A: Status: preliminary; nucleic acid sequence not shown; translation not shown  
A: Molecule type: DNA  
A: Residues: 1-295 <COL>  
A: Cross-references: UNIPROT:Q50719; UNIPARC:UPI000013C263; GB:Z77165; GB:AL123456; NID:9  
A: Experimental source: strain H37RV  
C: Genetics:  
A: Gene: RV3406

Query Match 86.2%; Score 25; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
|||  
Db 43 KVVFF 47

## RESULT 74

A99074

Hypothetical protein ABC-MSP [imported] - Streptococcus pneumoniae (strain R6)

C: Species: Streptococcus pneumoniae  
C: Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C: Accession: A99074  
R: Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A: Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A: Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A: Reference number: A97872; MUID:21429245; PMID:11544234  
A: Accession: A99074  
A: Status: preliminary  
A: Molecule type: DNA  
A: Residues: 1-302 <KUR>  
A: Cross-references: UNIPROT:Q8DNN8; UNIPARC:UPI00000E36B3; GB:AE007317; PIDN:AAL00422.1;  
C: Genetics:

A: Gene: ABC-MSP  
C: Superfamily: inner membrane protein ugpa

Query Match 86.2%; Score 25; DB 2; Length 302;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
|||  
Db 118 KVVFFA 123

## RESULT 75

B35961

Hypothetical 21K protein - Pseudomonas syringae pv. savastanoi

C: Species: Pseudomonas syringae pv. savastanoi  
C: Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 09-Jul-2004  
C: Accession: B35961  
R: Roberto, F.F.; Klee, H.; White, F.; Nordeen, R.; Kosuge, T.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5797-5801, 1990  
A: Title: Expression and fine structure of the gene encoding N(epsilon)-(indole-3-acetyl)  
A: Reference number: A35961; MUID:90332669; PMID:2377619  
A: Accession: B35961  
A: Status: preliminary  
A: Molecule type: DNA  
A: Residues: 1-302 <ROB>  
A: Cross-references: UNIPROT:P18205; UNIPARC:UPI000013B36E; GB:M35373; NID:g151286; PIDN:

Query Match 86.2%; Score 25; DB 2; Length 302;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
:||||  
Db 197 QVVFFA 202

Search completed: December 29, 2005, 17:49:17  
Job time : 14.9677 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 , Search time 3.29032 Seconds  
(without alignments)  
13.656 Million cell updates/sec

Title: US-10-009-122-9

Perfect score: 29

Sequence: 1 KVPFPA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/2/pubaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	26	89.7	19	6	US-10-923-605-5
2	26	89.7	19	6	US-10-934-818-5
3	26	89.7	40	7	US-11-016-706-36
4	26	89.7	40	7	US-11-098-674-12
5	26	89.7	42	6	US-10-923-605-1
6	26	89.7	42	6	US-10-934-818-1
7	26	89.7	42	7	US-11-016-706-37
8	26	89.7	43	6	US-10-934-818-6
9	26	89.7	43	6	US-10-250-581-1
10	26	89.7	43	6	US-10-250-581-1
11	26	89.7	770	6	US-10-982-545-15
12	26	89.7	770	6	US-10-789-273-38
13	25	86.2	660	7	US-11-186-284-125
14	25	86.2	708	6	US-10-821-234-917
15	24	82.8	229	6	US-10-131-826A-410
16	24	82.8	269	6	US-10-467-657-330
17	24	82.8	311	6	US-10-793-626-2450
18	24	82.8	400	6	US-10-793-626-1056
19	24	82.8	3623	6	US-10-995-561-593
20	23	79.3	50	6	US-10-467-657-7892
21	23	79.3	167	7	US-11-210-316-18
22	23	79.3	239	6	US-10-467-657-432
23	23	79.3	265	6	US-10-793-626-2500
24	23	79.3	347	6	US-10-467-657-2014
25	23	79.3	402	6	US-10-467-657-9070

26	79.3	426	6	US-10-467-657-2120	Sequence 2120, Ap
27	79.3	481	6	US-10-995-561-959	Sequence 959, App
28	79.3	510	7	US-11-210-316-22	Sequence 22, Appl
29	79.3	524	6	US-10-689-742-13	Sequence 13, Appl
30	79.3	539	7	US-11-210-316-26	Sequence 26, Appl
31	79.3	677	6	US-10-131-826A-230	Sequence 230, App
32	79.3	2233	6	US-10-873-528-2	Sequence 2, Appl
33	79.3	5	7	US-11-098-674-1	Sequence 1, Appl
34	75.9	43	6	US-10-467-657-7886	Sequence 7886, Ap
35	75.9	47	6	US-10-467-657-5436	Sequence 5436, Ap
36	75.9	182	6	US-10-793-626-2836	Sequence 2836, Ap
37	75.9	190	6	US-10-467-657-3436	Sequence 3436, Ap
38	75.9	211	6	US-10-821-234-1372	Sequence 1372, Ap
39	75.9	278	6	US-10-957-569-45	Sequence 45, Appl
40	75.9	440	7	US-11-082-389-106	Sequence 106, App
41	75.9	482	6	US-10-793-626-24	Sequence 24, Appl
42	75.9	522	7	US-11-080-991-104	Sequence 104, App
43	75.9	528	6	US-10-793-626-1930	Sequence 1930, Ap
44	75.9	533	6	US-10-467-657-2868	Sequence 2868, Ap
45	75.9	569	7	US-11-082-389-104	Sequence 104, App
46	75.9	1061	7	US-11-000-463-347	Sequence 347, App
47	75.9	1091	7	US-11-000-463-348	Sequence 348, App
48	75.9	3507	7	US-11-075-185-7	Sequence 7, Appl
49	72.4	83	6	US-10-510-386-114	Sequence 114, App
50	72.4	98	6	US-10-467-657-4746	Sequence 4746, Ap
51	72.4	105	6	US-10-467-657-9209	Sequence 9209, Ap
52	72.4	137	6	US-10-821-234-1701	Sequence 1701, Ap
53	72.4	140	6	US-10-467-657-2486	Sequence 2486, Ap
54	72.4	155	6	US-10-467-657-2420	Sequence 2420, Ap
55	72.4	179	6	US-10-467-657-2232	Sequence 2232, Ap
56	72.4	210	6	US-10-467-657-6318	Sequence 6318, Ap
57	72.4	211	6	US-10-467-657-6932	Sequence 6932, Ap
58	72.4	215	6	US-10-131-826A-4	Sequence 4, Appl
59	72.4	228	6	US-10-467-657-568	Sequence 568, App
60	72.4	228	6	US-10-467-657-4838	Sequence 4838, Ap
61	72.4	233	6	US-10-821-234-1322	Sequence 1322, Ap
62	72.4	266	6	US-10-995-561-544	Sequence 544, App
63	72.4	267	6	US-10-995-561-543	Sequence 543, App
64	72.4	312	7	US-11-055-822-16	Sequence 16, Appl
65	72.4	330	6	US-10-793-626-2476	Sequence 2476, Ap
66	72.4	330	6	US-10-793-626-2734	Sequence 2734, Ap
67	72.4	337	6	US-10-485-517-234	Sequence 234, App
68	72.4	338	6	US-10-878-556A-19	Sequence 19, Appl
69	72.4	344	6	US-10-131-826A-376	Sequence 376, App
70	72.4	355	6	US-10-467-657-7996	Sequence 7996, Ap
71	72.4	358	7	US-11-055-822-572	Sequence 572, App
72	72.4	358	7	US-11-055-822-836	Sequence 836, App
73	72.4	406	6	US-10-467-657-7420	Sequence 7420, Ap
74	72.4	414	6	US-10-878-556A-1	Sequence 1, Appl
75	72.4	432	7	US-11-194-246-308	Sequence 308, App
76	72.4	448	6	US-10-763-712A-69	Sequence 69, Appl
77	72.4	448	6	US-10-763-712A-112	Sequence 112, App
78	72.4	449	6	US-10-821-234-1075	Sequence 1075, Ap
79	72.4	449	6	US-10-467-657-678	Sequence 678, App
80	72.4	450	6	US-10-467-657-7094	Sequence 7094, Ap
81	72.4	450	6	US-10-467-657-8028	Sequence 8028, Ap
82	72.4	450	6	US-10-763-712A-76	Sequence 76, Appl
83	72.4	451	6	US-10-467-657-7104	Sequence 7104, Ap
84	72.4	453	7	US-11-082-389-198	Sequence 198, App
85	72.4	508	7	US-11-082-389-178	Sequence 178, App
86	72.4	525	7	US-11-082-389-350	Sequence 350, App
87	72.4	560	6	US-10-623-155-225	Sequence 225, App
88	72.4	563	6	US-10-821-234-1067	Sequence 1067, Ap
89	72.4	601	6	US-10-467-657-7120	Sequence 7120, Ap
90	72.4	635	6	US-10-821-234-1673	Sequence 1673, Ap
91	72.4	739	7	US-11-082-389-94	Sequence 94, Appl
92	72.4	817	6	US-10-793-626-2948	Sequence 2948, Ap
93	72.4	858	6	US-10-613-744-6	Sequence 6, Appl
94	72.4	896	7	US-11-192-219-3	Sequence 3, Appl
95	72.4	898	7	US-11-166-730-3	Sequence 3, Appl
96	72.4	902	7	US-11-057-058-64	Sequence 64, Appl
97	72.4	923	7	US-11-192-219-4	Sequence 4, Appl
98	72.4	1013	7	US-11-103-957-9	Sequence 9, Appl

99	21	72.4	1165	7	US-11-192-219-2	Sequence 2, Appli	172	20	69.0	329	6	US-10-524-647-80	Sequence 80, Appl
100	21	72.4	1217	7	US-11-074-176-252	Sequence 252, App	173	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap
101	21	72.4	7968	7	US-11-186-731-5	Sequence 5, Appli	174	20	69.0	341	6	US-10-524-647-27	Sequence 27, Appl
102	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	175	20	69.0	348	6	US-10-821-234-1402	Sequence 1402, Ap
103	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	176	20	69.0	355	6	US-10-454-437-102	Sequence 102, App
104	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	177	20	69.0	356	7	US-11-012-762-46	Sequence 46, Appl
105	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	178	20	69.0	362	7	US-11-012-762-62	Sequence 62, Appl
106	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	179	20	69.0	364	6	US-10-131-826A-186	Sequence 186, App
107	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	180	20	69.0	370	6	US-10-821-234-1105	Sequence 1105, Ap
108	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	181	20	69.0	370	7	US-11-073-605-2	Sequence 2, Appli
109	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	182	20	69.0	370	7	US-11-073-605-2	Sequence 2, Appli
110	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	183	20	69.0	386	7	US-11-012-762-44	Sequence 44, Appl
111	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	184	20	69.0	389	7	US-11-069-642-18	Sequence 18, Appl
112	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	185	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
113	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	186	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
114	20	69.0	43	7	US-11-075-400-28	Sequence 28, Appl	187	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
115	20	69.0	52	6	US-10-467-657-2216	Sequence 2216, Ap	188	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
116	20	69.0	54	6	US-10-467-657-4978	Sequence 4978, Ap	189	20	69.0	418	6	US-10-467-657-5788	Sequence 5788, Ap
117	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	190	20	69.0	423	6	US-10-525-710-44	Sequence 44, Appl
118	20	69.0	76	6	US-10-467-657-5690	Sequence 5690, Ap	191	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, Ap
119	20	69.0	80	6	US-10-986-501-200	Sequence 200, App	192	20	69.0	443	6	US-10-793-626-1860	Sequence 1860, Ap
120	20	69.0	86	6	US-10-467-657-3962	Sequence 3962, Ap	193	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
121	20	69.0	91	6	US-10-821-234-1703	Sequence 1703, Ap	194	20	69.0	445	6	US-10-454-437-312	Sequence 312, App
122	20	69.0	98	6	US-10-467-657-3376	Sequence 3376, Ap	195	20	69.0	445	7	US-11-082-389-376	Sequence 376, App
128	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	196	20	69.0	445	7	US-11-103-240-32	Sequence 32, Appl
129	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appl	202	20	69.0	456	6	US-10-467-657-4150	Sequence 4150, Ap
130	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appli	203	20	69.0	456	6	US-10-467-657-6352	Sequence 6352, Ap
131	20	69.0	134	6	US-10-793-626-2374	Sequence 2374, Ap	204	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
132	20	69.0	137	6	US-10-793-626-530	Sequence 530, App	205	20	69.0	492	6	US-10-793-626-770	Sequence 770, App
133	20	69.0	139	6	US-10-467-657-5728	Sequence 5728, Ap	206	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appl
134	20	69.0	164	6	US-10-793-626-2478	Sequence 2478, Ap	208	20	69.0	496	7	US-11-067-121-12	Sequence 12, Appl
135	20	69.0	165	6	US-10-467-657-4990	Sequence 4990, Ap	209	20	69.0	508	7	US-11-075-185-26	Sequence 26, Appl
136	20	69.0	175	6	US-10-965-694-23	Sequence 23, Appl	210	20	69.0	522	6	US-10-995-561-1030	Sequence 1030, Ap
137	20	69.0	182	6	US-10-467-657-3510	Sequence 3510, Ap	211	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
138	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	212	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
139	20	69.0	183	6	US-10-467-657-8138	Sequence 8138, Ap	212	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
140	20	69.0	196	6	US-10-793-626-630	Sequence 630, App	213	20	69.0	582	7	US-11-090-439-58	Sequence 58, Appl
141	20	69.0	200	6	US-10-524-198-2	Sequence 2, Appli	214	20	69.0	585	7	US-11-012-762-6	Sequence 6, Appli
142	20	69.0	200	7	US-11-073-605-3	Sequence 3, Appli	215	20	69.0	592	6	US-10-467-657-4888	Sequence 4888, Ap
143	20	69.0	204	6	US-10-467-657-5874	Sequence 5874, Ap	216	20	69.0	601	7	US-11-103-957-3	Sequence 3, Appli
144	20	69.0	210	6	US-10-986-501-126	Sequence 126, App	217	20	69.0	615	6	US-10-995-561-940	Sequence 940, App
145	20	69.0	216	6	US-10-467-657-8102	Sequence 8102, Ap	218	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
146	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	219	20	69.0	657	7	US-11-080-991-48	Sequence 48, Appl
147	20	69.0	221	6	US-10-467-657-290	Sequence 290, App	220	20	69.0	662	6	US-10-995-561-943	Sequence 943, App
148	20	69.0	221	6	US-10-467-657-5750	Sequence 5750, Ap	221	20	69.0	690	6	US-10-131-826A-306	Sequence 306, App
149	20	69.0	231	6	US-10-689-742-132	Sequence 132, App	222	20	69.0	702	6	US-10-995-561-942	Sequence 942, App
150	20	69.0	254	6	US-10-467-657-6144	Sequence 6144, Ap	223	20	69.0	721	6	US-10-467-962B-49	Sequence 49, Appl
151	20	69.0	272	6	US-10-632-150-46	Sequence 46, Appl	224	20	69.0	738	7	US-11-147-047-48	Sequence 48, Appl
152	20	69.0	272	7	US-11-073-457-46	Sequence 46, Appl	225	20	69.0	741	6	US-10-467-657-6266	Sequence 6266, Ap
153	20	69.0	272	7	US-11-073-460-46	Sequence 46, Appl	226	20	69.0	747	7	US-11-018-018-1	Sequence 1, Appli
154	20	69.0	288	6	US-10-467-657-1272	Sequence 1272, Ap	227	20	69.0	747	7	US-11-047-757-1	Sequence 1, Appli
155	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appl	228	20	69.0	754	6	US-10-995-561-941	Sequence 941, App
156	20	69.0	292	7	US-11-102-883-24	Sequence 24, Appl	229	20	69.0	797	6	US-10-995-561-802	Sequence 802, App
157	20	69.0	296	6	US-10-467-657-7686	Sequence 7686, Ap	230	20	69.0	852	6	US-10-467-657-5004	Sequence 5004, Ap
158	20	69.0	296	6	US-10-965-972-8	Sequence 8, Appli	231	20	69.0	916	6	US-10-467-657-4242	Sequence 4242, Ap
159	20	69.0	296	7	US-11-102-978-7	Sequence 7, Appli	232	20	69.0	926	6	US-10-841-129-2	Sequence 2, Appli
160	20	69.0	314	7	US-11-018-018-4	Sequence 4, Appli	233	20	69.0	928	6	US-10-841-129-4	Sequence 4, Appli
161	20	69.0	314	7	US-11-047-757-4	Sequence 4, Appli	234	20	69.0	984	7	US-11-055-822-508	Sequence 508, App
162	20	69.0	315	6	US-10-524-647-25	Sequence 25, Appl	235	20	69.0	984	7	US-11-055-822-594	Sequence 594, App
163	20	69.0	317	6	US-10-995-561-798	Sequence 798, App	236	20	69.0	989	6	US-10-821-234-975	Sequence 975, App
164	20	69.0	319	6	US-10-467-657-640	Sequence 640, App	237	20	69.0	1070	6	US-11-147-047-49	Sequence 49, Appl
165	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	238	20	69.0	1278	6	US-10-995-561-952	Sequence 952, App
166	20	69.0	322	6	US-11-073-605-4	Sequence 4, Appli	239	20	69.0	1451	7	US-11-046-346-1	Sequence 1, Appli
167	20	69.0	324	6	US-10-467-657-7692	Sequence 7692, Ap	240	20	69.0	1857	7	US-11-102-217-2	Sequence 2, Appli
168	20	69.0	324	6	US-10-467-657-8440	Sequence 8440, Ap	241	20	69.0	2261	6	US-10-995-561-600	Sequence 600, App
169	20	69.0	325	6	US-10-454-437-142	Sequence 142, App	242	20	69.0	2261	7	US-11-055-309A-9	Sequence 9, Appli
170	20	69.0	329	6	US-10-524-647-2	Sequence 2, Appli	243	20	69.0	2261	7	US-11-055-309A-10	Sequence 10, Appl
171	20	69.0	329	6	US-10-524-647-23	Sequence 23, Appl	244	20	69.0	2504	6	US-10-647-956A-8	Sequence 8, Appli

Sequence 44, Appl  
Sequence 836, App  
Sequence 837, App  
Sequence 838, App  
Sequence 839, App  
Sequence 840, App  
Sequence 841, App  
Sequence 842, App  
Sequence 843, App  
Sequence 844, App  
Sequence 845, App  
Sequence 846, App  
Sequence 847, App  
Sequence 848, App  
Sequence 849, App  
Sequence 850, App  
Sequence 851, App  
Sequence 852, App  
Sequence 853, App  
Sequence 854, App  
Sequence 855, App  
Sequence 856, App  
Sequence 857, App  
Sequence 858, App  
Sequence 859, App  
Sequence 860, App  
Sequence 861, App  
Sequence 862, App  
Sequence 863, App  
Sequence 864, App  
Sequence 865, App  
Sequence 866, App  
Sequence 867, App  
Sequence 868, App  
Sequence 869, App  
Sequence 870, App  
Sequence 871, App  
Sequence 872, App  
Sequence 873, App  
Sequence 874, App  
Sequence 875, App  
Sequence 876, App  
Sequence 877, App  
Sequence 878, App  
Sequence 879, App  
Sequence 880, App  
Sequence 881, App  
Sequence 882, App  
Sequence 883, App  
Sequence 884, App  
Sequence 885, App  
Sequence 886, App  
Sequence 887, App  
Sequence 888, App  
Sequence 889, App  
Sequence 890, App  
Sequence 891, App  
Sequence 892, App  
Sequence 893, App  
Sequence 894, App  
Sequence 895, App  
Sequence 896, App  
Sequence 897, App  
Sequence 898, App  
Sequence 899, App  
Sequence 900, App  
Sequence 901, App  
Sequence 902, App  
Sequence 903, App  
Sequence 904, App  
Sequence 905, App  
Sequence 906, App  
Sequence 907, App  
Sequence 908, App  
Sequence 909, App  
Sequence 910, App  
Sequence 911, App  
Sequence 912, App  
Sequence 913, App  
Sequence 914, App  
Sequence 915, App  
Sequence 916, App  
Sequence 917, App  
Sequence 918, App  
Sequence 919, App  
Sequence 920, App  
Sequence 921, App  
Sequence 922, App  
Sequence 923, App  
Sequence 924, App  
Sequence 925, App  
Sequence 926, App  
Sequence 927, App  
Sequence 928, App  
Sequence 929, App  
Sequence 930, App  
Sequence 931, App  
Sequence 932, App  
Sequence 933, App  
Sequence 934, App  
Sequence 935, App  
Sequence 936, App  
Sequence 937, App  
Sequence 938, App  
Sequence 939, App  
Sequence 940, App  
Sequence 941, App  
Sequence 942, App  
Sequence 943, App  
Sequence 944, App  
Sequence 945, App  
Sequence 946, App  
Sequence 947, App  
Sequence 948, App  
Sequence 949, App  
Sequence 950, App  
Sequence 951, App  
Sequence 952, App  
Sequence 953, App  
Sequence 954, App  
Sequence 955, App  
Sequence 956, App  
Sequence 957, App  
Sequence 958, App  
Sequence 959, App  
Sequence 960, App  
Sequence 961, App  
Sequence 962, App  
Sequence 963, App  
Sequence 964, App  
Sequence 965, App  
Sequence 966, App  
Sequence 967, App  
Sequence 968, App  
Sequence 969, App  
Sequence 970, App  
Sequence 971, App  
Sequence 972, App  
Sequence 973, App  
Sequence 974, App  
Sequence 975, App  
Sequence 976, App  
Sequence 977, App  
Sequence 978, App  
Sequence 979, App  
Sequence 980, App  
Sequence 981, App  
Sequence 982, App  
Sequence 983, App  
Sequence 984, App  
Sequence 985, App  
Sequence 986, App  
Sequence 987, App  
Sequence 988, App  
Sequence 989, App  
Sequence 990, App  
Sequence 991, App  
Sequence 992, App  
Sequence 993, App  
Sequence 994, App  
Sequence 995, App  
Sequence 996, App  
Sequence 997, App  
Sequence 998, App  
Sequence 999, App  
Sequence 1000, App

ALIGNMENTS

RESULT 1  
US-10-923-605-5  
; Sequence 5, Application US/10923605  
; Publication No. US2005024972A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004740US  
; CURRENT APPLICATION NUMBER: US/10/923,605  
; PRIOR FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: US/09/322,289

Query Match 89.7%; Score 26; DB 6; Length 19;  
Best Local Similarity 83.3%; Pred. No. 2.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 4 KLVFFA 9

RESULT 3  
US-11-016-706-36  
; Sequence 36, Application US/11016706  
; Publication No. US2005024433A1  
; GENERAL INFORMATION:  
; APPLICANT: CASTILLO, GERARDO  
; APPLICANT: LAKE, THOMAS P.

Query Match 89.7%; Score 26; DB 6; Length 19;  
Best Local Similarity 83.3%; Pred. No. 2.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 4 KLVFFA 9

RESULT 3  
US-10-934-818-5  
; Sequence 5, Application US/10934818  
; Publication No. US2005025512A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; PRIOR FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28  
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue  
; OTHER INFORMATION: inserted and two added Gly residues  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)\_  
; OTHER INFORMATION: Xaa = acetyl histidine  
US-10-934-818-5

Query Match 89.7%; Score 26; DB 6; Length 19;  
Best Local Similarity 83.3%; Pred. No. 2.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 4 KLVFFA 9

; APPLICANT: NGUYEN, BETH P.  
; APPLICANT: SANDERS, VIRGINIA J.  
; APPLICANT: SNOW, ALAN D.  
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
; FILE REFERENCE: PROTEO.P03C13  
; CURRENT APPLICATION NUMBER: US/11/016,706  
; PRIOR FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 09/962,955  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 36  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-016-706-36

Query Match 89.7%; Score 26; DB 7; Length 40;  
Best Local Similarity 83.3%; Pred. No. 5.5;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

## RESULT 4

US-11-098-674-12  
; Sequence 12, Application US/11098674  
; Publication No. US20050267029A1  
; GENERAL INFORMATION:  
; APPLICANT: Ancsin, John B.  
; APPLICANT: Elimova, Elena  
; APPLICANT: Kisilevsky, Robert  
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their  
; FILE REFERENCE: PTQ-0066  
; CURRENT APPLICATION NUMBER: US/11/098,674  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 60/559,122  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-098-674-12

Query Match 89.7%; Score 26; DB 7; Length 40;  
Best Local Similarity 83.3%; Pred. No. 5.5;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

## RESULT 5

US-10-923-605-1  
; Sequence 1, Application US/10923605  
; Publication No. US20050249727A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004740US  
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: US/09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide  
US-10-923-605-1

Query Match 89.7%; Score 26; DB 6; Length 42;  
Best Local Similarity 83.3%; Pred. No. 5.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

## RESULT 6

US-10-934-818-1  
; Sequence 1, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide  
US-10-934-818-1

Query Match 89.7%; Score 26; DB 6; Length 42;  
Best Local Similarity 83.3%; Pred. No. 5.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

## RESULT 7

US-11-016-706-37  
; Sequence 37, Application US/11016706  
; Publication No. US20050244334A1  
; GENERAL INFORMATION:  
; APPLICANT: CASTILLO, GERARDO  
; APPLICANT: LAKE, THOMAS P.  
; APPLICANT: NGUYEN, BETH P.  
; APPLICANT: SANDERS, VIRGINIA J.  
; APPLICANT: SNOW, ALAN D.  
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
; FILE REFERENCE: PROTEO.P03C13  
; CURRENT APPLICATION NUMBER: US/11/016,706  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 09/962,955  
; PRIOR FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 37  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-016-706-37

Query Match 89.7%; Score 26; DB 7; Length 42;  
Best Local Similarity 83.3%; Pred. No. 5.7;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

## RESULT 8

US-10-934-818-6  
; Sequence 6, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 152703-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide  
US-10-934-818-6

Query Match 89.7%; Score 26; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 5.9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

## RESULT 9

US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 89.7%; Score 26; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 5.9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

## RESULT 10

US-10-250-581-1  
; Sequence 1, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 1  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-250-581-1

Query Match 89.7%; Score 26; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 5.9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 16 KLVFFA 21

## RESULT 11

US-10-982-545-15  
; Sequence 15, Application US/10982545  
; Publication No. US20050244890A1  
; GENERAL INFORMATION:

; APPLICANT: Davies, Huw Alun  
; APPLICANT: McGuire, James  
; APPLICANT: Simonsen, Anja Hvild  
; APPLICANT: Blennow, Kaj  
; APPLICANT: Podust, Vladimir  
; APPLICANT: CIPHERGEN Biosystems, Inc.  
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease  
; FILE REFERENCE: 016866-011550US  
; CURRENT APPLICATION NUMBER: US/10/982,545  
; CURRENT FILING DATE: 2004-11-06  
; PRIOR APPLICATION NUMBER: US 60/518,360  
; PRIOR FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US 60/526,753  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: US 60/546,423  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/547,250  
; PRIOR FILING DATE: 2004-02-23  
; PRIOR APPLICATION NUMBER: US 60/558,896  
; PRIOR FILING DATE: 2004-04-02  
; PRIOR APPLICATION NUMBER: US 60/572,617  
; PRIOR FILING DATE: 2004-05-18  
; PRIOR APPLICATION NUMBER: US 60/586,503  
; PRIOR FILING DATE: 2004-07-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),  
OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,  
OTHER INFORMATION: Alzheimer's disease amyloid protein

FEATURE: SIGNAL  
LOCATION: (1)..(17)  
OTHER INFORMATION: signal peptide  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(40)  
OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40  
OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (18)..(687)  
OTHER INFORMATION: soluble APP-alpha  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (18)..(671)  
OTHER INFORMATION: soluble APP-beta  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (672)..(770)  
OTHER INFORMATION: C99  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (672)..(713)  
OTHER INFORMATION: beta-amyloid protein 42  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (672)..(711)  
OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid  
OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (688)..(770)  
OTHER INFORMATION: C83  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (688)..(713)  
OTHER INFORMATION: P3(42)  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (688)..(711)  
OTHER INFORMATION: P3(40)  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (712)..(770)  
OTHER INFORMATION: gamma-CTF (59)  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (714)..(770)  
OTHER INFORMATION: gamma-CTF (57)  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (721)..(770)  
OTHER INFORMATION: gamma-CTF (50)  
FEATURE:

NAME/KEY: PEPTIDE  
LOCATION: (740)..(770)  
OTHER INFORMATION: C31  
US-10-982-545-15

Query Match 89.7%; Score 26; DB 6; Length 770;  
Best Local Similarity 83.3%; Pred. No. 92;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 687 KLVFFA 692

RESULT 12

US-10-789-273-38  
Sequence 38, Application US/10789273  
Publication No. US20050249725A1  
GENERAL INFORMATION:  
APPLICANT: Basi, Guriq  
APPLICANT: Saidanna, Jose  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
FILE REFERENCE: ELN-002CP  
CURRENT APPLICATION NUMBER: US/10/789,273  
CURRENT FILING DATE: 2004-02-27  
PRIOR APPLICATION NUMBER: US/10/388,389  
PRIOR FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US 10/010,942  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US 60/251,892  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 770  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-789-273-38

Query Match 89.7%; Score 26; DB 6; Length 770;  
Best Local Similarity 83.3%; Pred. No. 92;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 687 KLVFFA 692

RESULT 13

US-11-186-284-125  
Sequence 125, Application US/11186284  
Publication No. US20050266493A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Berger, Allison  
APPLICANT: Guillemette, Tracy L.  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Thibodeau, Stephen N.  
APPLICANT: Burgart, Lawrence J.  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
THERAPY OF COLON CANCER  
FILE REFERENCE: MPM01-029P2RNM  
CURRENT APPLICATION NUMBER: US/11/186,284  
CURRENT FILING DATE: 2005-07-21  
PRIOR APPLICATION NUMBER: US/10/301,822  
PRIOR FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 60/339,971  
PRIOR FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: US 60/361,978  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/381,988  
PRIOR FILING DATE: 2002-05-20  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 125  
LENGTH: 660  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-11-186-284-125

Query Match 86.2%; Score 25; DB 7; Length 660;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 Db 531 KAVFFA 536

RESULT 14  
 US-10-821-234-917  
 ; Sequence 917, Application US/10821234  
 ; Publication No. US20050255114A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Labat, Ivan  
 ; APPLICANT: Stache-Crain, Birgit  
 ; APPLICANT: Andermani, Susan  
 ; APPLICANT: Tang, Y. Tom  
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 ; FILE REFERENCE: 821A  
 ; CURRENT APPLICATION NUMBER: US/10/821,234  
 ; CURRENT FILING DATE: 2004-04-07  
 ; PRIOR APPLICATION NUMBER: US 60/462,047  
 ; PRIOR FILING DATE: 2003-04-07  
 ; NUMBER OF SEQ ID NOS: 1704  
 ; SOFTWARE: pt\_seq\_genes Version 1.0  
 ; SEQ ID NO 917  
 ; LENGTH: 708  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-821-234-917

Query Match 86.2%; Score 25; DB 6; Length 708;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 Db 579 KAVFFA 584

RESULT 15  
 US-10-131-826A-410  
 ; Sequence 410, Application US/10131826A  
 ; Publication No. US20050245730A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C128  
 ; CURRENT APPLICATION NUMBER: US/10/131,826A  
 ; CURRENT FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: 60/049911  
 ; PRIOR FILING DATE: 1997-06-18  
 ; PRIOR APPLICATION NUMBER: 60/056974  
 ; PRIOR FILING DATE: 1997-08-26  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059115  
 ; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059122  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059184  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059263  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 60/059352  
 ; PRIOR FILING DATE: 1997-09-19  
 ; PRIOR APPLICATION NUMBER: 60/059588  
 ; PRIOR FILING DATE: 1997-09-19  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 410  
 ; LENGTH: 229  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-131-826A-410

Query Match 82.8%; Score 24; DB 6; Length 229;  
 Best Local Similarity 80.0%; Pred. No. 79;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
 Db 118 KVIFF 122

RESULT 16  
 US-10-467-657-330  
 ; Sequence 330, Application US/10467657  
 ; Publication No. US20050260581A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SpA  
 ; APPLICANT: FONTANA Maria Rita  
 ; APPLICANT: PIZZA Mariagrazia  
 ; APPLICANT: MASIGNANI Vega  
 ; APPLICANT: MONACI Elisabetta  
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/467,657  
 ; CURRENT FILING DATE: 2003-08-11  
 ; PRIOR APPLICATION NUMBER: GB-0103424.8  
 ; PRIOR FILING DATE: 2001-02-12  
 ; NUMBER OF SEQ ID NOS: 9218  
 ; SOFTWARE: SeqWin99, version 1.04  
 ; SEQ ID NO 330  
 ; LENGTH: 269  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria gonorrhoeae  
 US-10-467-657-330

Query Match 82.8%; Score 24; DB 6; Length 269;  
 Best Local Similarity 80.0%; Pred. No. 92;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
 Db 11 KVIFF 15

RESULT 17  
 US-10-793-626-2450  
 ; Sequence 2450, Application US/10793626  
 ; Publication No. US20050255478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PU3480US  
 ; CURRENT APPLICATION NUMBER: US/10/793,626  
 ; CURRENT FILING DATE: 2004-03-04  
 ; PRIOR APPLICATION NUMBER: 60/164,258



; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2450  
; LENGTH: 311  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2450

Query Match 82.8%; Score 24; DB 6; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6  
DB 296 VVFFA 300  
|||

RESULT 18  
US-10-793-626-1056  
; Sequence 1056, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMBERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1056  
; LENGTH: 400  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1056

Query Match 82.8%; Score 24; DB 6; Length 400;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5  
DB 7 KIVFF 11  
|:|

RESULT 19  
US-10-995-561-593  
; Sequence 593, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 593  
; LENGTH: 3623  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-593

Query Match 82.8%; Score 24; DB 6; Length 3623;  
Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5  
DB 2544 KVVPF 2548  
|||

RESULT 20  
US-10-467-657-7892  
; Sequence 7892, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 7892  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-7892

Query Match 79.3%; Score 23; DB 6; Length 50;  
Best Local Similarity 60.0%; Pred. No. 30;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5  
DB 33 KIIFP 37  
|:|

RESULT 21  
US-11-210-316-18  
; Sequence 18, Application US/11210316  
; Publication No. US20050282278A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; TITLE OF INVENTION: Plant Sugar Transport Proteins  
; FILE REFERENCE: BB1163USDIV  
; CURRENT APPLICATION NUMBER: US/11/210,316  
; CURRENT FILING DATE: 2005-08-24  
; PRIOR APPLICATION NUMBER: US/10/051,902  
; PRIOR FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 60/083,044  
; PRIOR FILING DATE: 1998-04-24  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 18  
; LENGTH: 167  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (34)  
; OTHER INFORMATION: Xaa = any amino acid  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (85)  
; OTHER INFORMATION: Xaa = any amino acid  
; FEATURE:

; NAME/KEY: UNSURE  
; LOCATION: (98)  
; OTHER INFORMATION: Xaa = any amino acid  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (112)  
; OTHER INFORMATION: Xaa = any amino acid  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (151)  
; OTHER INFORMATION: Xaa = any amino acid  
US-11-210-316-18

Query Match 79.3%; Score 23; DB 7; Length 167;  
Best Local Similarity 80.0%; Pred. No. 96;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KVFFA 6  
Db 105 KVFFA 109  
|:|:|

RESULT 22  
US-10-467-657-432  
; Sequence 432, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 432  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-432

Query Match 79.3%; Score 23; DB 6; Length 239;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFFA 6  
Db 128 KVIFA 133  
|:|:|

RESULT 23  
US-10-793-626-2500  
; Sequence 2500, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2500  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2500

Query Match 79.3%; Score 23; DB 6; Length 265;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFFA 6  
Db 230 KVFFA 235  
|:|:|

RESULT 24  
US-10-467-657-2014  
; Sequence 2014, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2014  
; LENGTH: 347  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2014

Query Match 79.3%; Score 23; DB 6; Length 347;  
Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6  
Db 73 IVFFA 77  
|:|:|

RESULT 25  
US-10-467-657-9070  
; Sequence 9070, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 9070  
; LENGTH: 402  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-9070

Query Match 79.3%; Score 23; DB 6; Length 402;  
Best Local Similarity 80.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6  
:||||  
Db 264 IVFFA 268

## RESULT 26

US-10-467-657-2120  
; Sequence 2120, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2120  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2120

Query Match 79.3%; Score 23; DB 6; Length 426;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6  
:||||  
Db 414 IVFFA 418

## RESULT 27

US-10-995-561-959  
; Sequence 959, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 959  
; LENGTH: 481  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-959

Query Match 79.3%; Score 23; DB 6; Length 481;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
:||||  
Db 275 KVVFFA 280

## RESULT 28

US-11-210-316-22  
; Sequence 22, Application US/11210316  
; Publication No. US20050282278A1

; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; TITLE OF INVENTION: Plant Sugar Transport Proteins  
; FILE REFERENCE: B81163USDIV  
; CURRENT APPLICATION NUMBER: US/11/210,316  
; CURRENT FILING DATE: 2005-08-24  
; PRIOR APPLICATION NUMBER: US/10/051,902  
; PRIOR FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 60/083,044  
; PRIOR FILING DATE: 1998-04-24  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 22  
; LENGTH: 510  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (102)  
; OTHER INFORMATION: Xaa = any amino acid  
US-11-210-316-22

Query Match 79.3%; Score 23; DB 7; Length 510;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6  
:||||  
Db 96 VVFFA 100

## RESULT 29

US-10-689-742-13  
; Sequence 13, Application US/10689742  
; Publication No. US20050250180A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M  
; APPLICANT: Lavallie, Edward R  
; APPLICANT: Racine, Lisa A  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Spaulding, Vikki  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 00766.000091.10  
; CURRENT APPLICATION NUMBER: US/10/689,742  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 09/746,783  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 524  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-689-742-13

Query Match 79.3%; Score 23; DB 6; Length 524;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6  
:||||  
Db 404 IVFFA 408

## RESULT 30

US-11-210-316-26  
; Sequence 26, Application US/11210316  
; Publication No. US20050282278A1

; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; TITLE OF INVENTION: Plant Sugar Transport Proteins  
; FILE REFERENCE: BB1163USDIV  
; CURRENT APPLICATION NUMBER: US/11/210,316  
; CURRENT FILING DATE: 2005-08-24  
; PRIOR APPLICATION NUMBER: US/10/051,902  
; PRIOR FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 60/083,044  
; PRIOR FILING DATE: 1998-04-24  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 26  
; LENGTH: 539  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-11-210-316-26

Query Match : 79.3%; Score 23; DB 7; Length 539;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6  
Db 121 VIFFA 125

RESULT 11  
US-10-131-826A-230  
; Sequence 230, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 230  
; LENGTH: 677  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-230

Query Match : 79.3%; Score 23; DB 6; Length 677;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6  
Db 557 VVFFA 561

RESULT 32  
US-10-873-528-2  
; Sequence 2, Application US/10873528  
; Publication No. US20050276814A1  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; CURRENT FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2233  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-2

Query Match : 79.3%; Score 23; DB 6; Length 2233;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFFFA 6  
Db 1895 KVQFFA 1900

RESULT 33  
US-11-098-674-1  
; Sequence 1, Application US/11098674  
; Publication No. US20050267029A1  
; GENERAL INFORMATION:  
; APPLICANT: Ancsin, John B.  
; APPLICANT: Elimova, Elena  
; APPLICANT: Kisilevsky, Robert  
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their  
; FILE REFERENCE: PTQ-0066  
; CURRENT APPLICATION NUMBER: US/11/098,674  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 60/559,122  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1

; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-098-674-1

Query Match 75.9%; Score 22; DB 7; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.3e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
|:|  
Db 1 KLVFF 5

RESULT 34  
US-10-467-657-7886  
; Sequence 7886, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: Seqwin99, version 1.04  
; SEQ ID NO 7886  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-7886

Query Match 75.9%; Score 22; DB 6; Length 43;  
Best Local Similarity 83.3%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFF 6  
|:|  
Db 14 KVRFF 19

RESULT 35  
US-10-467-657-5436  
; Sequence 5436, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: Seqwin99, version 1.04  
; SEQ ID NO 5436  
; LENGTH: 47  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-5436

Query Match 75.9%; Score 22; DB 6; Length 47;  
Best Local Similarity 80.0%; Pred. No. 47;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5  
|:|  
Db 36 KVVFF 40

RESULT 36  
US-10-793-626-2836  
; Sequence 2836, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PUS480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatencIn Ver. 2.1  
; SEQ ID NO 2836  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2836

Query Match 75.9%; Score 22; DB 6; Length 182;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFF 6  
|:|  
Db 14 KVVFF 19

RESULT 37  
US-10-467-657-3436  
; Sequence 3436, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: Seqwin99, version 1.04  
; SEQ ID NO 3436  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3436

Query Match 75.9%; Score 22; DB 6; Length 190;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFF 6  
|:|  
Db 46 KTVFF 51

```
RESULT 38
US-10-821-234-1372
; Sequence 1372, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1372

Query Match      75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
Db      33 KTVYFA 38

RESULT 39
US-10-957-569-45
; Sequence 45, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
; APPLICANT: COOK, Zhihong et al.
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; TITLE OF INVENTION: THEROP
; FILE REFERENCE: 2750-1577PUS3
; CURRENT APPLICATION NUMBER: US/10/957,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/950,321
; PRIOR FILING DATE: 2004-09-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-957-569-45

Query Match      75.9%; Score 22; DB 6; Length 278;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
Db      55 KVLFF 59

RESULT 40
US-11-082-389-106
; Sequence 106, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
```

```
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 106
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-106

Query Match      75.9%; Score 22; DB 7; Length 440;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
Db      333 RVVFF 337

RESULT 41
US-10-793-626-24
; Sequence 24, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-24

Query Match      75.9%; Score 22; DB 6; Length 482;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
Db      388 KVLFFA 393
```

```
RESULT 42
US-11-080-991-104
; Sequence 104, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-104
```

```
Query Match 75.9%; Score 22; DB 7; Length 522;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 VVFFA 6
DB 260 IIFFA 264
```

```
RESULT 43
US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930
```

```
Query Match 75.9%; Score 22; DB 6; Length 528;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVF 5
DB 477 KLVFF 481
```

```
RESULT 44
US-10-467-657-2868
; Sequence 2868, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
```

```
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2868
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2868
```

```
Query Match 75.9%; Score 22; DB 6; Length 533;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 VVFFA 6
DB 371 IIFFA 375
```

```
RESULT 45
US-11-082-389-104
; Sequence 104, Application US/11082389
; Publication No. US2005024935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TRANSPORT
; FILE REFERENCE: BGI-131CPGN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 104
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-104
```

```
Query Match 75.9%; Score 22; DB 7; Length 569;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 KVVFF 5  
Db 462 RVVFF 466

## RESULT 46

US-11-000-463-347  
; Sequence 347, Application US/11000463  
; Publication No. US20050266423A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Qian, Xiaohong B.  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhou, Ping  
; APPLICANT: Cao, Yi-Cheng  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 785CIP4CN  
; CURRENT APPLICATION NUMBER: US/11/000,463  
; CURRENT FILING DATE: 2004-11-29  
; PRIOR APPLICATION NUMBER: 10/291,265  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: PCT/US01/02623  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/922,279  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 347  
; LENGTH: 1061  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-000-463-347

Query Match 75.9%; Score 22; DB 7; Length 1061;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 131 KVDFFA 136

## RESULT 47

US-11-000-463-348  
; Sequence 348, Application US/11000463  
; Publication No. US20050266423A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Qian, Xiaohong B.  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhou, Ping  
; APPLICANT: Cao, Yi-Cheng  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

FILE REFERENCE: 785CIP4CN  
; CURRENT APPLICATION NUMBER: US/11/000,463  
; CURRENT FILING DATE: 2004-11-29  
; PRIOR APPLICATION NUMBER: 10/291,265  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: PCT/US01/02623  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/922,279  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 1091  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-000-463-348

Query Match 75.9%; Score 22; DB 7; Length 1091;  
Best Local Similarity 83.3%; Pred. No. 9.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 131 KVDFFA 136

## RESULT 48

US-11-075-185-7  
; Sequence 7, Application US/11075185  
; Publication No. US20050266434A1  
; GENERAL INFORMATION:  
; APPLICANT: REEVES, CHRISTOPHER D  
; APPLICANT: JULIEN, BRYAN  
; APPLICANT: REID, RALPH  
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS  
; FILE REFERENCE: 010099.03  
; CURRENT APPLICATION NUMBER: US/11/075,185  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: US 60/551,103  
; PRIOR FILING DATE: 2004-03-08  
; PRIOR APPLICATION NUMBER: US 60/568,290  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 3507  
; TYPE: PRT  
; ORGANISM: Sorangium cellulosum  
US-11-075-185-7

Query Match 75.9%; Score 22; DB 7; Length 3507;  
Best Local Similarity 83.3%; Pred. No. 2.8e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 565 KVVFFA 570

## RESULT 49

US-10-510-386-114  
; Sequence 114, Application US/10510386  
; Publication No. US20050244922A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Jens Tonne



```
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-114
```

```
Query Match 72.4%; Score 21; DB 6; Length 83;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 VVFEA 6
Db 17 VLFEA 21
```

```
RESULT 50
US-10-467-657-4746
; Sequence 4746, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4746
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4746
```

```
Query Match 72.4%; Score 21; DB 6; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVF 5
Db 62 KIVFY 66
```

```
RESULT 51
US-10-467-657-9209
; Sequence 9209, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
```

```
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9209
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9209
```

```
Query Match 72.4%; Score 21; DB 6; Length 105;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KVVFEA 6
Db 3 QTVFEA 8
```

```
RESULT 52
US-10-821-234-1701
; Sequence 1701, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1701
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1701
```

```
Query Match 72.4%; Score 21; DB 6; Length 137;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KVVF 5
Db 28 KVTF 32
```

```
RESULT 53
US-10-467-657-2486
; Sequence 2486, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2486
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2486
```

Query Match 72.4%; Score 21; DB 6; Length 140;  
Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFP 5  
Db 89 KVIYF 93

RESULT 54  
US-10-467-657-2420  
; Sequence 2420, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2420  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2420

Query Match 72.4%; Score 21; DB 6; Length 155;  
Best Local Similarity 80.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6  
Db 18 MVFFA 22

RESULT 55  
US-10-467-657-2232  
; Sequence 2232, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2232  
; LENGTH: 179  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2232

Query Match 72.4%; Score 21; DB 6; Length 179;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 18 MVFFA 22

Db 107 KVVSEA 112

RESULT 56  
US-10-467-657-6318  
; Sequence 6318, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6318  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6318

Query Match 72.4%; Score 21; DB 6; Length 210;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFP 5  
Db 116 KAVFP 120

RESULT 57  
US-10-467-657-6932  
; Sequence 6932, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6932  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6932

Query Match 72.4%; Score 21; DB 6; Length 211;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6  
Db 19 LVFFA 23

RESULT 58  
US-10-131-826A-4  
; Sequence 4, Application US/10131826A  
; Publication No. US20050245730A1

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match          72.4%; Score 21; DB 6; Length 215;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VVFFA 6
Db      166 LVFFA 170

RESULT 59
US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; CURRENT APPLICATION NUMBER: US/10/467,657

```

```

; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

Query Match          72.4%; Score 21; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VVFFA 6
Db      156 LVFFA 160

RESULT 60
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; CURRENT APPLICATION NUMBER: US/10/467,657

```

```
; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match      72.4%; Score 21; DB 6; Length 233;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VVFFA 6
Db      166 LVFFA 170

RESULT 62
US-10-995-561-544
; Sequence 544, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(266)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-995-561-544

Query Match      72.4%; Score 21; DB 6; Length 266;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFF 5
Db      152 KVTFF 156

RESULT 63
US-10-995-561-543
; Sequence 543, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 543
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(267)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-995-561-543

Query Match      72.4%; Score 21; DB 6; Length 267;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; ORGANISM: Corynebacterium glutamicum
US-11-055-822-16

Query Match      72.4%; Score 21; DB 7; Length 312;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
Db      133 EVVFF 137

RESULT 65
US-10-793-626-2476
; Sequence 2476, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2476
; LENGTH: 330
```

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2476

Query Match 72.4%; Score 21; DB 6; Length 330;  
Best Local Similarity 60.0%; Pred. No. 5e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5  
|::||  
DB 3 KIMFF 7

RESULT 66  
US-10-793-626-2734  
; Sequence 2734, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2734  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2734

Query Match 72.4%; Score 21; DB 6; Length 330;  
Best Local Similarity 60.0%; Pred. No. 5e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5  
|::||  
DB 3 KIMFF 7

RESULT 67  
US-10-485-517-234  
; Sequence 234, Application US/10485517  
; Publication No. US20050256299A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Sheffield  
; APPLICANT: Biosynex Incorporated  
; APPLICANT: Foster, Simon  
; APPLICANT: Mond, James  
; TITLE OF INVENTION: Antigenic Polypeptides  
; FILE REFERENCE: P100629WO  
; CURRENT APPLICATION NUMBER: US/10/485,517  
; CURRENT FILING DATE: 2004-02-02  
; PRIOR APPLICATION NUMBER: GB 0118825.9  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: GB 0200349.9  
; PRIOR FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 424  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 234  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-485-517-234

Query Match 72.4%; Score 21; DB 6; Length 337;  
Best Local Similarity 80.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVPF 5  
|::||  
DB 175 KVAFP 179

RESULT 68  
US-10-878-556A-19  
; Sequence 19, Application US/10878556A  
; Publication No. US20050266399A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoffmann La-Roche Inc.  
; TITLE OF INVENTION: HCV regulated protein expression  
; FILE REFERENCE: 21762  
; CURRENT APPLICATION NUMBER: US/10/878,556A  
; CURRENT FILING DATE: 2004-06-28  
; NUMBER OF SEQ ID NOS: 199  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: sw\_hum/cn03\_human  
; DATABASE ENTRY DATE: 2001-10-16  
US-10-878-556A-19

Query Match 72.4%; Score 21; DB 6; Length 338;  
Best Local Similarity 60.0%; Pred. No. 5.1e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5  
|::||  
DB 76 KLIFF 80

RESULT 69  
US-10-131-826A-376  
; Sequence 376, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115

```
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-131-826A-376

Query Match      72.4%; Score 21; DB 6; Length 344;
Best Local Similarity 60.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
Db      279 KLIPF 283

RESULT 70
US-10-467-657-7996
; Sequence 7996, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7996
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-7996

Query Match      72.4%; Score 21; DB 6; Length 355;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
Db      5 KTTFFA 10

RESULT 71
US-11-055-822-572
; Sequence 572, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
```

```
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 572
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-11-055-822-572

Query Match      72.4%; Score 21; DB 7; Length 358;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
Db      61 KIVVFA 66

RESULT 72
US-11-055-822-836
; Sequence 836, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
```

```
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 836
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-055-822-836

Query Match          72.4%; Score 21; DB 7; Length 358;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |:|||
Db 61 KIWFPA 66

RESULT 73
US-10-467-657-7420
; Sequence 7420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7420
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7420

Query Match          72.4%; Score 21; DB 6; Length 406;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |:|||
Db 310 KTAFPA 315

RESULT 74
US-10-878-556A-1
; Sequence 1, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (307)..(307)
```

```
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: haugp:006101-3-0
; DATABASE ENTRY DATE: 2003-02-16
US-10-878-556A-1

Query Match          72.4%; Score 21; DB 6; Length 414;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
   |:|||
Db 59 VMFFA 63

RESULT 75
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MEI
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308

Query Match          72.4%; Score 21; DB 7; Length 432;
Best Local Similarity 60.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
   |:|||
Db 4 KILFF 8

Search completed: December 29, 2005, 18:50:18
Job time : 4.29032 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds  
(without alignments)  
37.818 Million cell updates/sec

Title: US-10-009-122-9  
Perfect score: 29  
Sequence: 1 KVFPPA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	3	US-09-867-847-18
2	29	100.0	6	3	US-09-867-847-26
3	29	100.0	6	3	US-09-915-092-8
4	29	100.0	6	3	US-09-915-092-16
5	29	100.0	6	3	US-09-747-408-9
6	29	100.0	6	3	US-09-747-408-17
7	29	100.0	6	5	US-10-728-028-8
8	29	100.0	6	5	US-10-728-028-16
9	29	100.0	6	5	US-10-825-958-16
10	29	100.0	6	5	US-10-825-958-24
11	29	100.0	37	4	US-10-641-924-7
12	29	100.0	37	4	US-10-642-255-7
13	29	100.0	60	4	US-10-437-963-173619
14	29	100.0	87	4	US-10-437-963-133986
15	29	100.0	109	4	US-10-437-963-105773
16	29	100.0	135	4	US-10-437-963-141578
17	29	100.0	175	4	US-10-437-963-122124
18	29	100.0	186	5	US-10-481-032A-214
19	29	100.0	186	5	US-10-481-032A-228
20	29	100.0	188	4	US-10-437-963-172476
21	29	100.0	198	4	US-10-437-963-172452
22	29	100.0	416	4	US-10-055-475-14
23	29	100.0	416	6	US-11-042-922-14
24	29	100.0	514	4	US-10-055-475-13
25	29	100.0	514	6	US-11-042-922-13
26	29	100.0	925	4	US-10-408-765A-2031
27	29	100.0	925	4	US-10-755-889-234

28	100.0	925	5	US-10-370-7158-8	Sequence 8, Appli
29	100.0	925	5	US-10-631-467-680	Sequence 680, App
30	100.0	925	5	US-10-631-467-747	Sequence 747, App
31	100.0	1144	3	US-09-870-759-124	Sequence 124, App
32	100.0	1144	3	US-09-751-708A-124	Sequence 124, App
33	100.0	1144	4	US-10-428-817A-120	Sequence 120, App
34	100.0	1144	5	US-10-937-758A-101	Sequence 101, App
35	100.0	1144	5	US-10-631-467-1388	Sequence 1388, App
36	100.0	1144	5	US-10-631-467-1464	Sequence 1464, Ap
37	100.0	1640	4	US-10-437-963-109646	Sequence 109646,
38	96.6	6	3	US-09-867-847-11	Sequence 11, Appl
39	96.6	6	3	US-09-867-847-19	Sequence 19, Appl
40	96.6	6	3	US-09-915-092-1	Sequence 1, Appli
41	96.6	6	3	US-09-915-092-9	Sequence 9, Appli
42	96.6	6	3	US-09-747-408-1	Sequence 1, Appli
43	96.6	6	3	US-09-747-408-10	Sequence 10, Appl
44	96.6	6	5	US-10-728-028-1	Sequence 1, Appli
45	96.6	6	5	US-10-728-028-9	Sequence 9, Appli
46	96.6	6	5	US-10-825-958-9	Sequence 9, Appli
47	96.6	6	5	US-10-825-958-17	Sequence 17, Appl
48	96.6	58	4	US-10-425-115-280164	Sequence 280164,
49	96.6	90	4	US-10-424-599-165325	Sequence 165325,
50	96.6	93	4	US-10-424-599-240310	Sequence 240310,
51	96.6	99	5	US-10-450-763-56957	Sequence 56957, A
52	93.1	564	6	US-11-097-143-12723	Sequence 12723, A
53	93.1	1443	6	US-11-097-143-32208	Sequence 32208, A
54	89.7	6	3	US-09-867-847-7	Sequence 7, Appli
55	89.7	6	3	US-09-867-847-20	Sequence 20, Appl
56	89.7	6	3	US-09-972-475-9	Sequence 9, Appli
57	89.7	6	3	US-09-915-092-10	Sequence 10, Appl
58	89.7	6	3	US-09-915-092-28	Sequence 28, Appl
59	89.7	6	3	US-09-956-625-25	Sequence 25, Appl
60	89.7	6	3	US-09-747-408-3	Sequence 3, Appli
61	89.7	6	3	US-09-747-408-11	Sequence 11, Appl
62	89.7	6	4	US-10-463-729-9	Sequence 9, Appli
63	89.7	6	5	US-10-728-028-10	Sequence 10, Appl
64	89.7	6	5	US-10-728-028-27	Sequence 27, Appl
65	89.7	6	5	US-10-728-028-28	Sequence 28, Appl
66	89.7	6	5	US-10-825-958-7	Sequence 7, Appli
67	89.7	6	5	US-10-825-958-18	Sequence 18, Appl
68	89.7	6	5	US-10-666-095-3	Sequence 3, Appli
69	89.7	7	3	US-09-867-847-12	Sequence 12, Appl
70	89.7	7	3	US-09-867-847-27	Sequence 27, Appl
71	89.7	7	3	US-09-867-847-28	Sequence 28, Appl
72	89.7	7	3	US-09-972-475-7	Sequence 7, Appli
73	89.7	7	3	US-09-915-092-2	Sequence 2, Appli
74	89.7	7	3	US-09-915-092-17	Sequence 17, Appl
75	89.7	7	3	US-09-915-092-18	Sequence 18, Appl
76	89.7	7	3	US-09-747-408-2	Sequence 2, Appli
77	89.7	7	3	US-09-747-408-18	Sequence 18, Appl
78	89.7	7	3	US-09-747-408-19	Sequence 19, Appl
79	89.7	7	4	US-10-463-729-7	Sequence 7, Appli
80	89.7	7	5	US-10-728-028-2	Sequence 2, Appli
81	89.7	7	5	US-10-728-028-17	Sequence 17, Appl
82	89.7	7	5	US-10-728-028-18	Sequence 18, Appl
83	89.7	7	5	US-10-825-958-10	Sequence 10, Appl
84	89.7	7	5	US-10-825-958-25	Sequence 25, Appl
85	89.7	7	5	US-10-825-958-26	Sequence 26, Appl
86	89.7	7	5	US-10-810-881A-128	Sequence 128, App
87	89.7	8	3	US-10-505-313-269	Sequence 269, App
88	89.7	8	3	US-09-850-061A-44	Sequence 44, Appl
89	89.7	8	3	US-09-972-475-5	Sequence 5, Appli
90	89.7	8	4	US-10-235-483-1	Sequence 1, Appli
91	89.7	8	4	US-10-463-729-5	Sequence 5, Appli
92	89.7	8	4	US-10-281-092-42	Sequence 42, Appl
93	89.7	8	4	US-10-721-774-44	Sequence 44, Appl
94	89.7	8	5	US-10-810-881A-125	Sequence 125, App
95	89.7	8	5	US-10-817-979-73	Sequence 73, Appl
96	89.7	9	3	US-09-867-847-9	Sequence 9, Appli
97	89.7	9	3	US-09-899-815-2	Sequence 2, Appli
98	89.7	9	3	US-09-747-408-20	Sequence 20, Appl
99	89.7	9	4	US-10-235-483-64	Sequence 64, Appl
100	89.7	9	4	US-10-619-454-3	Sequence 3, Appli



101	26	89.7	9	4	US-10-619-454-25	Sequence 25, Appl	174	26	89.7	12	6	US-11-012-797A-33	Sequence 33, Appl
102	26	89.7	9	4	US-10-619-454-28	Sequence 28, Appl	175	26	89.7	13	4	US-10-281-458-1	Sequence 1, Appl
103	26	89.7	9	4	US-10-619-454-57	Sequence 57, Appl	176	26	89.7	13	5	US-10-625-854-127	Sequence 127, App
104	26	89.7	9	4	US-10-619-454-157	Sequence 157, App	177	26	89.7	13	5	US-10-625-854-140	Sequence 140, App
105	26	89.7	10	3	US-09-867-847-29	Sequence 29, Appl	178	26	89.7	14	3	US-09-992-800-5	Sequence 5, Appl
106	26	89.7	10	3	US-09-915-092-19	Sequence 19, Appl	179	26	89.7	14	3	US-09-992-994-5	Sequence 5, Appl
107	26	89.7	10	3	US-10-889-999-20	Sequence 20, Appl	180	26	89.7	14	3	US-10-385-065-5	Sequence 5, Appl
108	26	89.7	10	5	US-10-889-999-21	Sequence 21, Appl	181	26	89.7	14	5	US-10-810-881A-114	Sequence 114, App
109	26	89.7	10	5	US-10-889-999-22	Sequence 22, Appl	182	26	89.7	14	5	US-10-505-313-2	Sequence 2, Appl
110	26	89.7	10	5	US-10-889-999-23	Sequence 23, Appl	183	26	89.7	14	5	US-10-625-854-115	Sequence 115, App
111	26	89.7	10	5	US-10-889-999-24	Sequence 24, Appl	184	26	89.7	14	5	US-10-625-854-128	Sequence 128, App
112	26	89.7	10	5	US-10-890-070-20	Sequence 20, Appl	185	26	89.7	14	5	US-10-625-854-141	Sequence 141, App
113	26	89.7	10	5	US-10-890-070-21	Sequence 21, Appl	186	26	89.7	14	6	US-11-063-350-5	Sequence 5, Appl
114	26	89.7	10	5	US-10-890-070-22	Sequence 22, Appl	187	26	89.7	15	3	US-09-972-475-14	Sequence 14, Appl
115	26	89.7	10	5	US-10-890-070-23	Sequence 23, Appl	188	26	89.7	15	3	US-09-996-357-9	Sequence 9, Appl
116	26	89.7	10	5	US-10-890-070-24	Sequence 24, Appl	189	26	89.7	15	4	US-10-235-483-56	Sequence 56, Appl
117	26	89.7	10	5	US-10-890-000-20	Sequence 20, Appl	190	26	89.7	15	4	US-10-235-483-57	Sequence 57, Appl
118	26	89.7	10	5	US-10-890-000-21	Sequence 21, Appl	191	26	89.7	15	4	US-10-235-483-58	Sequence 58, Appl
119	26	89.7	10	5	US-10-890-000-22	Sequence 22, Appl	192	26	89.7	15	4	US-10-235-483-60	Sequence 60, Appl
120	26	89.7	10	5	US-10-890-000-23	Sequence 23, Appl	193	26	89.7	15	4	US-10-235-483-61	Sequence 61, Appl
121	26	89.7	10	5	US-10-890-000-24	Sequence 24, Appl	194	26	89.7	15	4	US-10-235-483-62	Sequence 62, Appl
122	26	89.7	10	5	US-10-823-463-20	Sequence 20, Appl	195	26	89.7	15	4	US-10-235-483-63	Sequence 63, Appl
123	26	89.7	10	5	US-10-823-463-21	Sequence 21, Appl	196	26	89.7	15	4	US-10-235-483-65	Sequence 65, Appl
124	26	89.7	10	5	US-10-823-463-22	Sequence 22, Appl	197	26	89.7	15	4	US-10-463-729-14	Sequence 14, Appl
125	26	89.7	10	5	US-10-823-463-23	Sequence 23, Appl	198	26	89.7	15	5	US-10-625-854-103	Sequence 103, App
126	26	89.7	10	5	US-10-823-463-24	Sequence 24, Appl	199	26	89.7	15	5	US-10-625-854-116	Sequence 116, App
127	26	89.7	10	5	US-10-728-028-19	Sequence 19, Appl	200	26	89.7	15	5	US-10-625-854-129	Sequence 129, App
128	26	89.7	10	5	US-10-822-968-20	Sequence 20, Appl	201	26	89.7	15	5	US-10-625-854-142	Sequence 142, App
129	26	89.7	10	5	US-10-822-968-21	Sequence 21, Appl	202	26	89.7	16	5	US-10-625-854-91	Sequence 91, Appl
130	26	89.7	10	5	US-10-822-968-22	Sequence 22, Appl	203	26	89.7	16	5	US-10-625-854-104	Sequence 104, App
131	26	89.7	10	5	US-10-822-968-23	Sequence 23, Appl	204	26	89.7	16	5	US-10-625-854-117	Sequence 117, App
132	26	89.7	10	5	US-10-822-968-24	Sequence 24, Appl	205	26	89.7	16	5	US-10-625-854-130	Sequence 130, App
133	26	89.7	10	5	US-10-777-792-20	Sequence 20, Appl	206	26	89.7	16	5	US-10-625-854-143	Sequence 143, App
134	26	89.7	10	5	US-10-777-792-21	Sequence 21, Appl	207	26	89.7	17	3	US-09-992-800-3	Sequence 3, Appl
135	26	89.7	10	5	US-10-777-792-22	Sequence 22, Appl	208	26	89.7	17	3	US-09-992-994-3	Sequence 3, Appl
136	26	89.7	10	5	US-10-777-792-23	Sequence 23, Appl	209	26	89.7	17	3	US-09-998-491-8	Sequence 8, Appl
137	26	89.7	10	5	US-10-777-792-24	Sequence 24, Appl	210	26	89.7	17	4	US-10-385-065-3	Sequence 3, Appl
138	26	89.7	10	5	US-10-825-958-27	Sequence 27, Appl	211	26	89.7	17	4	US-10-451-367-26	Sequence 26, Appl
139	26	89.7	10	5	US-10-890-071-20	Sequence 20, Appl	212	26	89.7	17	4	US-10-475-281-8	Sequence 8, Appl
140	26	89.7	10	5	US-10-890-071-21	Sequence 21, Appl	213	26	89.7	17	4	US-10-810-919-3	Sequence 3, Appl
141	26	89.7	10	5	US-10-890-071-22	Sequence 22, Appl	214	26	89.7	17	5	US-10-684-346-24	Sequence 24, Appl
142	26	89.7	10	5	US-10-890-071-23	Sequence 23, Appl	215	26	89.7	17	5	US-10-997-078-46	Sequence 46, Appl
143	26	89.7	10	5	US-10-890-071-24	Sequence 24, Appl	216	26	89.7	17	5	US-10-997-700-19	Sequence 19, Appl
144	26	89.7	10	5	US-10-890-024-20	Sequence 20, Appl	217	26	89.7	17	6	US-11-063-350-3	Sequence 3, Appl
145	26	89.7	10	5	US-10-890-024-21	Sequence 21, Appl	218	26	89.7	17	6	US-11-066-697-950	Sequence 950, App
146	26	89.7	10	5	US-10-890-024-22	Sequence 22, Appl	219	26	89.7	17	6	US-11-066-697-983	Sequence 983, App
147	26	89.7	10	5	US-10-890-024-23	Sequence 23, Appl	220	26	89.7	19	3	US-09-823-242-5	Sequence 5, Appl
148	26	89.7	10	5	US-10-890-024-24	Sequence 24, Appl	221	26	89.7	19	3	US-10-429-216-5	Sequence 5, Appl
149	26	89.7	10	5	US-10-928-926-20	Sequence 20, Appl	222	26	89.7	19	4	US-10-816-022-5	Sequence 5, Appl
150	26	89.7	10	5	US-10-928-926-21	Sequence 21, Appl	223	26	89.7	19	4	US-10-816-529-5	Sequence 5, Appl
151	26	89.7	10	5	US-10-928-926-22	Sequence 22, Appl	224	26	89.7	19	4	US-10-815-353-5	Sequence 5, Appl
152	26	89.7	10	5	US-10-928-926-23	Sequence 23, Appl	225	26	89.7	19	4	US-10-815-391-5	Sequence 5, Appl
153	26	89.7	10	5	US-10-928-926-24	Sequence 24, Appl	226	26	89.7	19	5	US-10-828-548-5	Sequence 5, Appl
154	26	89.7	10	6	US-11-058-757-20	Sequence 20, Appl	227	26	89.7	19	5	US-10-816-380-5	Sequence 5, Appl
155	26	89.7	10	6	US-11-058-757-21	Sequence 21, Appl	228	26	89.7	19	5	US-10-889-999-75	Sequence 75, Appl
156	26	89.7	10	6	US-11-058-757-22	Sequence 22, Appl	229	26	89.7	19	5	US-10-890-070-75	Sequence 75, Appl
157	26	89.7	10	6	US-11-058-757-23	Sequence 23, Appl	230	26	89.7	19	5	US-10-890-000-75	Sequence 75, Appl
158	26	89.7	10	6	US-11-058-757-24	Sequence 24, Appl	231	26	89.7	19	5	US-10-788-666-5	Sequence 5, Appl
159	26	89.7	11	3	US-09-988-842-9	Sequence 9, Appl	232	26	89.7	19	5	US-10-923-471-5	Sequence 5, Appl
160	26	89.7	11	3	US-09-988-842-25	Sequence 25, Appl	233	26	89.7	19	5	US-10-823-463-75	Sequence 75, Appl
161	26	89.7	11	4	US-10-235-483-14	Sequence 14, Appl	234	26	89.7	19	5	US-10-923-469-5	Sequence 5, Appl
162	26	89.7	11	4	US-10-050-200-33	Sequence 33, Appl	235	26	89.7	19	5	US-10-933-559-5	Sequence 5, Appl
163	26	89.7	11	4	US-10-237-673-20	Sequence 20, Appl	236	26	89.7	19	5	US-10-815-404-5	Sequence 5, Appl
164	26	89.7	11	5	US-10-464-117-13	Sequence 13, Appl	237	26	89.7	19	5	US-10-934-603-5	Sequence 5, Appl
165	26	89.7	11	5	US-10-772-230-9	Sequence 9, Appl	238	26	89.7	19	5	US-10-923-474-5	Sequence 5, Appl
166	26	89.7	12	3	US-09-772-230-25	Sequence 25, Appl	239	26	89.7	19	5	US-10-884-892-5	Sequence 5, Appl
167	26	89.7	12	3	US-09-867-847-8	Sequence 8, Appl	240	26	89.7	19	5	US-10-822-968-75	Sequence 75, Appl
168	26	89.7	12	4	US-10-481-180-671	Sequence 671, App	241	26	89.7	19	5	US-10-777-792-75	Sequence 75, Appl
169	26	89.7	12	5	US-10-810-881A-115	Sequence 115, App	242	26	89.7	19	5	US-10-890-071-75	Sequence 75, Appl
170	26	89.7	12	5	US-10-810-881A-117	Sequence 117, App	243	26	89.7	19	5	US-10-890-024-75	Sequence 75, Appl
171	26	89.7	12	5	US-10-508-586-2	Sequence 2, Appl	244	26	89.7	19	5	US-10-934-819-5	Sequence 5, Appl
172	26	89.7	12	5	US-10-508-586-3	Sequence 3, Appl	245	26	89.7	19	5	US-10-923-267-5	Sequence 5, Appl
173	26	89.7	12	5	US-10-625-854-139	Sequence 139, App	246	26	89.7	19	5	US-10-928-926-75	Sequence 75, Appl

247 26 89.7 19 6 US-11-058-757-75 Sequence 75, Appl  
248 26 89.7 19 6 US-11-108-102-5 Sequence 5, Appl  
249 26 89.7 20 3 US-09-908-943A-25 Sequence 25, Appl  
250 26 89.7 20 4 US-10-481-180-710 Sequence 710, Appl  
251 26 89.7 20 5 US-10-801-487-25 Sequence 25, Appl  
252 26 89.7 20 5 US-10-801-938-25 Sequence 25, Appl  
253 26 89.7 20 5 US-10-801-509-25 Sequence 25, Appl  
254 26 89.7 20 5 US-10-801-486-25 Sequence 25, Appl  
255 26 89.7 20 5 US-10-801-493-25 Sequence 25, Appl  
256 26 89.7 24 5 US-10-728-246-5 Sequence 5, Appl  
257 26 89.7 24 5 US-10-728-246-6 Sequence 6, Appl  
258 26 89.7 25 4 US-10-481-180-724 Sequence 724, Appl  
259 26 89.7 26 3 US-09-792-079-11 Sequence 11, Appl  
260 26 89.7 26 4 US-10-159-279-11 Sequence 11, Appl  
261 26 89.7 28 3 US-09-867-847-4 Sequence 4, Appl  
262 26 89.7 28 3 US-09-865-294-66 Sequence 66, Appl  
263 26 89.7 28 3 US-09-792-079-5 Sequence 5, Appl  
264 26 89.7 28 4 US-10-159-279-5 Sequence 5, Appl  
265 26 89.7 28 4 US-10-363-082-2 Sequence 2, Appl  
266 26 89.7 28 4 US-10-433-385-7 Sequence 7, Appl  
267 26 89.7 28 4 US-10-390-472-4 Sequence 4, Appl  
268 26 89.7 28 4 US-10-741-205-36 Sequence 36, Appl  
269 26 89.7 28 4 US-10-416-262B-7 Sequence 7, Appl  
270 26 89.7 28 4 US-10-481-180-735 Sequence 735, Appl  
271 26 89.7 28 4 US-10-478-308-4 Sequence 4, Appl  
272 26 89.7 28 4 US-10-478-307-4 Sequence 4, Appl  
273 26 89.7 28 5 US-10-861-614-66 Sequence 66, Appl  
274 26 89.7 28 5 US-10-825-958-4 Sequence 4, Appl  
275 26 89.7 28 6 US-11-091-309-3 Sequence 3, Appl  
276 26 89.7 28 6 US-11-066-697-959 Sequence 959, Appl  
277 26 89.7 28 6 US-11-066-697-965 Sequence 965, Appl  
278 26 89.7 28 6 US-11-066-697-976 Sequence 976, Appl  
279 26 89.7 28 6 US-11-066-697-992 Sequence 992, Appl  
280 26 89.7 28 6 US-11-066-697-1003 Sequence 1003, Appl  
281 26 89.7 30 3 US-09-861-847-1 Sequence 1, Appl  
282 26 89.7 30 4 US-10-301-488A-1 Sequence 1, Appl  
283 26 89.7 30 4 US-10-666-423-1 Sequence 1, Appl  
284 26 89.7 30 4 US-10-617-876-9 Sequence 9, Appl  
285 26 89.7 30 4 US-10-619-454-24 Sequence 24, Appl  
286 26 89.7 30 4 US-10-301-448-1 Sequence 1, Appl  
287 26 89.7 30 5 US-10-775-562-5 Sequence 5, Appl  
288 26 89.7 32 4 US-10-732-862A-99 Sequence 99, Appl  
289 26 89.7 33 3 US-09-930-915A-295 Sequence 295, Appl  
290 26 89.7 33 4 US-10-082-014-84 Sequence 84, Appl  
291 26 89.7 33 4 US-10-372-076-85 Sequence 85, Appl  
292 26 89.7 33 4 US-10-732-862A-98 Sequence 98, Appl  
293 26 89.7 33 4 US-10-806-006-295 Sequence 295, Appl  
294 26 89.7 33 4 US-10-677-074-85 Sequence 85, Appl  
295 26 89.7 33 4 US-10-805-913-295 Sequence 295, Appl  
296 26 89.7 33 4 US-10-481-180-746 Sequence 746, Appl  
297 26 89.7 35 3 US-09-867-847-3 Sequence 3, Appl  
298 26 89.7 35 3 US-09-972-475-16 Sequence 16, Appl  
299 26 89.7 35 4 US-10-463-729-16 Sequence 16, Appl  
300 26 89.7 35 5 US-10-825-958-3 Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-867-847-18  
; Sequence 18, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-09-867-847-18  
  
Query Match 100.0%; Score 29; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KVVFFA 6  
Db 1 KVVFFA 6  
  
RESULT 2  
US-09-867-847-26  
; Sequence 26, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; NAME/KEY: MOD\_RES  
; LOCATION: (6)  
; OTHER INFORMATION: AMIDATION  
US-09-867-847-26  
  
Query Match 100.0%; Score 29; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KVVFFA 6  
Db 1 KVVFFA 6  
  
RESULT 3  
US-09-915-092-8  
; Sequence 8, Application US/09915092  
; Publication No. US2002011571A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Chalfour, Robert

```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-8

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVWFFA 6
      |||||
Db      1 KVWFFA 6

RESULT 4
US-09-915-092-16
; Sequence 16, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-16

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVWFFA 6
      |||||
Db      1 KVWFFA 6

RESULT 5
US-09-747-408-9
; Sequence 9, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

US-10-009-122-9.rapbm

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVWFFA 6
      |||||
Db      1 KVWFFA 6

RESULT 6
US-09-747-408-17
; Sequence 17, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVWFFA 6
      |||||
Db      1 KVWFFA 6

RESULT 7
US-10-728-028-8
; Sequence 8, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-8

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 8
US-10-728-028-16
; Sequence 16, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-16

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 9
US-10-825-958-16
; Sequence 16, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-16

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 10
US-10-825-958-24
; Sequence 24, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-24

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 11
US-10-641-924-7
; Sequence 7, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: cNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 53035AUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
```

; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-641-924-7

Query Match 100.0%; Score 29; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
| | | | |  
DB 18 KVVFFA 23

RESULT 12  
US-10-642-255-7  
; Sequence 7, Application US/10642255  
; Publication No. US20040120930A1  
; GENERAL INFORMATION:  
; APPLICANT: Dole, William P.  
; APPLICANT: Kauser, Katalin  
; APPLICANT: Qian, Hu Sheng  
; APPLICANT: Rubanyi, Gabor  
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant  
; FILE REFERENCE: eNOS  
; CURRENT APPLICATION NUMBER: US/10/642,255  
; CURRENT FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: US 60/403,637  
; PRIOR FILING DATE: 2002-08-16  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-642-255-7

Query Match 100.0%; Score 29; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
| | | | |  
DB 18 KVVFFA 23

RESULT 13  
US-10-437-963-173619  
; Sequence 173619, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 173619  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Oryza sativa

; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_71639C.1.pap  
US-10-437-963-173619

Query Match 100.0%; Score 29; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
| | | | |  
DB 4 KVVFFA 9

RESULT 14  
US-10-437-963-133986  
; Sequence 133986, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 133986  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_35803C.1.pap  
US-10-437-963-133986

Query Match 100.0%; Score 29; DB 4; Length 87;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
| | | | |  
DB 6 KVVFFA 11

RESULT 15  
US-10-437-963-105773  
; Sequence 105773, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 105773  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102988C.1.pep  
US-10-437-963-105773

Query Match 100.0%; Score 29; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
| | | | |  
Db 4 KVVFFA 9

## RESULT 16

US-10-437-963-141578

; Sequence 141578, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 141578

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_42668C.1.pep

US-10-437-963-141578

Query Match 100.0%; Score 29; DB 4; Length 135;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
| | | | |  
Db 4 KVVFFA 9

## RESULT 17

US-10-437-963-122124

; Sequence 122124, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 122124

; LENGTH: 175

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)-(175)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_25081C.1.pep

US-10-437-963-122124

Query Match 100.0%; Score 29; DB 4; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
| | | | |  
Db 4 KVVFFA 9

## RESULT 18

US-10-481-032A-214

; Sequence 214, Application US/10481032A

; Publication No. US20050177901A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Cheng, Wenglong

; APPLICANT: Briggs, Steven

; APPLICANT: Cooper, Bret

; APPLICANT: Goff, Stephen A.

; APPLICANT: Moughamer, Todd

; APPLICANT: Glazebrook, Jane

; APPLICANT: Katagiri, Fumiaki

; APPLICANT: Kreps, Joel

; APPLICANT: Provart, Nicolas

; APPLICANT: Rickes, Darrell

; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES

; FILE REFERENCE: 60148USPT

; CURRENT APPLICATION NUMBER: US/10/481,032A

; PRIOR FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 60/300,112

; PRIOR FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: US 60/325,277

; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: US 60/342,327

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: PCT/IB02/02450

; PRIOR FILING DATE: 2002-06-21

; NUMBER OF SEQ ID NOS: 1201

; SOFTWARE: PatentIn Ver. 2.2

; SEQ ID NO 214

; LENGTH: 186

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-481-032A-214

Query Match 100.0%; Score 29; DB 5; Length 186;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
| | | | |  
Db 4 KVVFFA 9

## RESULT 19

US-10-481-032A-228

; Sequence 228, Application US/10481032A

; Publication No. US20050177901A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Cheng, Wenglong

; APPLICANT: Briggs, Steven

; APPLICANT: Cooper, Bret

; APPLICANT: Goff, Stephen A.

; APPLICANT: Moughamer, Todd

; APPLICANT: Glazebrook, Jane

; APPLICANT: Katagiri, Fumiaki

; APPLICANT: Kreps, Joel  
; APPLICANT: Provart, Nicolas  
; APPLICANT: Ricke, Darrell  
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES  
; FILE REFERENCE: 60148USPCT  
; CURRENT APPLICATION NUMBER: US/10/481,032A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: US 60/300,112  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/325,277  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 60/342,327  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: PCT/IB02/02450  
; PRIOR FILING DATE: 2002-06-21  
; NUMBER OF SEQ ID NOS: 1201  
; SOFTWARE: PatentIn Ver. 2.2  
; SEQ ID NO 228  
; LENGTH: 186  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-481-032A-228

Query Match 100.0%; Score 29; DB 5; Length 186;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
Db 4 KVVFFA 9

RESULT 20  
US-10-437-963-172476  
; Sequence 172476, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 172476  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; NAME/KEY: unsure  
; LOCATION: (1)..(188)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_70608C.1.pep  
US-10-437-963-172476

Query Match 100.0%; Score 29; DB 4; Length 188;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
Db 4 KVVFFA 9

RESULT 21

US-10-437-963-172452  
; Sequence 172452, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 172452  
; LENGTH: 198  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; NAME/KEY: unsure  
; LOCATION: (1)..(198)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_70587C.1.pep  
US-10-437-963-172452

Query Match 100.0%; Score 29; DB 4; Length 198;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
Db 4 KVVFFA 9

RESULT 22  
US-10-055-475-14  
; Sequence 14, Application US/10055475  
; Publication No. US20030022855A1  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Paul B.  
; APPLICANT: Kang, Dong-Chul  
; APPLICANT: Gopalkrishnan, Rahul V.  
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND  
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT  
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)  
; CURRENT APPLICATION NUMBER: US/10/055,475  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: PCT/US01/06960  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 09/515,363  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 416  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-055-475-14

Query Match 100.0%; Score 29; DB 4; Length 416;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
Db 57 KVVFFA 62

RESULT 23  
 US-11-042-922-14  
 ; Sequence 14, Application US/11042922  
 ; Publication No. US20050186211A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fisher, Paul B.  
 ; APPLICANT: Kang, Dong-Chul  
 ; APPLICANT: Gopalakrishnan, Rahul V.  
 ; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND  
 ; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT  
 ; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)  
 ; CURRENT APPLICATION NUMBER: US/11/042,922  
 ; CURRENT FILING DATE: 2005-01-24  
 ; PRIOR APPLICATION NUMBER: 10/055,475  
 ; PRIOR FILING DATE: 2002-01-22  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06960  
 ; PRIOR FILING DATE: 2001-02-28  
 ; PRIOR APPLICATION NUMBER: 09/515,363  
 ; PRIOR FILING DATE: 2000-02-29  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 14  
 ; LENGTH: 416  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-11-042-922-14

Query Match 100.0%; Score 29; DB 6; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 57 KVVFFA 62

RESULT 24  
 US-10-055-475-13  
 ; Sequence 13, Application US/10055475  
 ; Publication No. US20030022855A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fisher, Paul B.  
 ; APPLICANT: Kang, Dong-Chul  
 ; APPLICANT: Gopalakrishnan, Rahul V.  
 ; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND  
 ; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT  
 ; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)  
 ; CURRENT APPLICATION NUMBER: US/10/055,475  
 ; CURRENT FILING DATE: 2002-01-22  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06960  
 ; PRIOR FILING DATE: 2001-02-28  
 ; PRIOR APPLICATION NUMBER: 09/515,363  
 ; PRIOR FILING DATE: 2000-02-29  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 514  
 ; TYPE: PRT  
 ; ORGANISM: sus scrofa  
 US-10-055-475-13

Query Match 100.0%; Score 29; DB 4; Length 514;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 57 KVVFFA 62

RESULT 25  
 US-11-042-922-13  
 ; Sequence 13; Application US/11042922

; Publication No. US20050186211A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fisher, Paul B.  
 ; APPLICANT: Kang, Dong-Chul  
 ; APPLICANT: Gopalakrishnan, Rahul V.  
 ; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND  
 ; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT  
 ; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)  
 ; CURRENT APPLICATION NUMBER: US/11/042,922  
 ; CURRENT FILING DATE: 2005-01-24  
 ; PRIOR APPLICATION NUMBER: 10/055,475  
 ; PRIOR FILING DATE: 2002-01-22  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06960  
 ; PRIOR FILING DATE: 2001-02-28  
 ; PRIOR APPLICATION NUMBER: 09/515,363  
 ; PRIOR FILING DATE: 2000-02-29  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 514  
 ; TYPE: PRT  
 ; ORGANISM: sus scrofa  
 US-11-042-922-13

Query Match 100.0%; Score 29; DB 6; Length 514;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 57 KVVFFA 62

RESULT 26  
 US-10-408-765A-2031  
 ; Sequence 2031, Application US/10408765A  
 ; Publication No. US20040101874A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Fahy, Eoin D.  
 ; APPLICANT: Zhang, Bing  
 ; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Taylor, Steven W.  
 ; APPLICANT: Glenn, Gary M.  
 ; APPLICANT: Warnock, Dale E.  
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 ; FILE REFERENCE: 660088.465  
 ; CURRENT APPLICATION NUMBER: US/10/408,765A  
 ; CURRENT FILING DATE: 2003-04-04  
 ; NUMBER OF SEQ ID NOS: 3077  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2031  
 ; LENGTH: 925  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-408-765A-2031

Query Match 100.0%; Score 29; DB 4; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 292 KVVFFA 297

RESULT 27  
 US-10-755-889-234  
 ; Sequence 234, Application US/10755889  
 ; Publication No. US20040171823A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company



```
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 234
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-234

Query Match      100.0%; Score 29; DB 4; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 28
US-10-370-715B-8
; Sequence 8, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
;   Patin Docket Preview
;   APPLICANT: BODARY, SARAH C.
;   APPLICANT: CLARK, HILLARY
;   APPLICANT: BRISDELL, HUNTE
;   APPLICANT: JACKMAN, JANET
;   APPLICANT: SCHOENFELD, JILL R.
;   APPLICANT: WILLIAMS, P. MICKEY
;   APPLICANT: WOOD, WILLIAM I.
;   APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 8
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-8

Query Match      100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 29
US-10-631-467-680
; Sequence 680, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
;   APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
```

```
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-680

Query Match      100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 30
US-10-631-467-747
; Sequence 747, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
;   APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive i
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 747
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-747

Query Match      100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 31
US-09-870-759-124
; Sequence 124, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
;   APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-124

Query Match      100.0%; Score 29; DB 3; Length 1144;
```

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 32  
US-09-751-708A-124  
; Sequence 124, Application US/09751708A  
; Publication No. US20030157113A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 751708  
; CURRENT APPLICATION NUMBER: US/09/751.708A  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 60/173,371  
; PRIOR FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 124  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-751-708A-124

Query Match 100.0%; Score 29; DB 3; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 33  
US-10-428-817A-120  
; Sequence 120, Application US/10428817A  
; Publication No. US20040214783A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 38373-189118  
; CURRENT APPLICATION NUMBER: US/10/428.817A  
; CURRENT FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: US 60/378,988  
; PRIOR FILING DATE: 2002-05-08  
; PRIOR APPLICATION NUMBER: US 60/389,366  
; PRIOR FILING DATE: 2002-06-15  
; PRIOR APPLICATION NUMBER: US 60/406,697  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: US 60/406,750  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/415,310  
; PRIOR FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: US 60/415,400  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: US 60/438,686  
; PRIOR FILING DATE: 2003-01-09  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 120  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-428-817A-120

Query Match 100.0%; Score 29; DB 4; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 34  
US-10-937-758A-101  
; Sequence 101, Application US/10937758A  
; Publication No. US20050112141A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: FILE REFERENCE 650884  
; CURRENT APPLICATION NUMBER: US/10/937,758A  
; CURRENT FILING DATE: 2004-09-08  
; PRIOR APPLICATION NUMBER: 09/650,884  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 101  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-937-758A-101

Query Match 100.0%; Score 29; DB 5; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 35  
US-10-631-467-1388  
; Sequence 1388, Application US/10631467  
; Publication No. US20050208496A1  
; GENERAL INFORMATION:  
; APPLICANT: Genox Research Inc.  
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive disease  
; FILE REFERENCE: 3462.1005-000  
; CURRENT APPLICATION NUMBER: US/10/631,467  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: JP 2003-077212  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: JP 2002-229312  
; PRIOR FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 2086  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1388  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-631-467-1388

Query Match 100.0%; Score 29; DB 5; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
Db 514 KVVFFA 519

RESULT 36  
US-10-631-467-1464  
; Sequence 1464, Application US/10631467  
; Publication No. US20050208496A1  
; GENERAL INFORMATION:  
; APPLICANT: Genox Research Inc.  
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive

```
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1464
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1464

Query Match 100.0%; Score 29; DB 5; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 37
US-10-437-963-109646
; Sequence 109646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109646
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13784C.1.pep
US-10-437-963-109646

Query Match 100.0%; Score 29; DB 4; Length 1640;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1596 KVVFFA 1601

RESULT 38
US-09-867-847-11
; Sequence 11, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
```

```
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-11

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KIVFFA 6

RESULT 39
US-09-867-847-19
; Sequence 19, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KIVFFA 6

RESULT 40
US-09-915-092-1
; Sequence 1, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
```

```

; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-1

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
      |:||||
Db      1 KVVFFA 6

```

```

RESULT 41
US-09-915-092-9
; Sequence 9, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-9

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
      |:||||
Db      1 KVVFFA 6

```

```

RESULT 42
US-09-747-408-1
; Sequence 1, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877

```

```

; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
      |:||||
Db      1 KVVFFA 6

```

```

RESULT 43
US-09-747-408-10
; Sequence 10, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
      |:||||
Db      1 KVVFFA 6

```

```

RESULT 44
US-10-728-028-1
; Sequence 1, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6

```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1

Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
        |:||||
Db       1 KIVFFA 6

RESULT 45
US-10-728-028-9
; Sequence 9, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xiangqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9

Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
        |:||||
Db       1 KIVFFA 6

RESULT 46
US-10-825-958-9
; Sequence 9, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-10-825-958-9

Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
        |:||||
Db       1 KIVFFA 6

RESULT 47
US-10-825-958-17
; Sequence 17, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-10-825-958-17

Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
        |:||||
Db       1 KIVFFA 6

RESULT 48
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
```

```
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280164
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_187087C.1.pep
; US-10-425-115-280164

Query Match          96.6%; Score 28; DB 4; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |:||||
Db 28 KIVFFA 33

RESULT 49
US-10-424-599-165325
; Sequence 165325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pep
; US-10-424-599-165325

Query Match          96.6%; Score 28; DB 4; Length 90;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |:||||
Db 21 KIVFFA 26

RESULT 50
US-10-424-599-240310
; Sequence 240310, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep
```

US-10-424-599-240310

```
Query Match          96.6%; Score 28; DB 4; Length 93;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
   |:||||
Db 34 KIVFFA 39
```

RESULT 51

```
US-10-450-763-56957
; Sequence 56957, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06
; NAME/KEY: misc feature
; LOCATION: (1)..(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
; US-10-450-763-56957
```

```
Query Match          96.6%; Score 28; DB 5; Length 99;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
   |:||||
Db 63 KIVFFA 68
```

RESULT 52

```
US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
```

```
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match          93.1%; Score 27; DB 6; Length 564;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
DB      53 KIFFA 58

RESULT 53
US-11-097-143-32208
; Sequence 32208, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32208
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32208

Query Match          93.1%; Score 27; DB 6; Length 1443;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
DB      1204 KIFFA 1209

; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32208
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32208

Query Match          93.1%; Score 27; DB 6; Length 1443;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
DB      1204 KIFFA 1209

; Sequence 7, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-7

Query Match          89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
DB      1 KLVFFA 6

RESULT 55
US-09-867-847-20
; Sequence 20, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-20

Query Match          89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 56
US-09-972-475-9
; Sequence 9, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972.475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-972-475-9
Query Match 89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 57
US-09-915-092-10
; Sequence 10, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
```

```
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-10
Query Match 89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 58
US-09-915-092-28
; Sequence 28, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(6)
; OTHER INFORMATION: D-amino acids
US-09-915-092-28
Query Match 89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 59
US-09-956-625-25
; Sequence 25, Application US/09956625
; Patent No. US2002011926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
```



```

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Antifibrillogenic agents
US-09-956-625-25

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 60
US-09-747-408-3
; Sequence 3, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 61
US-09-747-408-11
; Sequence 11, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 62
US-10-463-729-9
; Sequence 9, Application US/10463729
; Publication No. US20040005307A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,729
; FILING DATE: 17-JUNE-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-463-729-9

Query Match      89.7%; Score 26; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 63
US-10-728-028-10
; Sequence 10, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert

```

```
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-728-028-10
```

```
Query Match      89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KVVFFA 6
Db      1 KLVFFA 6
```

```
RESULT 64
US-10-728-028-27
; Sequence 27, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-728-028-27
```

```
Query Match      89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KVVFFA 6
Db      1 KLVFFA 6
```

```
RESULT 65
US-10-728-028-28
; Sequence 28, Application US/10728028
```

```
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-728-028-28
```

```
Query Match      89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KVVFFA 6
Db      1 KLVFFA 6
```

```
RESULT 66
US-10-825-958-7
; Sequence 7, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; US-10-825-958-7
```

```
Query Match      89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KVVFFA 6
Db      1 KLVFFA 6
```

RESULT 67  
US-10-825-958-18  
; Sequence 18, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; NAME/KEY: MOD\_RES  
; LOCATION: (6)  
; OTHER INFORMATION: AMIDATION  
US-10-825-958-18

Query Match 89.7%; Score 26; DB 5; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVFFA 6  
Db 1 KLVFFA 6

RESULT 68  
US-10-666-095-3  
; Sequence 3, Application US/10666095  
; Publication No. US2005019187A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammer, Robert P.  
; APPLICANT: Fu, Yanwen  
; APPLICANT: Aucoin, Jed P.  
; APPLICANT: Miller, Tod J.  
; APPLICANT: McLaughlin, Mark L.  
; APPLICANT: McCarley, Robin L.  
; TITLE OF INVENTION: Anti-fibril Peptides  
; FILE REFERENCE: 0212.1 Hammer  
; CURRENT APPLICATION NUMBER: US/10/666,095  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: 60/412,081  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-666-095-3

Query Match 89.7%; Score 26; DB 5; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVFFA 6

Db 1 KLVFFA 6  
|:||||  
RESULT 69  
US-09-867-847-12  
; Sequence 12, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-09-867-847-12

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVFFA 6  
|:||||  
Db 2 KLVFFA 7

RESULT 70  
US-09-867-847-27  
; Sequence 27, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-09-867-847-27

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVFFA 6  
|:||||  
Db 2 KLVFFA 7

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

## RESULT 71

US-09-867-847-28  
; Sequence 28, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lisa  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; NAME/KEY: MOD\_RES  
; LOCATION: (7)  
; OTHER INFORMATION: AMIDATION  
US-09-867-847-28

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

## RESULT 72

US-09-972-475-7  
; Sequence 7, Application US/09972475  
; Patent No. US20020098173A1  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/972,475  
; FILING DATE: 04-Oct-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/617,267

; FILING DATE: <Unknown>  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PFI-002CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-972-475-7

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 2 KLVFFA 7

## RESULT 73

US-09-915-092-2  
; Sequence 2, Application US/09915092  
; Publication No. US20020115717A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; TITLE OF INVENTION: USSS THEREOF  
; FILE REFERENCE: NRI-139  
; CURRENT APPLICATION NUMBER: US/09/915,092  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220,808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-092-2

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 2 KLVFFA 7

## RESULT 74

US-09-915-092-17  
; Sequence 17, Application US/09915092  
; Publication No. US20020115717A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND

; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: NBI-139  
; CURRENT APPLICATION NUMBER: US/09/915,092  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220,808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-092-17

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
Db 1 KLVFFA 6  
|:|||||

RESULT 75  
US-09-915-092-18  
; Sequence 18, Application US/09915092  
; Publication No. US20020115717A1  
; GENERAL INFORMATION:  
; APPLICANT: Gervais, Francine  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Migneault, David  
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND  
; FILE REFERENCE: NBI-139  
; CURRENT APPLICATION NUMBER: US/09/915,092  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/220,808  
; PRIOR FILING DATE: 2000-07-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-092-18

Query Match 89.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KVVFFA 6  
Db 1 KLVFFA 6  
|:|||||

Search completed: December 29, 2005, 18:49:45  
Job time : 67.2903 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds  
(without alignments)  
24.763 Million cell updates/sec

Title: US-10-009-122-9  
Perfect score: 29  
Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Issued Patents AA.\*  
1: /cgm2\_6/ptodata/1/iaa/5\_COMB.pep.\*  
2: /cgm2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgm2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgm2\_6/ptodata/1/iaa/PCITUS\_COMB.pep.\*  
5: /cgm2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	2	US-09-747-408-9
2	29	100.0	6	2	US-09-747-408-17
3	29	100.0	77	2	US-09-513-999C-6921
4	29	100.0	1144	1	US-08-147-812-5
5	29	100.0	1144	1	US-08-319-866-12
6	29	100.0	1144	2	US-09-123-708-2
7	29	100.0	1144	2	US-09-123-624-2
8	29	100.0	1144	2	US-09-661-258-5
9	29	100.0	1144	2	US-08-809-917-12
10	29	100.0	1144	2	US-09-419-371-12
11	28	96.6	6	2	US-09-747-408-1
12	28	96.6	6	2	US-09-747-408-10
13	28	96.6	123	2	US-09-902-540-13513
14	26	89.7	6	1	US-08-612-785B-9
15	26	89.7	6	2	US-08-703-675C-32
16	26	89.7	6	2	US-08-617-267C-9
17	26	89.7	6	2	US-09-747-408-3
18	26	89.7	6	2	US-09-747-408-11
19	26	89.7	7	1	US-08-127-904-14
20	26	89.7	7	1	US-08-612-785B-7
21	26	89.7	7	2	US-08-703-675C-30
22	26	89.7	7	2	US-08-617-267C-7
23	26	89.7	7	2	US-09-264-709A-13
24	26	89.7	7	2	US-09-747-408-2
25	26	89.7	7	2	US-09-747-408-18
26	26	89.7	7	2	US-09-747-408-19
27	26	89.7	7	4	PCT-US94-10475-14

28	26	89.7	8	1	US-08-612-785B-5	Sequence 5, Appli
29	26	89.7	8	1	US-08-630-645-1	Sequence 1, Appli
30	26	89.7	8	2	US-08-703-675C-28	Sequence 28, Appl
31	26	89.7	8	2	US-08-617-267C-5	Sequence 5, Appli
32	26	89.7	8	2	US-09-095-106A-44	Sequence 44, Appl
33	26	89.7	8	2	US-08-766-596A-1	Sequence 1, Appli
34	26	89.7	8	2	US-09-668-314C-73	Sequence 73, Appl
35	26	89.7	8	4	PCT-US96-10220-1	Sequence 1, Appli
36	26	89.7	9	2	US-08-766-596A-64	Sequence 64, Appl
37	26	89.7	9	2	US-09-747-408-20	Sequence 20, Appl
38	26	89.7	10	2	US-08-970-833-3	Sequence 3, Appli
39	26	89.7	10	2	US-09-724-961-20	Sequence 20, Appl
40	26	89.7	10	2	US-09-724-961-21	Sequence 21, Appl
41	26	89.7	10	2	US-09-724-961-22	Sequence 22, Appl
42	26	89.7	10	2	US-09-724-961-23	Sequence 23, Appl
43	26	89.7	10	2	US-09-724-961-24	Sequence 24, Appl
44	26	89.7	10	2	US-09-580-018-20	Sequence 20, Appl
45	26	89.7	10	2	US-09-580-018-21	Sequence 21, Appl
46	26	89.7	10	2	US-09-580-018-22	Sequence 22, Appl
47	26	89.7	10	2	US-09-580-018-23	Sequence 23, Appl
48	26	89.7	10	2	US-09-580-018-24	Sequence 24, Appl
49	26	89.7	10	2	US-09-724-551-20	Sequence 20, Appl
50	26	89.7	10	2	US-09-724-551-21	Sequence 21, Appl
51	26	89.7	10	2	US-09-724-551-22	Sequence 22, Appl
52	26	89.7	10	2	US-09-724-551-23	Sequence 23, Appl
53	26	89.7	10	2	US-09-724-551-24	Sequence 24, Appl
54	26	89.7	10	2	US-09-724-940-20	Sequence 20, Appl
55	26	89.7	10	2	US-09-724-940-21	Sequence 21, Appl
56	26	89.7	10	2	US-09-724-940-22	Sequence 22, Appl
57	26	89.7	10	2	US-09-724-940-23	Sequence 23, Appl
58	26	89.7	10	2	US-09-724-940-24	Sequence 24, Appl
59	26	89.7	11	1	US-08-630-645-14	Sequence 14, Appl
60	26	89.7	11	2	US-08-766-596A-14	Sequence 14, Appl
61	26	89.7	11	2	US-09-988-842-9	Sequence 9, Appli
62	26	89.7	11	2	US-09-988-842-25	Sequence 25, Appl
63	26	89.7	11	4	PCT-US96-10220-14	Sequence 14, Appl
64	26	89.7	14	2	US-09-594-366-5	Sequence 5, Appli
65	26	89.7	14	2	US-09-992-800-5	Sequence 5, Appli
66	26	89.7	15	1	US-08-612-785B-14	Sequence 14, Appl
67	26	89.7	15	1	US-08-612-785B-37	Sequence 37, Appl
68	26	89.7	15	2	US-08-617-267C-14	Sequence 14, Appl
69	26	89.7	15	2	US-08-766-596A-56	Sequence 56, Appl
70	26	89.7	15	2	US-08-766-596A-57	Sequence 57, Appl
71	26	89.7	15	2	US-08-766-596A-58	Sequence 58, Appl
72	26	89.7	15	2	US-08-766-596A-60	Sequence 60, Appl
73	26	89.7	15	2	US-08-766-596A-61	Sequence 61, Appl
74	26	89.7	15	2	US-08-766-596A-62	Sequence 62, Appl
75	26	89.7	15	2	US-08-766-596A-63	Sequence 63, Appl
76	26	89.7	15	2	US-08-766-596A-65	Sequence 65, Appl
77	26	89.7	17	2	US-09-264-709A-2	Sequence 2, Appli
78	26	89.7	17	2	US-09-594-366-3	Sequence 3, Appli
79	26	89.7	17	2	US-09-623-548A-950	Sequence 950, App
80	26	89.7	17	2	US-09-623-548A-983	Sequence 983, App
81	26	89.7	17	2	US-09-992-800-3	Sequence 3, Appli
82	26	89.7	17	2	US-09-657-276-950	Sequence 950, App
83	26	89.7	17	2	US-09-657-276-983	Sequence 983, App
84	26	89.7	19	2	US-08-970-833-11	Sequence 11, Appl
85	26	89.7	19	2	US-09-723-384-5	Sequence 5, Appli
86	26	89.7	19	2	US-09-724-961-75	Sequence 75, Appl
87	26	89.7	19	2	US-09-724-552-5	Sequence 5, Appli
88	26	89.7	19	2	US-09-580-018-75	Sequence 75, Appl
89	26	89.7	19	2	US-09-723-927-5	Sequence 5, Appli
90	26	89.7	19	2	US-09-724-489-5	Sequence 5, Appli
91	26	89.7	19	2	US-09-724-477-5	Sequence 5, Appli
92	26	89.7	19	2	US-09-723-762-5	Sequence 5, Appli
93	26	89.7	19	2	US-09-201-430-5	Sequence 5, Appli
94	26	89.7	19	2	US-09-724-551-75	Sequence 75, Appl
95	26	89.7	19	2	US-10-815-353-5	Sequence 5, Appli
96	26	89.7	19	2	US-10-816-529-5	Sequence 5, Appli
97	26	89.7	19	2	US-10-815-391-5	Sequence 5, Appli
98	26	89.7	19	2	US-10-816-022-5	Sequence 5, Appli
99	26	89.7	19	2	US-09-724-940-75	Sequence 75, Appl
100	26	89.7	19	2	US-10-934-609-5	Sequence 5, Appli

101	26	89.7	19	2	US-10-884-892-5	Sequence 5, Appli	174	26	89.7	38	2	US-09-623-548A-1002	Sequence 1002, Ap
102	26	89.7	20	2	US-08-970-833-10	Sequence 10, Appli	175	26	89.7	38	2	US-09-657-276-975	Sequence 975, App
103	26	89.7	20	2	US-09-724-953-33	Sequence 33, Appl	176	26	89.7	38	2	US-09-657-276-1002	Sequence 1002, Ap
104	26	89.7	20	2	US-09-724-567-33	Sequence 33, Appl	177	26	89.7	39	1	US-08-304-585-5	Sequence 5, Appli
105	26	89.7	20	2	US-09-979-953-33	Sequence 33, Appl	178	26	89.7	39	1	US-08-302-808-2	Sequence 2, Appli
106	26	89.7	20	2	US-09-585-817-33	Sequence 33, Appl	179	26	89.7	39	1	US-08-609-090-7	Sequence 7, Appli
107	26	89.7	26	1	US-08-304-585-7	Sequence 37, Appli	180	26	89.7	39	1	US-08-682-245A-1	Sequence 1, Appli
108	26	89.7	28	1	US-08-346-849-4	Sequence 4, Appli	181	26	89.7	39	1	US-08-986-948-2	Sequence 2, Appli
109	26	89.7	28	1	US-08-302-808-7	Sequence 7, Appli	182	26	89.7	40	1	US-07-744-767A-1	Sequence 1, Appli
110	26	89.7	28	1	US-08-609-090-2	Sequence 2, Appli	183	26	89.7	40	1	US-08-235-400-2	Sequence 2, Appli
111	26	89.7	28	1	US-08-986-948-7	Sequence 7, Appli	184	26	89.7	40	1	US-08-476-464A-2	Sequence 2, Appli
112	26	89.7	28	1	US-08-293-284A-4	Sequence 4, Appli	185	26	89.7	40	1	US-08-304-585-1	Sequence 1, Appli
113	26	89.7	28	1	US-08-461-216-2	Sequence 2, Appli	186	26	89.7	40	1	US-08-304-585-8	Sequence 8, Appli
114	26	89.7	28	2	US-09-388-890-2	Sequence 2, Appli	187	26	89.7	40	1	US-08-302-808-3	Sequence 3, Appli
115	26	89.7	28	2	US-09-388-890-3	Sequence 3, Appli	188	26	89.7	40	1	US-08-433-734-1	Sequence 1, Appli
116	26	89.7	28	2	US-09-388-890-4	Sequence 4, Appli	189	26	89.7	40	1	US-08-609-090-8	Sequence 8, Appli
117	26	89.7	28	2	US-09-388-890-5	Sequence 5, Appli	190	26	89.7	40	1	US-07-737-371E-69	Sequence 69, Appli
118	26	89.7	28	2	US-09-388-890-6	Sequence 6, Appli	191	26	89.7	40	1	US-08-682-245A-2	Sequence 2, Appli
119	26	89.7	28	2	US-09-388-890-7	Sequence 7, Appli	192	26	89.7	40	1	US-08-986-948-3	Sequence 3, Appli
120	26	89.7	28	2	US-09-388-890-8	Sequence 8, Appli	193	26	89.7	40	1	US-08-461-216-1	Sequence 1, Appli
121	26	89.7	28	2	US-09-388-890-9	Sequence 9, Appli	194	26	89.7	40	2	US-08-959-148-1	Sequence 1, Appli
122	26	89.7	28	2	US-09-388-890-10	Sequence 10, Appl	195	26	89.7	40	2	US-09-242-724-22	Sequence 22, Appl
123	26	89.7	28	2	US-09-388-890-12	Sequence 12, Appl	196	26	89.7	40	2	US-08-723-661B-1	Sequence 1, Appli
124	26	89.7	28	2	US-09-388-890-13	Sequence 13, Appl	197	26	89.7	40	2	US-08-062-365-3	Sequence 3, Appli
125	26	89.7	28	2	US-09-388-890-14	Sequence 14, Appl	198	26	89.7	40	2	US-09-133-866-1	Sequence 1, Appli
126	26	89.7	28	2	US-09-264-709A-1	Sequence 1, Appli	199	26	89.7	40	2	US-09-861-847A-7	Sequence 7, Appli
127	26	89.7	28	2	US-08-723-661B-2	Sequence 2, Appli	200	26	89.7	40	2	US-09-861-847A-8	Sequence 8, Appli
128	26	89.7	28	2	US-09-660-954-2	Sequence 2, Appli	201	26	89.7	40	2	US-09-988-842-3	Sequence 3, Appli
129	26	89.7	28	2	US-09-660-954-3	Sequence 3, Appli	202	26	89.7	40	2	US-10-455-218-1	Sequence 1, Appli
130	26	89.7	28	2	US-09-660-954-4	Sequence 4, Appli	203	26	89.7	40	2	US-10-151-614-1	Sequence 1, Appli
131	26	89.7	28	2	US-09-660-954-5	Sequence 5, Appli	204	26	89.7	40	2	US-09-623-548A-956	Sequence 956, App
132	26	89.7	28	2	US-09-660-954-6	Sequence 6, Appli	205	26	89.7	40	2	US-09-623-548A-962	Sequence 962, App
133	26	89.7	28	2	US-09-660-954-7	Sequence 7, Appli	206	26	89.7	40	2	US-09-623-548A-968	Sequence 968, App
134	26	89.7	28	2	US-09-660-954-8	Sequence 8, Appli	207	26	89.7	40	2	US-09-623-548A-978	Sequence 978, App
135	26	89.7	28	2	US-09-660-954-9	Sequence 9, Appli	208	26	89.7	40	2	US-09-623-548A-989	Sequence 989, App
136	26	89.7	28	2	US-09-660-954-10	Sequence 10, Appl	209	26	89.7	40	2	US-08-623-548A-995	Sequence 995, App
137	26	89.7	28	2	US-09-660-954-12	Sequence 12, Appl	210	26	89.7	40	2	US-09-657-276-956	Sequence 956, App
138	26	89.7	28	2	US-09-660-954-13	Sequence 13, Appl	211	26	89.7	40	2	US-09-657-276-962	Sequence 962, App
139	26	89.7	28	2	US-09-660-954-14	Sequence 14, Appl	212	26	89.7	40	2	US-09-657-276-968	Sequence 968, App
140	26	89.7	28	2	US-08-898-300-4	Sequence 4, Appli	213	26	89.7	40	2	US-09-657-276-978	Sequence 978, App
141	26	89.7	28	2	US-08-824-513-4	Sequence 4, Appli	214	26	89.7	40	2	US-09-657-276-989	Sequence 989, App
142	26	89.7	28	2	US-09-623-548A-959	Sequence 959, App	215	26	89.7	40	2	US-09-657-276-995	Sequence 995, App
143	26	89.7	28	2	US-09-623-548A-965	Sequence 965, App	216	26	89.7	40	2	US-09-657-276-1005	Sequence 1005, Ap
144	26	89.7	28	2	US-09-623-548A-976	Sequence 976, App	217	26	89.7	40	2	US-09-962-955D-36	Sequence 36, Appl
145	26	89.7	28	2	US-09-623-548A-992	Sequence 992, App	218	26	89.7	40	2	US-09-962-955D-36	Sequence 36, Appl
146	26	89.7	28	2	US-09-623-548A-1003	Sequence 1003, Ap	219	26	89.7	40	4	PCT-US92-06700-1	Sequence 1, Appli
147	26	89.7	28	2	US-09-657-276-959	Sequence 959, App	220	26	89.7	41	1	US-07-819-361-1	Sequence 1, Appli
148	26	89.7	28	2	US-09-657-276-965	Sequence 965, App	221	26	89.7	41	1	US-08-302-808-4	Sequence 4, Appli
149	26	89.7	28	2	US-09-657-276-976	Sequence 976, App	222	26	89.7	41	1	US-08-682-245A-3	Sequence 3, Appli
150	26	89.7	28	2	US-09-657-276-992	Sequence 992, App	223	26	89.7	41	1	US-08-986-948-4	Sequence 4, Appli
151	26	89.7	28	2	US-09-657-276-1003	Sequence 1003, Ap	224	26	89.7	42	1	US-07-744-767A-2	Sequence 2, Appli
152	26	89.7	28	2	US-09-865-294A-66	Sequence 66, Appl	225	26	89.7	42	1	US-08-179-574-1	Sequence 1, Appli
153	26	89.7	30	1	US-08-609-090-3	Sequence 3, Appli	226	26	89.7	42	1	US-08-271-162-5	Sequence 5, Appli
154	26	89.7	30	2	US-08-861-847A-1	Sequence 1, Appli	227	26	89.7	42	1	US-08-347-144-1	Sequence 1, Appli
155	26	89.7	33	1	US-08-609-090-4	Sequence 4, Appli	228	26	89.7	42	1	US-08-462-859A-19	Sequence 19, Appl
156	26	89.7	34	1	US-08-475-579A-4	Sequence 4, Appli	229	26	89.7	42	1	US-08-123-659A-19	Sequence 19, Appl
157	26	89.7	35	1	US-08-304-585-6	Sequence 6, Appli	230	26	89.7	42	1	US-08-464-247A-19	Sequence 19, Appl
158	26	89.7	35	1	US-08-612-785B-16	Sequence 16, Appl	231	26	89.7	42	1	US-08-464-248A-19	Sequence 19, Appl
159	26	89.7	35	1	US-08-612-785B-36	Sequence 36, Appl	232	26	89.7	42	1	US-08-476-464A-1	Sequence 1, Appli
160	26	89.7	35	1	US-08-612-785B-38	Sequence 38, Appl	233	26	89.7	42	1	US-08-304-585-2	Sequence 2, Appli
161	26	89.7	35	1	US-08-612-785B-38	Sequence 40, Appl	234	26	89.7	42	1	US-08-302-808-5	Sequence 5, Appli
162	26	89.7	35	2	US-08-617-267C-16	Sequence 16, Appl	235	26	89.7	42	1	US-08-268-348A-1	Sequence 1, Appli
163	26	89.7	35	2	US-09-623-548A-979	Sequence 979, App	236	26	89.7	42	1	US-08-268-348A-2	Sequence 2, Appli
164	26	89.7	35	2	US-09-623-548A-1006	Sequence 1006, Ap	237	26	89.7	42	1	US-08-268-348A-3	Sequence 3, Appli
165	26	89.7	35	2	US-09-657-276-979	Sequence 979, App	238	26	89.7	42	1	US-08-268-348A-4	Sequence 4, Appli
166	26	89.7	35	2	US-08-609-090-6	Sequence 6, Appli	239	26	89.7	42	1	US-08-268-348A-5	Sequence 5, Appli
167	26	89.7	36	2	US-09-861-847A-6	Sequence 6, Appli	240	26	89.7	42	1	US-08-268-348A-6	Sequence 6, Appli
168	26	89.7	36	2	US-09-861-847A-11	Sequence 11, Appl	241	26	89.7	42	1	US-08-433-734-2	Sequence 2, Appli
169	26	89.7	36	2	US-08-302-808-1	Sequence 1, Appli	242	26	89.7	42	1	US-07-737-371E-72	Sequence 72, Appl
170	26	89.7	38	1	US-08-302-808-1	Sequence 1, Appli	243	26	89.7	42	1	US-08-422-333-4	Sequence 4, Appli
171	26	89.7	38	1	US-07-737-371E-68	Sequence 68, Appl	244	26	89.7	42	1	US-08-682-245A-4	Sequence 4, Appli
172	26	89.7	38	1	US-08-986-948-1	Sequence 1, Appli	245	26	89.7	42	1	US-08-986-948-5	Sequence 5, Appli
173	26	89.7	38	2	US-09-623-548A-975	Sequence 975, App	246	26	89.7	42	1		

```

247 26 89.7 42 2 US-08-717-551A-2
248 26 89.7 42 2 US-09-388-890-1
249 26 89.7 42 2 US-09-005-215-20
250 26 89.7 42 2 US-09-242-724-23
251 26 89.7 42 2 US-08-922-930-2
252 26 89.7 42 2 US-09-660-954-1
253 26 89.7 42 2 US-08-923-055-2
254 26 89.7 42 2 US-08-922-889-2
255 26 89.7 42 2 US-09-731-460-1
256 26 89.7 42 2 US-09-133-866-2
257 26 89.7 42 2 US-09-723-384-1
258 26 89.7 42 2 US-09-724-961-42
259 26 89.7 42 2 US-09-724-552-1
260 26 89.7 42 2 US-09-580-018-42
261 26 89.7 42 2 US-10-455-218-2
262 26 89.7 42 2 US-09-723-527-1
263 26 89.7 42 2 US-09-724-489-1
264 26 89.7 42 2 US-09-724-477-1
265 26 89.7 42 2 US-09-723-762-1
266 26 89.7 42 2 US-09-201-430-1
267 26 89.7 42 2 US-09-724-551-42
268 26 89.7 42 2 US-10-815-353-1
269 26 89.7 42 2 US-10-278-181-1
270 26 89.7 42 2 US-10-816-529-1
271 26 89.7 42 2 US-09-623-548A-955
272 26 89.7 42 2 US-09-623-548A-961
273 26 89.7 42 2 US-09-623-548A-967
274 26 89.7 42 2 US-09-623-548A-988
275 26 89.7 42 2 US-09-623-548A-994
276 26 89.7 42 2 US-10-815-391-1
277 26 89.7 42 2 US-10-816-022-1
278 26 89.7 42 2 US-09-724-553-34
279 26 89.7 42 2 US-09-657-276-955
280 26 89.7 42 2 US-09-657-276-961
281 26 89.7 42 2 US-09-657-276-967
282 26 89.7 42 2 US-09-657-276-988
283 26 89.7 42 2 US-09-657-276-994
284 26 89.7 42 2 US-09-724-567-34
285 26 89.7 42 2 US-09-724-940-42
286 26 89.7 42 2 US-09-865-294A-65
287 26 89.7 42 2 US-09-979-952-34
288 26 89.7 42 2 US-09-585-817-34
289 26 89.7 42 2 US-09-962-355D-37
290 26 89.7 42 2 US-09-706-574A-20
291 26 89.7 42 2 US-10-934-609-1
292 26 89.7 42 2 US-10-884-892-1
293 26 89.7 42 2 PCT-US92-06700-2
294 26 89.7 42 4 PCT-US93-00325-1
295 26 89.7 42 4 PCT-US93-08302-5
296 26 89.7 42 6 5220013-12
297 26 89.7 42 6 5220013-14
298 26 89.7 42 6 5223482-12
299 26 89.7 43 1 US-08-235-400-1
300 26 89.7 43 1 US-08-437-067-1

```

# ALIGNMENTS

```

RESULT 1
US-09-747-408-9
; Sequence 9, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

```

```

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 1 KVVFFA 6

RESULT 2
US-09-747-408-17
; Sequence 17, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 1 KVVFFA 6

RESULT 3
US-09-513-999C-6921
; Sequence 6921, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6921
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6921

Query Match 100.0%; Score 29; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 14;

```



Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 38 KVVFFA 43

## RESULT 4

US-08-147-812-5  
; Sequence 5, Application US/08147812  
; Patent No. 5766909  
; GENERAL INFORMATION:  
; APPLICANT: Xie, Qiao-wen  
; APPLICANT: Nathan, Carl F.  
; APPLICANT: Mumford, Richard A.  
; APPLICANT: Calaycay, Jimmy Ramos  
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: 126 East Lincoln Avenue  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07065

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh Centris650  
; OPERATING SYSTEM: Macintosh 7.0.1  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,812  
; FILING DATE: No. 5766909 Available  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/841,841  
; FILING DATE: 02-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wallen, John W III  
; REGISTRATION NUMBER: 35,403  
; REFERENCE/DOCKET NUMBER: 186581A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-3905  
; TELEFAX: (908) 594-4720  
; TELEX: 138825  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1144 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-147-812-5  
Query Match 100.0%; Score 29; DB 1; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 514 KVVFFA 519

## RESULT 5

US-08-319-866-12  
; Sequence 12, Application US/08319866  
; Patent No. 5929223  
; GENERAL INFORMATION:  
; APPLICANT: Tully, Timothy P.  
; APPLICANT: Yin, Jerry C.  
; APPLICANT: Regulski, Michael  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/319,866  
; FILING DATE: 7-OCT-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:

FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL94-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1144 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-319-866-12

Query Match 100.0%; Score 29; DB 1; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 514 KVVFFA 519

## RESULT 6

US-09-123-708-2  
; Sequence 2, Application US/09123708  
; Patent No. 6146887  
; GENERAL INFORMATION:  
; APPLICANT: SCHRADER, Juergen  
; APPLICANT: GOEDECKE, Axel  
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC  
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
; FILE REFERENCE: 51169-2003  
; CURRENT APPLICATION NUMBER: US/09/123,708  
; CURRENT FILING DATE: 1998-07-28  
; EARLIER APPLICATION NUMBER: 08/553,503  
; EARLIER FILING DATE: 1996-03-01  
; EARLIER APPLICATION NUMBER: P4411402.8  
; EARLIER FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Cytomegalovirus  
; US-09-123-708-2

Query Match 100.0%; Score 29; DB 2; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

|||||

Db 514 KVVFFA 519

RESULT 7

US-09-123-624-2

Sequence 2, Application US/09123624

Patent No. 6149936

GENERAL INFORMATION:

APPLICANT: SCHRADER, Jurgen

APPLICANT: GODECKE, Axel

TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

FILE REFERENCE: 511169-2004

CURRENT APPLICATION NUMBER: US/09/123,624

CURRENT FILING DATE: 1998-07-28

PRIOR APPLICATION NUMBER: 08/553,503

PRIOR FILING DATE: 1996-03-01

PRIOR APPLICATION NUMBER: 4411402.8

PRIOR FILING DATE: 1994-03-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 2

LENGTH: 1144

TYPE: PRT

ORGANISM: Mus musculus

US-09-123-624-2

Query Match 100.0%; Score 29; DB 2; Length 1144;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

Db 514 KVVFFA 519

RESULT 8

US-09-661-258-5

Sequence 5, Application US/09661258

Patent No. 6620616

GENERAL INFORMATION:

APPLICANT: Stuehr, Dennis J.

APPLICANT: Adak, Subrata

TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants

FILE REFERENCE: 26473/04028

CURRENT APPLICATION NUMBER: US/09/661,258

CURRENT FILING DATE: 2000-09-13

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patent in version 3.1

SEQ ID NO 5

LENGTH: 1144

TYPE: PRT

ORGANISM: Mus musculus

US-09-661-258-5

Query Match 100.0%; Score 29; DB 2; Length 1144;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

Db 514 KVVFFA 519

RESULT 9

US-08-809-917-12

Sequence 12, Application US/08809917

Patent No. 6689557

GENERAL INFORMATION:

APPLICANT:

APPLICANT: APPLICANT

TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES

TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/809,917

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13198

FILING DATE:

APPLICATION NUMBER: US 08/361,063

FILING DATE: 21-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/319,866

FILING DATE: 07-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240

TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1144 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-809-917-12

Query Match 100.0%; Score 29; DB 2; Length 1144;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

Db 514 KVVFFA 519

RESULT 10

US-09-419-371-12

Sequence 12, Application US/09419371

Patent No. 6890516

GENERAL INFORMATION:

APPLICANT: Tully, Timothy P.

APPLICANT: Yin, Jerry Chi-Ping

TITLE OF INVENTION: Cloning and Characterizing of Genes

TITLE OF INVENTION: Associated With Long-Term Memory

FILE REFERENCE: CSHL94-03A3Z

CURRENT APPLICATION NUMBER: US/09/419,371

CURRENT FILING DATE: 1999-10-14

PRIOR APPLICATION NUMBER: 08/809,917

PRIOR FILING DATE: 1997-07-07

PRIOR APPLICATION NUMBER: PCT/US95/13198

PRIOR FILING DATE: 1995-10-06

PRIOR APPLICATION NUMBER: 08/361,063

PRIOR FILING DATE: 1994-12-21

PRIOR APPLICATION NUMBER: 08/319,866

PRIOR FILING DATE: 1994-10-07

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

;  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-419-371-12

Query Match 100.0%; Score 29; DB 2; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 514 KVVFFA 519

## RESULT 11

US-09-747-408-1  
; Sequence 1, Application US/09747408  
; Patent No. 6670399  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-408-1

Query Match 96.6%; Score 28; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 1 KVVFFA 6

## RESULT 12

US-09-747-408-10  
; Sequence 10, Application US/09747408  
; Patent No. 6670399  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/171,877  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-747-408-10

Query Match 96.6%; Score 28; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||

Db 1 KVVFFA 6

## RESULT 13

US-09-902-540-13513  
; Sequence 13513, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 13513  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-13513

Query Match 96.6%; Score 28; DB 2; Length 123;  
Best Local Similarity 83.3%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 52 KVVFFA 57

## RESULT 14

US-08-612-785B-9  
; Sequence 9, Application US/08612785B  
; Patent No. 5854204  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
; TITLE OF INVENTION: Aggregation  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/612,785B  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP3  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-612-785B-9

Query Match 89.7%; Score 26; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 15  
US-08-703-675C-32  
; Sequence 32, Application US/08703675C  
; Patent No. 6303567  
; GENERAL INFORMATION:  
; APPLICANT: Findexis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/703,675C  
; FILING DATE: 27-AUG-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/616,081  
; FILING DATE: 14-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kara, Catherine J.  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: PPI-016CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)742-4214  
; TELEFAX: (617)227-7400  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-703-675C-32

Query Match 89.7%; Score 26; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 16  
US-08-617-267C-9  
; Sequence 9, Application US/08617267C  
; Patent No. 6319498  
; GENERAL INFORMATION:  
; APPLICANT: Findexis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/617,267C  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-617-267C-9

Query Match 89.7%; Score 26; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 17  
US-09-747-408-3  
; Sequence 3, Application US/09747408  
; Patent No. 6670399  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan M.  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: Compounds And Methods For Modulating  
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy  
; FILE REFERENCE: NBI-088  
; CURRENT APPLICATION NUMBER: US/09/747,408

```
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match      89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 18
US-09-747-408-11
; Sequence 11, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match      89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 19
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Amnestic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; COMPUTER: Wang PC

; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,904
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
US-08-127-904-14

Query Match      89.7%; Score 26; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 20
US-08-612-785B-7
; Sequence 7, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
```

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-612-785B-7

Query Match 89.7%; Score 26; DB 1; Length 7;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
Db 2 KLVFFA 7

## RESULT 21

US-08-703-675C-30  
Sequence 30, Application US/08703675C  
Patent No. 6303567  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/703.675C  
FILING DATE: 27-AUG-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/616,081  
FILING DATE: 14-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kara, Catherine J.  
REGISTRATION NUMBER: 41,106  
REFERENCE/DOCKET NUMBER: PPI-016CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-703-675C-30

Query Match 89.7%; Score 26; DB 2; Length 7;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 2 KLVFFA 7

RESULT 22  
US-08-617-267C-7  
Sequence 7, Application US/08617267C  
Patent No. 6319498  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Modulators of Amyloid Aggregation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C  
FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-617-267C-7

Query Match 89.7%; Score 26; DB 2; Length 7;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
Db 2 KLVFFA 7

## RESULT 23

US-09-264-709A-13  
Sequence 13, Application US/09264709A  
Patent No. 6320024  
GENERAL INFORMATION:  
APPLICANT: Roberts, Eugene  
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and  
FILE OF INVENTION: Improve the Quality of Life  
FILE REFERENCE: 2124-310  
CURRENT APPLICATION NUMBER: US/09/264,709A  
CURRENT FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: 08/797,782  
PRIOR FILING DATE: 1997-02-07

```
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-13

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 24
US-09-747-408-2
; Sequence 2, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 2 KLVFFA 7

RESULT 25
US-09-747-408-18
; Sequence 18, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 26
US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 27
PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amnestic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
```

REGISTRATION NUMBER: 16,541  
REFERENCE/DOCKET NUMBER: None  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 626-3564 or 783-6030  
TELEFAX: (202) 783-6031  
TELEX: None  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7  
TYPE: Amino Acid  
STRANDEDNESS:  
TOPOLOGY: Unknown  
PCT-US94-10475-14

Query Match 89.7%; Score 26; DB 4; Length 7;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 28  
US-08-612-785B-5  
Sequence 5, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
TITLE OF INVENTION: Aggregation  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612.785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PFI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-612-785B-5

Query Match 89.7%; Score 26; DB 1; Length 8;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 3 KLVFFA 8

RESULT 29  
US-08-630-645-1  
Sequence 1, Application US/08630645  
Patent No. 5948763  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,645  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-630-645-1

Query Match 89.7%; Score 26; DB 1; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 30  
US-08-703-675C-28  
Sequence 28, Application US/08703675C  
Patent No. 6303567  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Modulators of -Amyloid Peptide  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:

Aggregation Comprising D-



ADDRESS: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/703,675C  
FILING DATE: 27-AUG-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/616,081  
FILING DATE: 14-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kara, Catherine J.  
REGISTRATION NUMBER: 41,106  
REFERENCE/DOCKET NUMBER: PPI-016CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-703-675C-28

Query Match 89.7%; Score 26; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 KVVFFA 6  
|:||||  
Db 3 KLVFFA 8

RESULT 31  
US-08-617-267C-5  
Sequence 5, Application US/08617267C  
Patent No. 6319498  
GENERAL INFORMATION:  
APPLICANT: Findels, Mark A. et al.  
TITLE OF INVENTION: Modulators of Amyloid Aggregation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSES: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C

FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-617-267C-5

Query Match 89.7%; Score 26; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 KVVFFA 6  
|:||||  
Db 3 KLVFFA 8

RESULT 32  
US-09-095-106A-44  
Sequence 44, Application US/09095106A  
Patent No. 6331440  
GENERAL INFORMATION:  
APPLICANT: NORDSTEDT, Christer  
APPLICANT: NASLUND, Jan  
APPLICANT: TYBERG, Johan  
APPLICANT: TJERNBERG, Lars O.  
APPLICANT: TERENIUS, Lars  
TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
FILE REFERENCE: 000500-124  
CURRENT APPLICATION NUMBER: US/09/095,106A  
CURRENT FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: US 60/009,386  
PRIOR FILING DATE: 1995-12-29  
PRIOR APPLICATION NUMBER: PCT/SE96/01621  
PRIOR FILING DATE: 1996-12-09  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 44  
LENGTH: 8  
TYPE: PPT  
ORGANISM: Amyloidosis  
US-09-095-106A-44

Query Match 89.7%; Score 26; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 33  
US-08-766-596A-1  
Sequence 1, Application US/08766596A  
Patent No. 6462171

GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BRAUMANN, Marc  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766.596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-1

Query Match 89.7%; Score 26; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 34  
US-09-668-314C-73  
Sequence 73, Application US/09668314C  
Patent No. 6844148  
GENERAL INFORMATION:  
APPLICANT: Guiney, et al  
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES  
FILE REFERENCE: 28341/628ONCP  
CURRENT APPLICATION NUMBER: US/09/668,314C  
CURRENT FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US 60/169,232  
PRIOR FILING DATE: 1999-12-06  
PRIOR APPLICATION NUMBER: US 09/416,901  
PRIOR FILING DATE: 1999-10-13  
PRIOR APPLICATION NUMBER: US 60/155,493  
PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: US 09/404,133  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: PCT/US99/20881  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 60/101,594  
PRIOR FILING DATE: 1998-09-24  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 73  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURES:  
OTHER INFORMATION: Synthetic peptide  
US-09-668-314C-73

Query Match 89.7%; Score 26; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 35  
PCT-US96-10220-1  
Sequence 1, Application PC/TUS9610220  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10220  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US96-10220-1

Query Match 89.7%; Score 26; DB 4; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;

```

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 KVVFFA 6
Db      1 KLVFFA 6

RESULT 36
US-08-766-596A-64
; Sequence 64, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-64

Query Match      89.7%; Score 26; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 KVVFFA 6
Db      2 KLVFFA 7

RESULT 37
US-09-747-408-20
; Sequence 20, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.

```

```

; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-20

Query Match      89.7%; Score 26; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 KVVFFA 6
Db      4 KLVFFA 9

RESULT 38
US-08-970-833-3
; Sequence 3, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Kieselring, Laura L.
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-970-833-3

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 KVVFFA 6
Db      1 KLVFFA 6

```

```
RESULT 39
US-09-724-961-20
; Sequence 20, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:|||||
Db      5 KLVFFA 10

RESULT 40
US-09-724-961-21
; Sequence 21, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:|||||
Db      5 KLVFFA 10

RESULT 41
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:|||||
Db      3 KLVFFA 8

RESULT 42
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

```
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21
```

```
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:|||||
Db      4 KLVFFA 9
```

```
RESULT 41
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22
```

```
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:|||||
Db      3 KLVFFA 8
```

```
RESULT 42
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US 09/724,961  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-961-23

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 2 KLVFFA 7

RESULT 43  
US-09-724-961-24  
; Sequence 24, Application US/09724961  
; Patent No. 6743427  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US 09/724,961  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-961-24

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 1 KLVFFA 6

RESULT 44  
US-09-580-018-20  
; Sequence 20, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US 09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-20

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:|||||  
Db 5 KLVFFA 10

RESULT 45  
US-09-580-018-21  
; Sequence 21, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US 09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-21

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 4 KLVFFA 9

RESULT 46  
US-09-580-018-22  
; Sequence 22, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-22

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 3 KLVFFA 8

RESULT 47  
US-09-580-018-23  
; Sequence 23, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-23

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KLVFFA 6  
|:||||  
Db 2 KLVFFA 7

RESULT 48  
US-09-580-018-24  
; Sequence 24, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-24

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
|:||||  
Db 1 KLVFFA 6

RESULT 49  
US-09-724-551-20  
; Sequence 20, Application US/09724551  
; Patent No. 6787637  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/724,551  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-551-20

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 KVVFFA 6
Db      5 KLVFFA 10

RESULT 50
US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      4 KLVFFA 9

RESULT 51
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      2 KLVFFA 7

RESULT 52
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      2 KLVFFA 7

RESULT 53
US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Best Local Similarity 83.3%; Pred. No. 8.4; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

## RESULT 54

US-09-724-940-20  
; Sequence 20, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-20

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KVVFFA 6  
|:||||  
Db 5 KLVFFA 10

## RESULT 55

US-09-724-940-21  
; Sequence 21, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-21

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KVVFFA 6  
|:||||  
Db 4 KLVFFA 9

## RESULT 56

US-09-724-940-22  
; Sequence 22, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-22

Query Match 89.7%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 8.4; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KVVFFA 6  
|:||||  
Db 3 KLVFFA 8



```

RESULT 57
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

```

```

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KLVFFA 6
       |:|||||
DB      2 KLVFFA 7

```

```

RESULT 58
US-09-724-940-24
; Sequence 24, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1

```

```

; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

```

```

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KLVFFA 6
       |:|||||
DB      1 KLVFFA 6

```

```

RESULT 59
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-630-645-14

```

```

Query Match      89.7%; Score 26; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KLVFFA 6
       |:|||||
DB      2 KLVFFA 7

```

```
RESULT 60
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-14

Query Match      89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
Db      2 KLVFFA 7

RESULT 61
US-09-988-842-9
; Sequence 9, Application US/099888842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match      89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
Db      2 KLVFFA 7

RESULT 62
US-09-988-842-25
; Sequence 25, Application US/099888842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match      89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
Db      2 KLVFFA 7

RESULT 63
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
```

```
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9
```

```
Query Match      89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KVVFFA 6
Db      2 KLVFFA 7
```

```
RESULT 62
US-09-988-842-25
; Sequence 25, Application US/099888842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25
```

```
Query Match      89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KVVFFA 6
Db      2 KLVFFA 7
```

```
RESULT 63
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-10220-14

```

```

Query Match      89.7%; Score 26; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
       |:||||
Db      2 KLVFFA 7

```

```

RESULT 64
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-5

```

```

Query Match      89.7%; Score 26; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
       |:||||
Db      4 KLVFFA 9

```

```

RESULT 65
US-09-992-800-5
; Sequence 5, Application US/0992800
; Patent No. 6872554
; GENERAL INFORMATION:

```

```

; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-5

Query Match      89.7%; Score 26; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      4 KLVFFA 9

RESULT 66
US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

```

; FRAGMENT TYPE: internal  
US-08-612-785B-14

Query Match 89.7%; Score 26; DB 1; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

## RESULT 67

US-08-612-785B-37  
; Sequence 37, Application US/08612785B  
; Patent No. 5854204  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
; TITLE OF INVENTION: Aggregation  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/612,785B  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-612-785B-37

Query Match 89.7%; Score 26; DB 1; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 6 KLVFFA 11

## RESULT 68

US-08-617-267C-14

; Sequence 14, Application US/08617267C  
; Patent No. 6319498  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/617,267C  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-617-267C-14

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|:||||  
Db 1 KLVFFA 6

## RESULT 69

US-08-766-596A-56  
; Sequence 56, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.

/ COUNTRY: USA  
/ ZIP: 20004  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/766,596A  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/630,645  
/ FILING DATE: 10-APR-1996  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/478,326  
/ FILING DATE: 06-JUN-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: YUN, Allen C.  
/ REGISTRATION NUMBER: 37,971  
/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-628-5197  
/ INFORMATION FOR SEQ ID NO: 56:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ US-08-766-596A-56

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 5 KLVFFA 10

RESULT 70  
US-08-766-596A-57  
; Sequence 57, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/766,596A  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/630,645  
/ FILING DATE: 10-APR-1996  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/478,326  
/ FILING DATE: 06-JUN-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: YUN, Allen C.  
/ REGISTRATION NUMBER: 37,971  
/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-628-5197  
/ TELEFAX: 202-737-3528  
/ INFORMATION FOR SEQ ID NO: 58:  
/ SEQUENCE CHARACTERISTICS:

/ FILING DATE: 10-APR-1996  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/478,326  
/ FILING DATE: 06-JUN-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: YUN, Allen C.  
/ REGISTRATION NUMBER: 37,971  
/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-628-5197  
/ TELEFAX: 202-737-3528  
/ INFORMATION FOR SEQ ID NO: 57:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ US-08-766-596A-57

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 5 KLVFFA 10

RESULT 71  
US-08-766-596A-58  
; Sequence 58, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/766,596A  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/630,645  
/ FILING DATE: 10-APR-1996  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/478,326  
/ FILING DATE: 06-JUN-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: YUN, Allen C.  
/ REGISTRATION NUMBER: 37,971  
/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-628-5197  
/ TELEFAX: 202-737-3528  
/ INFORMATION FOR SEQ ID NO: 58:  
/ SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-58

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
Db 5 KLVFFA 10

## RESULT 72

US-08-766-596A-60  
Sequence 60, Application US/08766596A  
Patent No. 6462171

## GENERAL INFORMATION:

APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
APPLICANT: FRANGIONE, Blas  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
TITLE OF INVENTION: DEPOSITS  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-60

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
Db 5 KLVFFA 10

Db 5 KLVFFA 10

## RESULT 73

US-08-766-596A-61  
Sequence 61, Application US/08766596A  
Patent No. 6462171

## GENERAL INFORMATION:

APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
APPLICANT: FRANGIONE, Blas  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
TITLE OF INVENTION: DEPOSITS  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-61

Query Match 89.7%; Score 26; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6  
Db 5 KLVFFA 10

## RESULT 74

US-08-766-596A-62  
Sequence 62, Application US/08766596A  
Patent No. 6462171

## GENERAL INFORMATION:

APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
APPLICANT: FRANGIONE, Blas  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

RESULT 75  
US-08-766-596A-63  
; Sequence 63, Application US/08766596A  
; Patent No. 6462171  
; GENERAL INFORMATION:  
; APPLICANT: SOTO-JARA, Claudio  
; APPLICANT: BAUMANN, Marc  
; APPLICANT: FRANGIONE, Blas  
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
; TITLE OF INVENTION: DEPOSITS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds  
(without alignments)  
32.238 Million cell updates/sec

Title: US-10-009-122-9  
Perfect score: 29  
Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4	AAB48482
2	29	100.0	6	4	AAB48490
3	29	100.0	6	4	AAB82630
4	29	100.0	6	4	AAB82638
5	29	100.0	6	5	AAU96818
6	29	100.0	6	5	AAU96826
7	29	100.0	6	5	AAU11664
8	29	100.0	6	5	AAU11656
9	29	100.0	6	6	AAE35452
10	29	100.0	6	8	ADQ37277
11	29	100.0	6	8	ADQ37321
12	29	100.0	6	8	ADQ37329
13	29	100.0	6	9	ADY37928
14	29	100.0	6	9	ADY37936
15	29	100.0	22	8	ADQ09761
16	29	100.0	23	8	ADT93984
17	29	100.0	37	3	AAB05910
18	29	100.0	37	3	ADK34080
19	29	100.0	37	8	ADL70727
20	29	100.0	77	3	AAQ02840
21	29	100.0	175	4	AAQ11219
22	29	100.0	186	7	ADC07962
23	29	100.0	186	7	ADC07948
24	29	100.0	190	4	AAW83792



98	26	89.7	7	2	AAW89376	AAW89376 Beta-amyl	171	26	89.7	9	9	AEA51417	AEA51417 C-A 16-23
99	26	89.7	7	4	AA567281	AA567281 Residues	172	26	89.7	9	9	AEA62825	AEA62825 Immunoon
100	26	89.7	7	4	AA48475	AA48475 Antifibri	173	26	89.7	9	9	AEA62828	AEA62828 Immunoon
101	26	89.7	7	4	AA48492	AA48492 Antifibri	174	26	89.7	10	3	AAV79388	AAV79388 Beta-amyl
102	26	89.7	7	4	AA48491	AA48491 Antifibri	175	26	89.7	10	4	AA46226	AA46226 Human APP
103	26	89.7	7	4	AA82624	AA82624 All-D pep	176	26	89.7	10	4	AA46225	AA46225 Human APP
104	26	89.7	7	4	AA82640	AA82640 All-D pep	177	26	89.7	10	4	AA46228	AA46228 Human APP
105	26	89.7	7	4	AA82639	AA82639 All-D pep	178	26	89.7	10	4	AA46224	AA46224 Human APP
106	26	89.7	7	5	ABG71007	ABG71007 Long form	179	26	89.7	10	4	AA46227	AA46227 Human APP
107	26	89.7	7	5	AB805155	AB805155 Beta amyl	180	26	89.7	10	4	AA82641	AA82641 All-D pep
108	26	89.7	7	5	AAU96827	AAU96827 Amyloid t	181	26	89.7	10	5	AAU96829	AAU96829 Amyloid t
109	26	89.7	7	5	AAU96812	AAU96812 Amyloid t	182	26	89.7	10	6	ABP57511	ABP57511 Different
110	26	89.7	7	5	AAU96828	AAU96828 Amyloid t	183	26	89.7	10	6	AAE35455	AAE35455 Beta pep
111	26	89.7	7	5	AB804920	AB804920 Human amy	184	26	89.7	10	8	ADQ37280	ADQ37280 Vaccine a
112	26	89.7	7	5	AAU11665	AAU11665 Peptide #	185	26	89.7	10	8	ADQ37371	ADQ37371 Amyloid-b
113	26	89.7	7	5	AAU11649	AAU11649 Peptide #	186	26	89.7	10	8	ADQ37374	ADQ37374 Amyloid-b
114	26	89.7	7	5	AAU11666	AAU11666 Peptide #	187	26	89.7	10	9	ADY37939	ADY37939 Amyloid-c
115	26	89.7	7	6	AB882630	AB882630 Beta fib	188	26	89.7	11	2	AAW32560	AAW32560 Antil-amyl
116	26	89.7	7	6	AAE35439	AAE35439 Beta pep	189	26	89.7	11	4	AAW52586	AAW52586 Peptide #
117	26	89.7	7	6	AAE35454	AAE35454 Beta pep	190	26	89.7	11	5	AAU99431	AAU99431 Human amy
118	26	89.7	7	6	AAE35453	AAE35453 Beta pep	191	26	89.7	11	5	AAE29504	AAE29504 Amyloid b
119	26	89.7	7	6	ADA90937	ADA90937 Solid-pha	192	26	89.7	11	6	ABU79013	ABU79013 Amyloidog
120	26	89.7	7	6	ADA90134	ADA90134 Anti-Abet	193	26	89.7	11	7	ABR84683	ABR84683 Aggreana
121	26	89.7	7	7	ADD20746	ADD20746 Human bet	194	26	89.7	11	7	ABW00147	ABW00147 Amyloid-b
122	26	89.7	7	7	ADF50855	ADF50855 Human cal	195	26	89.7	12	6	ABR91837	ABR91837 P. papata
123	26	89.7	7	8	ADJ64058	ADJ64058 Human bet	196	26	89.7	12	6	AAE35464	AAE35464 Beta pep
124	26	89.7	7	8	ADP64922	ADP64922 Beta-amyl	197	26	89.7	12	6	AAE35435	AAE35435 Beta pep
125	26	89.7	7	8	ADQ37278	ADQ37278 Vaccine a	198	26	89.7	12	6	AAE35466	AAE35466 Beta pep
126	26	89.7	7	8	ADQ37314	ADQ37314 Antifibri	199	26	89.7	12	7	ADD20745	ADD20745 Human bet
127	26	89.7	7	8	ADQ37263	ADQ37263 Vaccine a	200	26	89.7	12	7	ADD20744	ADD20744 Human bet
128	26	89.7	7	8	ADQ37279	ADQ37279 Vaccine a	201	26	89.7	12	8	ADJ71476	ADJ71476 N-termina
129	26	89.7	7	8	ADQ37330	ADQ37330 Antifibri	202	26	89.7	12	8	ADQ37407	ADQ37407 Amyloid-b
130	26	89.7	7	8	ADQ37331	ADQ37331 Antifibri	203	26	89.7	12	8	ADQ37289	ADQ37289 Vaccine a
131	26	89.7	7	8	ADQ37351	ADQ37351 Beta-amyl	204	26	89.7	12	8	ADQ37259	ADQ37259 Vaccine a
132	26	89.7	7	9	ADY37922	ADY37922 Amyloid-c	205	26	89.7	12	9	ADZ08890	ADZ08890 Human bet
133	26	89.7	7	9	ADY37938	ADY37938 Amyloid-t	206	26	89.7	12	9	ADZ08892	ADZ08892 Human bet
134	26	89.7	7	9	ADY37937	ADY37937 Amyloid-t	207	26	89.7	13	6	AAE35465	AAE35465 Beta pep
135	26	89.7	7	9	ADZ08903	ADZ08903 Human bet	208	26	89.7	13	6	AAE35467	AAE35467 Beta pep
136	26	89.7	8	2	AAW02310	AAW02310 Beta-amyl	209	26	89.7	13	6	ADA37467	ADA37467 Human amy
137	26	89.7	8	2	AAW45967	AAW45967 Peptide d	210	26	89.7	13	8	ADJ71477	ADJ71477 N-termina
138	26	89.7	8	2	AAW32551	AAW32551 Amyloidog	211	26	89.7	13	8	ADJ71464	ADJ71464 N-termina
139	26	89.7	8	2	AAW89374	AAW89374 Beta-amyl	212	26	89.7	13	8	ADQ37408	ADQ37408 Amyloid-b
140	26	89.7	8	4	AAE10663	AAE10663 Human amy	213	26	89.7	13	8	ADQ37290	ADQ37290 Vaccine a
141	26	89.7	8	4	AAE02615	AAE02615 Human amy	214	26	89.7	14	6	ADA89887	ADA89887 Beta-A4 s
142	26	89.7	8	5	ABG71005	ABG71005 Long form	215	26	89.7	14	6	ADJ71452	ADJ71452 N-termina
143	26	89.7	8	5	AB878624	AB878624 Human alp	216	26	89.7	14	8	ADJ71465	ADJ71465 N-termina
144	26	89.7	8	5	AB805153	AB805153 Beta amyl	217	26	89.7	14	8	ADJ71478	ADJ71478 N-termina
145	26	89.7	8	6	ABU09765	ABU09765 Amyloidog	218	26	89.7	14	9	ADZ08889	ADZ08889 Human bet
146	26	89.7	8	6	ABR61959	ABR61959 Human amy	219	26	89.7	15	2	AAW02334	AAW02334 Beta-amyl
147	26	89.7	8	7	ABW00134	ABW00134 Beta-amyl	220	26	89.7	15	2	AAW89358	AAW89358 Beta-amyl
148	26	89.7	8	8	ADJ64056	ADJ64056 Human bet	221	26	89.7	15	2	AAW89354	AAW89354 Beta-amyl
149	26	89.7	8	8	ADQ37385	ADQ37385 Antifibri	222	26	89.7	15	5	ABG71014	ABG71014 Long form
150	26	89.7	8	8	ADQ37349	ADQ37349 Beta-amyl	223	26	89.7	15	5	ABW05162	ABW05162 Beta amyl
151	26	89.7	8	9	ADZ08900	ADZ08900 Human bet	224	26	89.7	15	5	AAE26271	AAE26271 Human bet
152	26	89.7	8	9	AEA51423	AEA51423 C-Abeta 1	225	26	89.7	15	6	ABU79057	ABU79057 Aggregati
153	26	89.7	8	9	AEA51420	AEA51420 A 16-22-C	226	26	89.7	15	6	ABU79064	ABU79064 Aggregati
154	26	89.7	8	9	AEA62831	AEA62831 Immunoon	227	26	89.7	15	6	ABU79059	ABU79059 Aggregati
155	26	89.7	8	9	AEA62834	AEA62834 Immunoon	228	26	89.7	15	6	ABU79060	ABU79060 Aggregati
156	26	89.7	9	2	AA452359	AA452359 Mutant am	229	26	89.7	15	6	ABU79055	ABU79055 Aggregati
157	26	89.7	9	4	AA484893	AA484893 Antifibri	230	26	89.7	15	6	ABU79056	ABU79056 Aggregati
158	26	89.7	9	5	AAU11667	AAU11667 Peptide #	231	26	89.7	15	6	ABU79062	ABU79062 Aggregati
159	26	89.7	9	6	ABP57517	ABP57517 Different	232	26	89.7	15	6	ABU79061	ABU79061 Aggregati
160	26	89.7	9	6	ABU79063	ABU79063 Aggregati	233	26	89.7	15	7	ABW00190	ABW00190 Peptide #
161	26	89.7	9	6	AAE35436	AAE35436 Beta pep	234	26	89.7	15	7	ABW00198	ABW00198 Peptide #
162	26	89.7	9	7	ABW00197	ABW00197 Peptide #	235	26	89.7	15	7	ABW00189	ABW00189 Peptide #
163	26	89.7	9	8	ADI36003	ADI36003 Amyloid b	236	26	89.7	15	7	ABW00193	ABW00193 Peptide #
164	26	89.7	9	8	ADI35849	ADI35849 Amyloid b	237	26	89.7	15	7	ABW00191	ABW00191 Peptide #
165	26	89.7	9	8	ADI35874	ADI35874 Amyloid b	238	26	89.7	15	7	ABW00196	ABW00196 Peptide #
166	26	89.7	9	8	ADI35871	ADI35871 Amyloid b	239	26	89.7	15	7	ABW00195	ABW00195 Peptide #
167	26	89.7	9	8	ADI35903	ADI35903 Amyloid b	240	26	89.7	15	7	ABW00194	ABW00194 Peptide #
168	26	89.7	9	8	ADQ37260	ADQ37260 Vaccine a	241	26	89.7	15	7	ADK82695	ADK82695 Beta-amyl
169	26	89.7	9	8	ADQ37332	ADQ37332 Antifibri	242	26	89.7	15	7	ADK82697	ADK82697 Beta-amyl
170	26	89.7	9	9	AEA51414	AEA51414 A 16-23-C	243	26	89.7	15	7	ADK82700	ADK82700 Beta-amyl

244	26	89.7	15	7	ADK92698	Adk92698 Beta-amyl
245	26	89.7	15	7	ADK92699	Adk92699 Beta-amyl
246	26	89.7	15	8	ADJ71466	Adj71466 N-termina
247	26	89.7	15	8	ADJ71453	Adj71453 N-termina
248	26	89.7	15	8	ADJ71479	Adj71479 N-termina
249	26	89.7	15	8	ADJ71440	Adj71440 N-termina
250	26	89.7	15	8	ADJ64065	Adj64065 Human bet
251	26	89.7	16	5	AAE26330	AAE26330 Human bet
252	26	89.7	16	8	ADJ71454	Adj71454 N-termina
253	26	89.7	16	8	ADJ71480	Adj71480 N-termina
254	26	89.7	16	8	ADJ71441	Adj71441 N-termina
255	26	89.7	16	8	ADJ71467	Adj71467 N-termina
256	26	89.7	16	8	ADJ71428	Adj71428 N-termina
257	26	89.7	17	2	AAE54703	AAE54703 Beta-amyl
258	26	89.7	17	2	AAW18880	AAW18880 Beta-amyl
259	26	89.7	17	4	AAW18880	AAW18880 Beta-amyl
260	26	89.7	17	4	AAW18880	AAW18880 Beta-amyl
261	26	89.7	17	4	AAW18880	AAW18880 Beta-amyl
262	26	89.7	17	5	AAW18880	AAW18880 Beta-amyl
263	26	89.7	17	6	AAW18880	AAW18880 Beta-amyl
264	26	89.7	17	6	AAW18880	AAW18880 Beta-amyl
265	26	89.7	17	8	ADG93165	ADG93165 Novel exp
266	26	89.7	17	8	ADJ65843	ADJ65843 Amyloid B
267	26	89.7	17	8	ADN02827	ADN02827 Mammalian
268	26	89.7	17	8	ADQ37291	ADQ37291 Vaccine a
269	26	89.7	17	8	ADL18447	ADL18447 Amyloid-b
270	26	89.7	18	3	AAW10963	AAW10963 Beta-amyl
271	26	89.7	18	3	AAW18882	AAW18882 AEDANS-be
272	26	89.7	19	2	AAW18881	AAW18881 Txp-Beta-
273	26	89.7	19	3	AAW17935	AAW17935 Beta-amyl
274	26	89.7	19	4	AAW49097	AAW49097 Human amy
275	26	89.7	19	4	AAW46201	AAW46201 Human APP
276	26	89.7	19	8	ADU24440	ADU24440 Novel glu
277	26	89.7	19	8	ADU24442	ADU24442 Novel glu
278	26	89.7	19	8	ADU46714	ADU46714 Amyloid b
279	26	89.7	19	8	ADU46716	ADU46716 Gln3 amyl
280	26	89.7	19	9	ADZ71366	ADZ71366 Human bet
281	26	89.7	19	9	ADZ71368	ADZ71368 Human bet
282	26	89.7	19	9	AEA35401	AEA35401 Novel QC
283	26	89.7	19	9	AEA35399	AEA35399 Novel QC
284	26	89.7	19	9	AEB92572	AEB92572 Glutamin
285	26	89.7	19	9	AEB92574	AEB92574 Glutamin
286	26	89.7	20	3	AAW79334	AAW79334 Beta-amyl
287	26	89.7	20	5	ABW06431	ABW06431 Beta-secr
288	26	89.7	20	6	ABW1876	ABW1876 P. papata
289	26	89.7	21	2	AAW30941	AAW30941 Human sec
290	26	89.7	21	8	ADU24439	ADU24439 Novel glu
291	26	89.7	21	8	ADU46713	ADU46713 Amyloid b
292	26	89.7	21	9	ADV86872	ADV86872 Beta-amyl
293	26	89.7	21	9	ADZ71365	ADZ71365 Human bet
294	26	89.7	21	9	AEA35398	AEA35398 Novel QC
295	26	89.7	21	9	AEB92571	AEB92571 Glutamin
296	26	89.7	22	2	ADR83670	ADR83670 Amyloidog
297	26	89.7	22	2	AAW52569	AAW52569 Alzheimer
298	26	89.7	24	9	ADW88085	ADW88085 T688 phos
299	26	89.7	24	9	AEW09195	AEW09195 Human bet
300	26	89.7	24	9	AEW09194	AEW09194 Human bet

ALIGNMENTS

RESULT 1  
 ID AAB48482 standard; peptide; 6 AA.  
 AC AAB48482;  
 XX  
 XX  
 DT 02-MAR-2001 (first entry)  
 DE Antifibrillogenic peptide #9.  
 XX  
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 XX Homo sapiens.  
 OS  
 PN WO200068263-A2.  
 XX  
 PD 16-NOV-2000.  
 XX  
 PF 04-MAY-2000; 2000WO-CA000515.  
 XX  
 PR 05-MAY-1999; 99US-0132592P.  
 XX  
 PA (NEUR-) NEUROCHEM INC.  
 XX  
 PI Chalfour R, Gervais F, Gupta A;  
 WPI; 2001-031852/04.  
 DR  
 PS Claim 7; Page 25; 46pp; English.  
 XX  
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein  
 CC  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 |||||  
 Db 1 KVVFFA 6  
 RESULT 2  
 AAB48490  
 ID AAB48490 standard; peptide; 6 AA.  
 XX  
 AC AAB48490;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Antifibrillogenic peptide #17.  
 XX  
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 6  
 FT /note= "C-terminal amide"  
 XX  
 PN WO200068263-A2.  
 XX  
 PD 16-NOV-2000.  
 XX  
 PF 04-MAY-2000; 2000WO-CA000515.  
 XX  
 PR 05-MAY-1999; 99US-0132592P.  
 XX  
 PA (NEUR-) NEUROCHEM INC.

XX PI Chalifour R, Gervais F, Gupta A;  
 XX DR WPI; 2001-031852/04.  
 XX PS Claim 7; Page 25; 46pp; English.  
 XX CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein  
 XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1 KVVFFA 6  
 RESULT 3  
 AAB82630  
 ID AAB82630 standard; peptide; 6 AA.  
 XX AC AAB82630;  
 XX DT 02-OCT-2001 (first entry)  
 XX DE All-D peptide used in Alzheimer's disease vaccine.  
 XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 1..6 /note= "all D-form residues"  
 FT Modified-site 6  
 XX PN WO200139796-A2.  
 XX PD 07-JUN-2001.  
 XX PF 29-NOV-2000; 2000WO-CA001413.  
 XX PR 29-NOV-1999; 99US-0168594P.  
 XX PR 28-NOV-2000; 2000US-00724842.  
 XX PA (NEUR-) NEUROCHEM INC.  
 XX PI Chalifour R, Hebert L, Kong X, Gervais F;  
 XX DR WPI; 2001-441458/47.  
 XX PT Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT which elicits production of antibodies to prevent fibrillogenesis and  
 PT associated cellular toxicity.  
 XX PS Disclosure; Page 11; 31pp; English.  
 XX CC The present sequence is that of an all-D peptide suitable for use for  
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self',  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients  
 XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1 KVVFFA 6  
 RESULT 4  
 AAB82638  
 ID AAB82638 standard; peptide; 6 AA.  
 XX AC AAB82638;  
 XX DT 02-OCT-2001 (first entry)  
 XX DE All-D peptide used in Alzheimer's disease vaccine.  
 XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 1..6 /note= "all D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"  
 XX PN WO200139796-A2.  
 XX PD 07-JUN-2001.  
 XX PF 29-NOV-2000; 2000WO-CA001413.  
 XX PR 29-NOV-1999; 99US-0168594P.  
 XX PR 28-NOV-2000; 2000US-00724842.  
 XX PA (NEUR-) NEUROCHEM INC.  
 XX PI Chalifour R, Hebert L, Kong X, Gervais F;  
 XX DR WPI; 2001-441458/47.  
 XX PT Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and  
 FT associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in  
 CC preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see A882622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in A882623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6  
 Db | | | | |  
 1 KVVFPA 6

RESULT 5  
 AAU96818  
 ID AAU96818 standard; peptide; 6 AA.

XX

AC AAU96818;

XX

DT 30-JUL-2002 (first entry)

XX

DE Amyloid targeting peptide #8.

XX

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

XX Synthetic.

OS

XX Key Location/Qualifiers

XX

FT Misc-difference 1. .6 /note= "Preferably D-form residue"

XX

FN WO200207781-A2.

XX

XX 31-JAN-2002.

XX

XX 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.  
 XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 FT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A-(A<sub>1</sub>)<sub>n</sub>-K-(A<sub>2</sub>)<sub>m</sub> where z = 0 - 1;  
 CC A<sub>1</sub> = an amyloid targeting moiety; A<sub>1</sub><sub>n</sub>-K = a linker moiety; and A<sub>2</sub><sub>m</sub> =  
 CC a labelling moiety. Also included are imaging amyloid deposition or  
 CC diagnosing an amyloid-related condition in a patient involving  
 CC administering (I) to the patient, and ultrasound imaging (I) in the  
 CC patient to determine the presence of amyloid or amyloid-related condition  
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising  
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and  
 CC instructions for the preparation and use of the radiopharmaceutical in  
 CC the imaging of amyloid or an amyloid-related condition. The agents are  
 CC used for imaging amyloid deposition and for diagnosing an amyloid related  
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible  
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6  
 Db | | | | |  
 1 KVVFPA 6

RESULT 6  
 AAU96826  
 ID AAU96826 standard; peptide; 6 AA.

XX

AC AAU96826;

XX

DT 30-JUL-2002 (first entry)

XX

DE Amyloid targeting peptide #16.

XX

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementia;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

XX Synthetic.

OS

XX Key Location/Qualifiers

XX Misc-difference 1. .6

```

FT FT /note= "Preferably D-form residue"
FT Modified-site 6
FT FT /note= "Ala is amidated"
XX PN WO200207781-A2.
XX PD 31-JAN-2002.
XX XX
XX XX 25-JUL-2001; 2001WO-CA001071.
XX PF
XX PR 25-JUL-2000; 2000US-0220808P.
XX PR 24-JUL-2001; 2001US-00915092.
XX XX
XX PA (NEUR-) NEUROCHEM INC.
XX XX
XX PI Gervais F, Kong X, Chalifour R, Migneault D;
XX XX WPI; 2002-371447/40.
XX XX
XX XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX FT plaques and/or for the treatment of amyloidosis disorders.
XX FT
XX PS Claim 49; Page 21; 57pp; English.
XX XX
XX CC The invention relates to an amyloid-targeting imaging agent comprising an
XX CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX CC agent is of general formula A-t-(A-1)n-k z-A-1 a-b (t) where z = 0 - 1;
XX CC A-t = an amyloid targeting moiety; A-1-n-k = a linker moiety; and A-1-a-b
XX CC = a labelling moiety. Also included are imaging amyloid deposition or
XX CC diagnosing an amyloid-related condition in a patient involving
XX CC administering (I) to the patient, and ultrasound imaging (I) in the
XX CC patient to determine the presence of amyloid or amyloid-related condition
XX CC ; and a kit for preparing a radiopharmaceutical preparation comprising
XX CC (I), a reducing agent, a buffering agent, a transchelating agent, and
XX CC instructions for the preparation and use of the radiopharmaceutical in
XX CC the imaging of amyloid or an amyloid-related condition. The agents are
XX CC used for imaging amyloid deposition and for diagnosing an amyloid related
XX CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX CC cerebral amyloidoses (transmissible virus dementia), familial CJD,
XX CC scrapie, transmissible mink encephalopathy, bovine spongiform
XX CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX CC amyloid angiopathy. The agents are capable of crossing the blood-brain
XX CC barrier and are capable of binding specifically to amyloid plaques. The
XX CC present sequence is a peptide forming the amyloid targeting moiety of the
XX CC agent of the invention
XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 1 KVVFFA 6

RESULT 7
AAU11664
ID AAU11664 standard; peptide; 6 AA.
XX AC AAU11664;
XX XX
XX DT 09-APR-2002 (first entry)
XX DE Peptide #17, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 1 KVVFFA 6

RESULT 8
AAU11656
ID AAU11656 standard; peptide; 6 AA.
XX AC AAU11656;
XX XX
XX DT 09-APR-2002 (first entry)
XX DE Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX OS Synthetic.
XX PN WO200185093-A2.
XX PD 15-NOV-2001.
XX PF 22-DEC-2000; 2000WO-IB002078.
XX PR 23-DEC-1999; 99US-0171877P.
XX XX
XX PA (NEUR-) NEUROCHEM INC.
XX XX
XX PI Green AM, Gervais F;
XX XX WPI; 2002-075222/10.
XX XX
XX XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX FT disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX FT inhibitor.
XX XX
XX XX Disclosure; Page 10; 68pp; English.
XX PS The present invention relates to a new method of inhibiting cerebral
XX CC amyloid angiopathy. The new method of the invention involves contacting a
XX CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX CC can be used for treating disease states characterised by cerebral amyloid
XX CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX CC The present sequence represents one of a group of peptides (AAU11648-
XX CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX CC was used in the invention to treat a disease state characterised by
XX CC cerebral amyloid angiopathy (CAA)
XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 1 KVVFFA 6

RESULT 8
AAU11656
ID AAU11656 standard; peptide; 6 AA.
XX AC AAU11656;
XX XX
XX DT 09-APR-2002 (first entry)
XX DE Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX OS Synthetic.
XX PN WO200185093-A2.
XX PD 15-NOV-2001.
XX PF 22-DEC-2000; 2000WO-IB002078.
XX PR 23-DEC-1999; 99US-0171877P.

```

XX PA (NEUR-) NEUROCHEM INC.  
 XX FI Green AM, Gervais F;  
 XX XX WPI; 2002-075222/10.  
 XX XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40  
 PT inhibitor.  
 XX XX Disclosure; Page 10; 68pp; English.  
 XX XX The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting a  
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
 CC The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)  
 XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVVFFFA 6  
 Db 1 KVVFFFA 6  
 RESULT 9  
 AAE35452  
 ID AAE35452 standard; peptide; 6 AA.  
 AC AAE35452;  
 DT 17-JUN-2003 (first entry)  
 DE Abeta peptide #23.  
 KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.  
 XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 1. .6  
 FT /note= "D-form residues"  
 FT Modified-site 6  
 FT /note= "C-terminal amide"  
 XX WO200296937-A2.  
 XX PD 05-DEC-2002.  
 XX 29-MAY-2002; 2002WO-CA000763.  
 XX 29-MAY-2001; 2001US-00867847.  
 XX (NEUR-) NEUROCHEM INC.  
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.  
 XX Prevention and/or treatment of an amyloid-related disease e.g.  
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.  
 XX Claim 1; Page 59; 44pp; English.  
 XX The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 XX invention  
 XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 29; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVVFFFA 6  
 Db 1 KVVFFFA 6  
 RESULT 10  
 ADQ37277  
 ID ADQ37277 standard; peptide; 6 AA.  
 XX ADQ37277;  
 AC ADQ37277;  
 XX 07-OCT-2004 (first entry)  
 XX Vaccine antigen amyloid-beta related amino acid sequence.  
 DE  
 XX amyloid-beta, amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; nontropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antichytoid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 1. .6  
 FT /note= "D-form residues"  
 FT Modified-site 6  
 FT /note= "amidated"  
 XX

PN	WO2004058239-A1.	ID	ADQ37321 standard; peptide; 6 AA.
XX	15-JUL-2004.	XX	ADQ37321;
XX	24-DEC-2003; 2003WO-CA002021.	XX	07-OCT-2004 (first entry)
XX	24-DEC-2002; 2002US-0436379P.	XX	Antifibrillogenic amyloidosis inhibiting peptide.
PR	23-JUN-2003; 2003US-0482214P.	DE	
XX	(NEUR-) NEUROCHEM INT LTD.	XX	amyloid-beta; amyloid-beta related disease;
PA		KW	amyloid-beta fibril formation; immune response; nootropic;
XX		KW	neuroprotective; cerebroprotective; haemostatic; ophthalmological;
PI	Gervais F, Bellini F;	KW	antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;
XX		KW	anticongulant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
XX		KW	cardiant; antidepressant; endocrine; hypnotic;
XX		KW	amyloid-beta fibril formation modulator; immune system modulator;
DR	WPI; 2004-543342/52.	KW	Alzheimer's disease; mild cognitive impairment;
XX		KW	mild-to-moderate cognitive impairment; vascular dementia;
PT	Composition for treating e.g. Alzheimer's disease comprises first agent	KW	cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
PT	that prevents or treats amyloid-beta related disease and second agent	KW	senile dementia; Down's syndrome; inclusion body myositis;
PT	that is either a peptide or peptidomimetic or an immune system modulator.	KW	age-related macular degeneration; hypothyroidism;
XX		KW	cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
PS	Disclosure; Page 67; 143pp; English.	KW	behavioural dysfunction; neurological condition; psychological condition;
XX		XX	vaccine antigen.
CC	The present invention describes compositions (C) comprising: (a) a first	OS	Synthetic.
CC	agent (a1) that prevents or treats amyloid-beta related disease; and (b)	PN	WO2004058239-A1.
CC	a second agent (a2) that is: (i) a peptide or peptidomimetic that	PD	15-JUL-2004.
CC	modulates amyloid-beta fibril formation or induces a prophylactic or	XX	
CC	therapeutic immune response against amyloid-beta fibril formation; or	XX	24-DEC-2003; 2003WO-CA002021.
CC	(ii) an immune system modulator that prevents or inhibits amyloid-beta	PR	24-DEC-2002; 2002US-0436379P.
CC	fibril formation. Also described is a kit comprising (C). (C) have	PR	23-JUN-2003; 2003US-0482214P.
CC	nootropic, neuroprotective, cerebroprotective, haemostatic,	XX	(NEUR-) NEUROCHEM INT LTD.
CC	ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,	XX	
CC	urophathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,	PI	Gervais F, Bellini F;
CC	neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,	XX	
CC	and can be used as amyloid-beta fibril formation modulators, and as	XX	WPI; 2004-543342/52.
CC	immune system modulators. (C) can be used for preventing or treating an	XX	
CC	amyloid-beta related disease e.g. Alzheimer's disease (including sporadic	XX	Composition for treating e.g. Alzheimer's disease comprises first agent
CC	mild-to-moderate cognitive impairment, vascular dementia, cerebral	PT	that prevents or treats amyloid-beta related disease and second agent
CC	Down's syndrome, inclusion body myositis, age-related macular	PT	that is either a peptide or peptidomimetic or an immune system modulator.
CC	degeneration, or a condition associated with Alzheimer's disease	PS	
CC	(including hypothyroidism, cerebrovascular disease, cardiovascular	XX	
CC	disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,	XX	
CC	aggression, or incontinence), a neurological condition (e.g. Huntington's	XX	
CC	disease, amyotrophic lateral sclerosis, acquired immunodeficiency,	XX	
CC	Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia	XX	
CC	with Lewy bodies, altered muscle tone, seizures, sensory loss, visual	XX	
CC	field deficits, incoordination, gait disturbance, transient ischaemic	XX	
CC	attack or stroke, transient alertness, attention deficit, frequent falls,	XX	
CC	syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural	XX	
CC	haematoma, brain tumour, posttraumatic brain injury, or posthypoxic	XX	
CC	damage), or a psychological condition (e.g. depression, delusions,	XX	
CC	illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep	XX	
CC	disturbance, insomnia, behavioural disinhibition, poor insight, suicidal	XX	
CC	ideation, depressed mood, irritability, anhedonia, social withdrawal, or	XX	
CC	excessive guilt)) in a subject e.g. human having a genomic mutation in an	XX	
CC	amyloid precursor protein gene, an ApoE gene, or a presenilin gene;	XX	
CC	having amyloid-beta deposits. The present sequence represents a peptide	XX	
CC	that can be used as a vaccine antigen in the exemplification of the	XX	
CC	present invention.	XX	
XX		XX	
SQ	Sequence 6 AA;	XX	
	Query Match 100.0%; Score 29; DB 8; Length 6;		
	Best Local Similarity 100.0%; Pred. No. 2e+06;		
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KVVFFA 6		
Db	1 KVVFFA 6		
RESULT 11			
ADQ37321			



CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 1 KVVFFA 6

RESULT 12

ADQ37329  
 ID ADQ37329 standard; peptide; 6 AA.

XX AC ADQ37329;

XX DT 07-OCT-2004 (first entry)

XX DE Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antihypertensive; vasotropic; cardiovascular; tranquiliser; uterine;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiac; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.

XX OS Synthetic.

XX FT Key Location/Qualifiers

XX FT Modified-site 6 /note= "amidated"

XX FN WO2004058239-A1.

XX PD 15-JUL-2004.

XX PF 24-DEC-2003; 2003WO-CA002021.

XX PR 24-DEC-2003; 2002US-0436379P.

XX PR 23-JUN-2003; 2003US-0482214P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Bellini F;

XX DR WPI; 2004-543342/52.

XX FT Composition for treating e.g. Alzheimer's disease comprises first agent

XX that prevents or treats amyloid-beta related disease and second agent

PT that is either a peptide or peptidomimetic or an immune system modulator.  
 XX Disclosure; Page 70; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,  
 CC uterine, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiac, antidepressant, endocrine and hypotonic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |||||  
 Db 1 KVVFFA 6

RESULT 13

ADY37928

ID ADY37928 standard; peptide; 6 AA.

XX AC ADY37928;

XX DT 19-MAY-2005 (first entry)

XX DE Amyloid-targeting peptide, SEQ ID NO:8, for use in imaging agent.

XX diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 KW transmissible spongiform encephalopathy; scrapie; BSE;  
 KW Alzheimer's disease; neurological disease; amyloidosis;  
 KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX FN US2005048000-A1.



PD 03-MAR-2005.  
 XX 03-DEC-2003; 2003US-00728028.  
 XX 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.  
 PR 29-JAN-2003; 2003US-0443291P.  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX Gervais F, Kong X, Chalifour R, Migneault D;  
 XX WPI; 2005-212201/22.  
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 PT related condition, e.g. Creutzfeldt-Jakob disease, bovine spongiform  
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.  
 XX Disclosure; SEQ ID NO 8; 34pp; English.  
 XX The invention relates to an amyloid-targeting imaging agent. The imaging  
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 CC a labeling moiety via a linking moiety, and is preferably able to cross  
 CC the blood-brain barrier. The invention also relates to a kit for  
 CC preparing a radiopharmaceutical preparation from the imaging agent of the  
 CC invention, a method for imaging amyloid deposition in a patient and a  
 CC method for diagnosing an amyloid-related condition in a patient. The  
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 CC related conditions such as Creutzfeldt-Jakob disease (CJD), Kuru,  
 CC transmissible cerebral amyloidosis (also known as transmissible virus  
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 CC mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.  
 XX Sequence 6 AA;  
 SQ Query Match 100.0%; Score 29; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1 KVVFFA 6  
 RESULT 14  
 ID ADY37936 standard; peptide; 6 AA.  
 XX ADY37936;  
 AC ADY37936;  
 XX 19-MAY-2005 (first entry)  
 XX Amyloid-targeting peptide, SEQ ID NO:16, for use in imaging agent.  
 XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
 XX transmissible spongiform encephalopathy; scrapie; BSE;  
 XX Alzheimers disease; neurological disease; amyloidosis;  
 XX non-insulin dependent diabetes; metabolic disorder.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FH Modified-site 6  
 FT

FT XX /note= "C-terminal amide"  
 XX PN US2005048000-A1.  
 XX PD 03-MAR-2005.  
 XX PF 03-DEC-2003; 2003US-00728028.  
 XX PR 25-JUL-2000; 2000US-0220808P.  
 PR 24-JUL-2001; 2001US-00915092.  
 PR 29-JAN-2003; 2003US-0443291P.  
 XX (NEUR-) NEUROCHEM INT LTD.  
 XX Gervais F, Kong X, Chalifour R, Migneault D;  
 XX WPI; 2005-212201/22.  
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-  
 PT related condition, e.g. Creutzfeldt-Jakob disease, bovine spongiform  
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.  
 XX Disclosure; SEQ ID NO 16; 34pp; English.  
 XX The invention relates to an amyloid-targeting imaging agent. The imaging  
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to  
 CC a labeling moiety via a linking moiety, and is preferably able to cross  
 CC the blood-brain barrier. The invention also relates to a kit for  
 CC preparing a radiopharmaceutical preparation from the imaging agent of the  
 CC invention, a method for imaging amyloid deposition in a patient and a  
 CC method for diagnosing an amyloid-related condition in a patient. The  
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-  
 CC related conditions such as Creutzfeldt-Jakob disease (CJD), Kuru,  
 CC transmissible cerebral amyloidosis (also known as transmissible virus  
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-  
 CC mediated diseases, dialysis-related amyloidosis, light chain-related  
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a  
 CC patient. The agent does not exhibit excessive toxicity or irritation,  
 CC does not induce an allergic response, and permits an earlier diagnosis of  
 CC amyloid-related conditions, thereby allowing earlier treatment and hence  
 CC prevention of the undesirable effects of such disorders. Sequences  
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as  
 CC the amyloid-targeting moiety in an imaging agent of the invention.  
 XX Sequence 6 AA;  
 SQ Query Match 100.0%; Score 29; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1 KVVFFA 6  
 RESULT 15  
 ID ADQ09761 standard; peptide; 22 AA.  
 XX ADQ09761;  
 AC ADQ09761;  
 XX 23-SEP-2004 (first entry)  
 XX Rice 26kDa globulin signal sequence SEQ ID NO:117.  
 XX prolamine; rice; plant; seed; transgenic plant; signal.  
 XX Oryza sativa.  
 XX WO2004056993-A1.  
 FN

XX PD 08-JUL-2004.  
 XX PF 09-DEC-2003; 2003WO-JP015753.  
 XX PR 20-DEC-2002; 2002JP-00369700.  
 XX PA (NAG-) NAT AGRIC & BIO-ORIENTED RES ORG.  
 XX PI Kuroda M;  
 XX DR WPI; 2004-525439/50.  
 XX DR N-PSDB; ADQ09760.  
 XX PT Novel nucleic acid molecule antisense to nucleic acid sequence encoding  
 PT prolamine, useful for reducing expression dose of protein in seed, and  
 PT for producing transgenic plant, preferably rice plant having reduced  
 PT storage protein.  
 XX Example 13; SEQ ID NO 117; 272pp; Japanese.  
 XX The present invention describes a nucleic acid molecule (I) comprising a  
 CC consecutive nucleic acid sequence (S1) of at least 15 bp in length and  
 CC complementary with a nucleic acid sequence encoding a prolamine  
 CC polypeptide or a nucleic acid sequence having a homology of at least  
 CC about 70% to (S1). Also described: (1) a nucleic acid molecule (NI)  
 CC comprising a nucleic acid sequence (A) having about 70% homology to a  
 CC nucleic acid sequence encoding a prolamine polypeptide and a nucleic acid  
 CC sequence (B) having about 70% homology to the complement of the nucleic  
 CC acid sequence encoding a prolamine polypeptide; (2) a factor (II) capable  
 CC of causing RNA interference of the gene sequence encoding a prolamine  
 CC polypeptide; (3) a nucleic acid cassette (III) containing (1); (4)  
 CC producing (III); (5) a vector (IV) comprising (1); (6) a plant cell (V)  
 CC containing (1) or (7); (9) a plant tissue (VI) comprising (V); (8) a plant (VII)  
 CC preparation produced from (VII) or (VIII); and (11) a composition  
 CC containing gene product of foreign gene produced from (VII) or (VIII).  
 CC (I) is useful for decreasing the expression level of a protein in the  
 CC seed of a plant, for expressing a foreign gene in the seed of a plant and  
 CC for decreasing the expression of a natural protein in the seed of a  
 CC plant. The method of decreasing the amount of expression level of a  
 CC protein in the seed of a plant involves providing (I), introducing (I)  
 CC into the cell of the plant, redifferentiating the cell, producing a  
 CC transgenic plant, and obtaining the seed from the transgenic plant. The  
 CC method after the step of introduction, further involves selecting the  
 CC cell introduced with (I), by determining resistance with respect to  
 CC antibiotics. The method of expressing a foreign gene in the seed of a  
 CC plant, involves providing (I) and the nucleic acid molecule encoding a  
 CC foreign gene product, introducing (I) and the nucleic acid molecule  
 CC encoding a foreign gene product into cell of the plant, re-  
 CC differentiating the cell, producing a transgenic plant, and obtaining the  
 CC seed from the transgenic plant. The method further involves isolating the  
 CC gene product of the foreign gene from the seed. (I) is useful for  
 CC producing transgenic plants having reduced expression of storage proteins  
 CC and for reducing the expression dose of a protein in a seed of a plant.  
 CC The present sequence represents a rice 26kDa globulin signal sequence,  
 CC which is used in the exemplification of the present invention.

Sequence 22 AA;

Query Match 100.0%; Score 29; DB 8; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 Db |||||  
 4 KVVFFA 9

RESULT 16  
 ADT93984  
 ID ADT93984 standard; peptide; 23 AA.  
 XX

AC ADT93984;  
 XX 27-JAN-2005 (first entry)  
 DT XX Rice 26 kDa peptide.  
 DE XX Storage protein; allergen specific T cell epitope;  
 XX vesicle anchoring signal; transgenic plant; rice albumen;  
 KW T cell epitope-attached peptide; 7crp; seed; glutelin; edible vaccine;  
 KW Japanese cedar pollen antigen; Cryj1; Cryj2; allergic disease; hay fever;  
 KW antiallergic; plant; 26 kDa.  
 XX Oryza sativa.  
 OS WO2004094637-A1.  
 XX 04-NOV-2004.  
 PD 23-APR-2004; 2004WO-JP005938.  
 PF 24-APR-2003; 2003JP-00120639.  
 PR (NORQ) NAT INST AGROBIOLOGICAL SCI.  
 XX Takaiwa F, Takagi H;  
 PI WPI; 2004-784905/77.  
 DR Novel DNA having sequence encoding allergen specific T-cell epitope  
 XX peptide, useful for accumulating T-cell epitope peptide in plants and for  
 PT treating allergic diseases such as pollinosis.  
 PT Disclosure; SEQ ID NO 5; 79pp; Japanese.

XX This invention relates to a DNA (I) having a sequence under the control  
 CC of a storage protein promoter, chosen from a sequence encoding storage  
 CC protein signal sequence at the 5' end of a sequence encoding allergen  
 CC specific T cell epitope peptide and/or a sequence encoding vesicle  
 CC anchoring signal sequence at the 3' end, and a DNA sequence encoding a  
 CC polypeptide having allergen specific T-cell epitope peptide inserted in  
 CC the variable region of a storage protein. Also disclosed is a vector (II)  
 CC for T-cell epitope accumulated plant preparation, and a method of  
 CC accumulating allergen specific T-cell epitope in a plant. The method  
 CC involves introducing (I) or (II) to a plant, obtaining DNA encoding  
 CC allergen specific T-cell epitope peptide, adding a DNA encoding a storage  
 CC protein signal sequence to the 5' end and/or a vesicle anchoring signal  
 CC sequence to the 3' end of the obtained DNA, and expressing the DNA in a  
 CC plant under the control of a storage protein promoter, or obtaining DNA  
 CC encoding allergen specific T-cell epitope peptide, inserting a DNA into  
 CC the variable region of storage protein of the plant and expressing the  
 CC peptide in the transgenic plant. The invention describes the accumulation  
 CC of human T cell epitope in rice albumen, a method of accumulating T cell  
 CC epitope-attached peptide (7crp) in seeds, a method of inserting the 7crp  
 CC into the variable region of glutelin (the major storage protein of rice),  
 CC and expressing and accumulating 7crp as part of the glutelin. The rice  
 CC capable of producing the 7crp is useful as an edible vaccine against  
 CC Japanese (Cryptomeria japonica) cedar pollen antigen. The pollen allergen  
 CC is Cryj1 or Cryj2. The T-cell epitope is integrated on an edible region  
 CC such as the seed of a plant. The method of the invention is useful for  
 CC producing a plant accumulated with allergen specific T-cell epitope, and  
 CC manufacturing a transgenic plant, preferably rice, integrated with T-cell  
 CC epitope. The method is useful for preventing or treating allergic disease  
 CC such as hay fever. The method enables the production of allergen specific  
 CC T-cell epitope at a low cost and also reduces the amount for  
 CC administration. The allergen specific T-cell epitope accumulated in a  
 CC seed is stable for storage. This sequence represents rice 26 kDa peptide.

Sequence 23 AA;

Query Match 100.0%; Score 29; DB 8; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 DB 4 KVVFFA 9

RESULT 17  
 AAB05910  
 ID AAB05910 standard; peptide; 37 AA.  
 XX  
 AC AAB05910;  
 XX  
 DT 16-OCT-2000 (first entry)  
 XX  
 DE Mouse inducible nitric oxide synthase calmodulin-binding region.  
 XX  
 KW Mouse; inducible nitric oxide synthase; iNOS;  
 KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;  
 KW AMP-activated protein kinase; AMPK; calmodulin; CaM;  
 KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;  
 KW obstructive airways disease.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200028076-A1.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PF 05-NOV-1999; 99WO-AU000968.  
 XX  
 PR 06-NOV-1998; 98AU-00006976.  
 XX  
 PA (SVIN-) ST VINCENTS INST MEDICAL RES.  
 XX  
 PI Stapleton DI, Chen Z, Michell BJ, Kemp BE, Mitchellhill KT;  
 XX  
 DR WPI; 2000-376583/32.  
 XX  
 PT Identifying modulators of AMP-activated protein kinase-mediated  
 PT activation of a nitric oxide synthase (NOS), for use in ischemic heart  
 PT disease, comprises testing for the increase or decrease in  
 PT phosphorylation of NOS.  
 XX  
 PS Example 4; Fig 5; 4lpp; English.  
 XX  
 CC The present sequence is the calmodulin (CaM)-binding region of mouse  
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of  
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-  
 CC arginine. The sequence is provided for comparison with endothelial nitric  
 CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is  
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of  
 CC Ca2+-CaM. Phosphorylation results in inhibition of eNOS. In the presence  
 CC of Ca2+-CaM, phosphorylation by AMPK occurs predominantly at Ser-117 and  
 CC eNOS is activated. Modulators which activate AMPK may be used in the  
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid  
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.  
 CC They may also be used for the treatment of pulmonary hypertension and  
 CC obstructive airways disease  
 XX  
 SQ Sequence 37 AA;  
 Query Match 100.0%; Score 29; DB 3; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 DB 18 KVVFFA 23

RESULT 18  
 ADK34080  
 ID ADK34080 standard; peptide; 37 AA.  
 XX

AC ADK34080;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human nNOS calmodulin binding domain peptide seqid 7.  
 XX  
 KW vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;  
 KW eNOS; endothelial nitric oxide synthase; angiogenesis;  
 KW microvascular dysfunction; human; calmodulin binding domain;  
 KW neuronal nitric oxide; nNOS.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004016761-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 15-AUG-2003; 2003WO-US025626.  
 XX  
 PR 16-AUG-2002; 2002US-0403637P.  
 XX  
 PA (SCHD ) SCHERING AG.  
 XX  
 PI Dole WP, Kauser K, Qian HS, Rubanyi G;  
 XX  
 DR WPI; 2004-203789/19.  
 XX  
 PT Treating critical limb ischemia (CLI), or angiogenesis comprises  
 PT administering to a patient a polynucleotide encoding a mammalian  
 PT endothelial nitric oxide synthase (eNOS) polypeptide.  
 XX  
 PS Example 1; SEQ ID NO 7; 82pp; English.  
 XX  
 CC The invention describes a method of creating critical limb ischaemia  
 CC (CLI) comprising administering to a patient a polynucleotide encoding a  
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also  
 CC described are: a method for treating angiogenesis by administering to a  
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular  
 CC dysfunction by administering to the patient the polynucleotide encoding  
 CC the eNOS polypeptide. The method is useful for treating critical limb  
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.  
 CC This is the amino acid sequence of a human neuronal nitric synthase  
 CC (nNOS) calmodulin binding domain peptide.  
 XX  
 SQ Sequence 37 AA;  
 Query Match 100.0%; Score 29; DB 8; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 DB 18 KVVFFA 23

RESULT 19  
 ADL70727  
 ID ADL70727 standard; peptide; 37 AA.  
 XX  
 AC ADL70727;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Mouse iNOS calmodulin-binding site amino acid sequence SEQ ID NO:7.  
 XX  
 KW mouse; endothelial nitric oxide synthase; eNOS; enzyme; mutant;  
 KW calmodulin-binding domain; vasotropic; antiarteriosclerotic; hypotensive;  
 KW antidiabetic; vulnery; antilipemic; anorectic;  
 KW reduced calcium dependence; ischaemia; atherosclerosis; hypertension;  
 KW diabetes; Raynaud's phenomenon; poor wound healing; hyperlipidaemia;  
 KW obesity; iNOS.  
 XX  
 OS Mus musculus.

```

XX WO2004016764-A2.
XX 26-FEB-2004.
XX 15-AUG-2003; 2003WO-US025745.
XX 16-AUG-2002; 2002US-0403638P.
XX (SCHD ) SCHERING AG.
XX Blasko E, Kauser K, Parkinson J;
XX WPI; 2004-203792/19.
XX
XX New isolated endothelial nitric oxide synthase polypeptide mutant, useful
XX for diagnosing or treating ischemia, atherosclerosis, hypertension,
XX diabetes, Raynaud's phenomenon, poor wound healing, hyperlipidemia or
XX obesity.
XX
XX Example 1; SEQ ID NO 7; 57pp; English.
XX
XX The present sequence represents the calmodulin-binding site of mouse iNOS
XX amino acid sequence. The present invention describes endothelial nitric
XX oxide synthase (eNOS) mutants having one or more mutations in an amino
XX acid sequence corresponding to a functional domain of a mammalian eNOS.
XX At least one of the mutations is at a position corresponding to an amino
XX acid residue in a calmodulin-binding domain that is phosphorylated in
XX mammalian cells, and not an amino acid substitution to Ala or Asp. Also
XX described: (1) an isolated eNOS polypeptide mutant that is substantially
XX homologous, or has a 95-99% sequence identity to the amino acid sequence
XX of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide
XX encoding the polypeptide mutant; (3) a recombinant vector comprising the
XX polynucleotide operably linked to at least one regulatory sequence; (4) a
XX pharmaceutical composition comprising the polypeptide mutant or the
XX polynucleotide; (5) a binding partner of the polypeptide mutant; (6)
XX modulating eNOS activity in a cell by administering to the cell the
XX polypeptide mutant; (7) modulating eNOS activity in a cell by
XX administering the polypeptide mutant or the polynucleotide to the cell,
XX such that the polypeptide mutant is expressed in the cell; (8) diagnosing
XX a condition associated with aberrant eNOS activity by contacting a cell
XX of a patient with the polynucleotide, and detecting a level of eNOS
XX activity indicative of the medical condition; and (9) prophylactic and
XX therapeutic methods of treating a condition associated with aberrant eNOS
XX activity by administering the polypeptide mutant or polynucleotide to the
XX patient. The eNOS mutant has vasotropic, antiarteriosclerotic,
XX hypotensive, antidiabetic, vulnary, antilipemic and anorectic
XX activities, and has reduced calcium dependence and increased activity.
XX The polypeptide mutant, polynucleotide and methods are useful for
XX diagnosing or treating a condition associated with aberrant eNOS
XX activity, e.g. ischaemia, atherosclerosis, hypertension, diabetes,
XX Raynaud's phenomenon, poor wound healing, hyperlipidaemia or obesity.
XX
XX Sequence 37 AA;
XX
XX Query Match 100.0%; Score 29; DB 8; Length 37;
XX Best Local Similarity 100.0%; Pred. No. 22;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KVVFFA 6
XX Db 18 KVVFFA 23
XX
XX RESULT 20
XX ARG02840
XX ID ARG02840 standard; protein; 77 AA.
XX AC
XX AAG02840;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein, SEQ ID NO: 6921.
XX

```

---

```

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000BP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX N-PSDB; AAC02846.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 13; SEQ ID NO 6921; 71pp + Sequence Listing; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number of
XX 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX tissues. EST sequences usually correspond mainly to the 3' untranslated
XX region (UTR) of the mRNA because they are often obtained from oligo-dT
XX primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX sequences derived from the 5' ends of mRNAs and even in those cases where
XX longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX are also used in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures. They are used to obtain upstream regulatory sequences
XX and to design expression and secretion vectors
XX
XX Sequence 77 AA;
XX
XX Query Match 100.0%; Score 29; DB 3; Length 77;
XX Best Local Similarity 100.0%; Pred. No. 46;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KVVFFA 6
XX Db 38 KVVFFA 43
XX
XX RESULT 21
XX AAO11219
XX ID AAO11219 standard; protein; 175 AA.
XX
XX AAO11219;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 25111.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX

```

PF 26-FEB-2001; 2001WO-US004927.  
 XX  
 PR 28-FEB-2000; 2000US-00515126.  
 PR 18-MAY-2000; 2000US-00577409.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Tang YT, Liu C, Drmanac RT;  
 PI  
 DR WPI; 2001-514838/56.  
 DR N-PSDB; AA191150.  
 XX  
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.  
 PT  
 XX Claim 20; SEQ ID NO 25111; 1399pp + Sequence Listing; English.  
 PS  
 XX The invention relates to human polynucleotides (AA179941-AA193841) and  
 CC the encoded proteins (AA00010-AA013910) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 175 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 175;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 DB 128 KVVFFA 133  
 RESULT 22  
 ADC07962  
 ID ADC07962 standard; protein; 186 AA.  
 XX  
 AC ADC07962;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Rice protein sequence Seq ID228 related to grain filling.  
 XX  
 KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;  
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
 KW gene; ds; plant.  
 XX  
 OS Oryza sativa.  
 XX  
 PN WO2003000905-A2.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-IB002450.  
 XX  
 PR 22-JUN-2001; 2001US-0300112P.  
 PR 26-SEP-2001; 2001US-0325277P.  
 PR 20-DEC-2001; 2001US-0342327P.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;  
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;

PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;  
 XX  
 XX WPI; 2003-229341/22.  
 DR N-PSDB; ADC07961.  
 XX  
 PT New plant genes encoding polypeptides having an activity involved in or  
 PT associated with the synthesis, metabolism or degradation of carbohydrates  
 PT in the plant grain useful in generating plants having improved  
 PT nutritional properties.  
 PT  
 XX Claim 15; SEQ ID NO 228; 130pp; English.  
 PS  
 XX This invention, in the area of plant biotechnology, relates to novel  
 CC polynucleotides comprising a nucleotide sequence encoding a protein which  
 CC is involved in or associated with the synthesis, metabolism or  
 CC degradation of carbohydrates in the plant grain and the expression of  
 CC which is up-regulated during grain filling. The plant is selected from  
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,  
 CC sugarcane, wheat, and rice. The invention may be useful for the  
 CC improvement of protein, oil, starch, fibre and moisture content of the  
 CC cereal grains. In addition, carbohydrate levels may be modified to a more  
 CC desirable level using the present invention. The present sequence is the  
 CC amino acid sequence of a rice protein of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 186 AA;  
 Query Match 100.0%; Score 29; DB 7; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 DB 4 KVVFFA 9  
 RESULT 23  
 ADC07948  
 ID ADC07948 standard; protein; 186 AA.  
 XX  
 AC ADC07948;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Rice protein sequence Seq ID214 related to grain filling.  
 XX  
 KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;  
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
 KW gene; ds; plant.  
 XX  
 OS Oryza sativa.  
 XX  
 PN WO2003000905-A2.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-IB002450.  
 XX  
 PR 22-JUN-2001; 2001US-0300112P.  
 PR 26-SEP-2001; 2001US-0325277P.  
 PR 20-DEC-2001; 2001US-0342327P.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;  
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;  
 XX  
 XX WPI; 2003-229341/22.  
 DR N-PSDB; ADC07947.

XX New plant genes encoding polypeptides having an activity involved in or  
PT associated with the synthesis, metabolism or degradation of carbohydrates  
PT in the plant grain useful in generating plants having improved  
PT nutritional properties.  
XX  
PS Claim 15; SEQ ID NO 214; 130pp; English.  
XX  
CC This invention, in the area of plant biotechnology, relates to novel  
CC polynucleotides comprising a nucleotide sequence encoding a protein which  
CC is involved in or associated with the synthesis, metabolism or  
CC degradation of carbohydrates in the plant grain and the expression of  
CC which is up-regulated during grain filling. The plant is selected from  
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,  
CC sugarbeet, wheat, and rice. The invention may be useful for the  
CC improvement of protein, oil, starch, fibre and moisture content of the  
CC cereal grains. In addition, carbohydrate levels may be modified to a more  
CC desirable level using the present invention. The present sequence is the  
CC amino acid sequence of a rice protein of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/publishedpct\_sequences.

XX SQ Sequence 186 AA;

Query Match 100.0%; Score 29; DB 7; Length 186;  
Best Local Similarity 100.0%; Pred. NO. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
Db 4 KVVFFA 9

RESULT 24

AAW83792  
ID AAW83792 standard; protein; 190 AA.

XX AC AAW83792;

XX DT 07-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen SEQ ID NO:11385.

XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis.

XX OS Homo sapiens.

XX PN W0200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001354.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-0216647P.

PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239315P.  
PR 13-OCT-2000; 2000US-0239317P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0241826P.  
PR 08-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249246P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249298P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-483426/52.  
DR N-PSDB; AAK56573.  
XX  
PT Nucleic acids encoding human immune/haematopoietic antigen polypeptides;  
PT useful for preventing, diagnosing and/or treating cancers and metastasis.  
XX  
XX Claim 1; SEQ ID NO 11385; 3071pp + Sequence Listing; English.  
XX  
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patients own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/haematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/haematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention  
XX  
SQ Sequence 190 AA;  
Query Match 100.0%; Score 29; DB 4; Length 190;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
Db 14 KVVFFA 19  
|||||  
RESULT 25  
ADQ66704  
ID ADQ66704 standard; protein; 854 AA.  
XX  
AC ADQ66704;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Novel human protein sequence #1677.  
XX  
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
KW gene therapy; diagnostic marker; morbid state; osteoporosis;  
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;  
KW cancer.  
XX  
OS Homo sapiens.  
XX  
PN EP1440981-A2.  
XX  
PD 28-JUL-2004.  
XX  
PF 21-JAN-2004; 2004EP-00001196.  
XX  
PR 21-JAN-2003; 2003JP-00102206.  
PR 09-MAY-2003; 2003JP-00131392.  
XX  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Nagai K, Irie R;  
XX  
DR WPI; 2004-535376/52.  
DR N-PSDB; ADQ64516.  
XX  
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,  
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX  
PS Claim 1; SEQ ID NO 3865; 2449pp; English.  
XX  
CC The invention relates to 2495 novel polynucleotides (I) and their encoded  
CC polypeptides, sequences hybridizing to these nucleotides, sequences  
CC encoding partial polypeptides and sequences having 70% or 90% identity to  
CC the nucleotide and protein sequences. The nucleotides and polypeptides  
CC are useful as diagnostic markers or therapeutic target for the diseases  
CC or morbid states. They are also useful for treating osteoporosis,  
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,  
CC dementia and various cancers. This sequence corresponds to a protein  
CC sequence of the invention.  
XX  
SQ Sequence 854 AA;  
Query Match 100.0%; Score 29; DB 8; Length 854;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
Db 221 KVVFFA 226  
|||||



RESULT 26  
ABM83252  
ID ABM83252 standard; protein; 922 AA.  
XX AC ADF76335;  
XX AC ADF76335;  
XX DT 26-FEB-2004 (first entry)  
XX DE 18-NOV-2004 (first entry)  
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:3501.  
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX OS Homo sapiens.  
XX PN WO2004023973-A2.  
XX PD 25-MAR-2004.  
XX PF 12-SEP-2002; 2003WO-US028227.  
XX PR 12-SEP-2002; 2002US-0410259P.  
XX PR 12-SEP-2002; 2002US-0410260P.  
XX PA (INCY-) INCYTE CORP.  
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patury S, Shi X, Suarez CJ;  
XX WPI; 2004-329368/30.  
XX DR N-PSDB; ACN41904.  
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
XX PT in diagnosing a condition, disease or disorder associated with human  
XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
XX PT in gene mapping.  
XX PS Claim 27; Page; 190pp; English.  
XX CC This invention relates to novel diagnostic and therapeutic polynucleotides  
XX CC selected from one of the 2722 sequences defined in the specification. A  
XX CC polynucleotide of the invention may have a use in gene therapy. The human  
XX CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
XX CC used to diagnose a particular condition, disease or disorder associated  
XX CC with human molecules, e.g. cell proliferative disorders,  
XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
XX CC disorder, neurological disorders, gastrointestinal disorders, or  
XX CC infections caused by virus, bacteria, fungi or parasite. The dithp  
XX CC molecules may also be used in genetic mapping, in identifying individuals  
XX CC from minute biological samples, in detecting single nucleotide  
XX CC polymorphisms, as molecular weight markers, and for somatic or germline  
XX CC gene therapy. The present sequence represents a dithp protein of the  
XX CC invention. Note: The sequence data for this patent is not represented in  
XX CC the printed specification, but was obtained in electronic format directly  
XX CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX SQ Sequence 922 AA;

Query Match 100.0%; Score 29; DB 8; Length 922;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||  
Db 291 KVVFFA 296

## RESULT 27

ADF76335  
ID ADF76335 standard; protein; 925 AA.  
XX AC ADF76335;  
XX AC ADF76335;  
XX DT 26-FEB-2004 (first entry)  
XX DE Novel human secreted and transmembrane protein SeqID 8.  
XX KW human; PRO; membrane bound protein; membrane bound receptor;  
XX KW cell proliferation; cell migration; cell differentiation;  
XX KW mitogenic factor; survival factor; cytotoxic factor;  
XX KW differentiation factor; neurotrophic factor; hormone; cell receptor;  
XX KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.  
XX OS Homo sapiens.  
XX PN WO2003072035-A2.  
XX PD 04-SEP-2003.  
XX PF 21-FEB-2003; 2003WO-US005241.  
XX PR 22-FEB-2002; 2002US-0359461P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Bodary SC, Clark HI, Hunte B, Jackman JK, Schoenfeld JR;  
PI Williams PM, Wood WI, Wu TD;  
XX WPI; 2003-721702/68.  
XX DR N-PSDB; ADF76334.  
XX PT New PRO polypeptides, useful for diagnosing and treating an immune  
XX PT related disorder, e.g. systemic lupus erythematosus, rheumatoid  
XX PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or  
XX PT diabetes mellitus.  
XX PS Claim 10; SEQ ID NO 8; 918pp; English.  
XX CC This invention relates to novel nucleic acids encoding human PRO secreted  
XX CC and transmembrane proteins. Extracellular proteins play important roles  
XX CC in the formation, differentiation and maintenance of multicellular  
XX CC organisms. The fate of many individual cells (for example proliferation,  
XX CC migration or differentiation) is typically governed by information  
XX CC received from other cells and the immediate environment. The information  
XX CC is often transmitted by secreted polypeptides (for example mitogenic  
XX CC factors, survival factors, cytotoxic factors, differentiation factors,  
XX CC neurotrophic factors and hormones) which are received and interpreted by diverse  
XX CC cell receptors or membrane bound proteins. These membrane bound proteins  
XX CC and receptors may be of use as pharmaceutical and diagnostic agents, such  
XX CC as in the blocking of receptor-ligand interactions. The current invention  
XX CC provides the amino acid sequences of novel human membrane bound receptors  
XX CC and proteins, along with the cDNA sequences encoding them. The novel  
XX CC proteins of the invention may have cytostatic activities through the  
XX CC stimulation of chondrocytes. The nucleic acids of the invention may be  
XX CC useful for the manufacture of a medicament for diagnosing or treating a  
XX CC tumour in a mammal. In addition, they may be useful for measuring or  
XX CC detecting the expression of a tumour associated gene. The present  
XX CC sequence is the amino acid sequence of a human PRO protein of the  
XX CC invention.  
XX SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 7; Length 925;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
|||||  
Db 292 KVVFFA 297



RESULT 28  
 ID ADJ70225 standard; protein; 925 AA.  
 XX AC ADJ70225;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Human heat mitochondrial protein as a therapeutic target SeqID2031.  
 XX KW mitochondrial; human; screening assay; diabetes mellitus;  
 XX KW Huntington's disease; osteoarthritis;  
 XX KW Leber's hereditary optic neuropathy; LHON;  
 XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 XX KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;  
 XX KW osteopathic; ophthalmological; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO2003087768-A2.  
 XX PD 23-OCT-2003.  
 XX PF 04-APR-2003; 2003WO-US010870.  
 XX PR 12-APR-2002; 2002US-0372843P.  
 XX PR 17-JUN-2002; 2002US-0389987P.  
 XX PR 20-SEP-2002; 2002US-0411418P.  
 XX PA (MITO-) MITOKOR.  
 XX PA (BUCK-) BUCK INST AGE RES.  
 XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
 PI Warnock DE;  
 XX WPI; 2003-845369/78.  
 XX DR Identifying a mitochondrial target for drug screening assays and for  
 PT treating diseases associated with altered mitochondrial function,  
 PT comprises detecting a modified polypeptide in a sample and correlating  
 PT with the disease.  
 XX PS Claim 1; SEQ ID NO 2031; 180pp; English.  
 XX CC This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, neurotropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cytostatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.  
 XX SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 7; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 292 KVVFFA 297

RESULT 29  
 ID ADJ75428 standard; protein; 925 AA.  
 XX AC ADJ75428;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Marker gene related amino acid sequence SEQ ID NO:680.  
 XX KW bronchial asthma; chronic obstructive pulmonary disease;  
 XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
 XX KW gene therapy; marker.  
 XX OS Homo sapiens.  
 XX PN EPI394274-A2.  
 XX PD 03-MAR-2004.  
 XX PF 04-AUG-2003; 2003EP-00254857.  
 XX PR 06-AUG-2002; 2002JP-00229312.  
 XX PR 20-MAR-2003; 2003JP-00077212.  
 XX PA (GENO-) GENOX RES INC.  
 XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuohara K;  
 XX WPI; 2004-193155/19.  
 XX DR Testing for bronchial asthma or chronic obstructive pulmonary disease by  
 PT comparing the expression level of a marker gene in a biological sample  
 PT from a subject with the expression level of the gene in a sample from a  
 PT healthy subject.  
 XX PS Example 11; SEQ ID NO 680; 241pp; English.  
 XX CC The present invention describes a method of testing for bronchial asthma  
 CC or chronic obstructive pulmonary disease. The method comprises  
 CC determining the expression level of a marker gene in a biological sample  
 CC from a subject, comparing the expression level determined with the  
 CC expression level of the marker gene in a biological sample from a healthy  
 CC subject, and judging whether the subject has bronchial asthma or chronic  
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
 CC genes (S1) whose expression levels increase when respiratory epithelial  
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
 CC whose expression levels decrease when respiratory epithelial cells are  
 CC stimulated with interleukin-13. Also described: (1) a reagent (1) for  
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
 CC (2) a kit for screening for a candidate compound for a therapeutic agent  
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
 CC an animal model for bronchial asthma or chronic obstructive pulmonary  
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
 CC method for producing an animal model for bronchial asthma or chronic  
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
 CC a marker gene or an antisense nucleic acid corresponding to a portion of  
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
 CC expression of the gene through an RNAi effect or an antibody recognising  
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
 CC probe has been immobilised to assay a marker gene. (1) has respiratory  
 CC and antiasthmatic activities, and can be used in gene therapy. The method  
 CC is useful for testing for or screening for a therapeutic agent for  
 CC bronchial asthma or chronic obstructive pulmonary disease. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



DE Human NF-kappaB pathway-associated protein SeqID234.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;

KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;

KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;

KW immunosuppressive; vulnery; gene therapy; immune disorder;

KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;

KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;

KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;

KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;

KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;

KW viral replication; host cell survival; evasion of immune response;

KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;

KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;

KW autoimmune disorder; hyper immune activity;

KW aberrant acute phase response; hypercongenital condition; birth defect;

KW necrotic lesion; wound; organ transplant rejection;

KW aberrant signal transduction; proliferating disorder; cancer;

KW HIV propagation; human.

XX Homo sapiens.

OS

XX

XX WO2004065577-A2.

XX

XX 05-AUG-2004.

XX

XX

XX 13-JAN-2004; 2004WO-US000798.

XX

XX 14-JAN-2003; 2003US-0440068P.

PR

XX 12-MAY-2003; 2003US-0469757P.

XX

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

PA

XX

XX Nadler SG, Neubauer MG, Feder JN, Carman J;

PI

XX

XX WPI; 2004-562168/54.

DR

XX N-PSDB; ADRI4232.

DR

XX

XX New isolated polynucleotides and polypeptides associated with NF-kappaB

PT pathway, useful for diagnosing, treating, or preventing disorders or

PT diseases associated with NF-kappaB pathway.

XX

XX

XX Claim 6; SEQ ID NO 234; 237pp; English.

PS

XX

XX This invention relates to the novel association of protein sequences (and

CC the genes which encode them) to the NF-kappaB pathway. The invention may

CC be useful for the production of compounds with an antiinflammatory,

CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,

CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,

CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or

CC vulnery activity or for gene therapy. The proteins and nucleotides are

CC useful for diagnosing, preventing, treating, or ameliorating conditions

CC or diseases associated with the NF-kappaB pathway. The condition is an

CC immune disorder, an inflammatory disorder, an inflammatory disorder

CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,

CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM

CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic

CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,

CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell

CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory

CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick

CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper

CC immune activity, disorders related to aberrant acute phase responses,

CC hypercongenital conditions, birth defects, necrotic lesions, wounds,

CC organ transplant rejection, conditions related to organ transplant

CC rejection, disorders related to aberrant signal transduction,

CC proliferating disorders, cancers and HIV propagation in cells infected

CC with other viruses. The present sequence is that of a human protein which

CC is subject to the novel association with the NF-kappaB pathway of the

CC invention. Note: This sequence does not appear in the specification but

CC was obtained by the indexer from Genbank.

XX

XX Sequence 925 AA;

XX

Query Match 100.0%; Score 29; DB 8; Length 925;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6

DB 292 KVFPPA 297

|||||

RESULT 33

ADP25011

ID ADP25011 standard; protein; 925 AA.

XX

AC ADP25011;

XX

DT 18-NOV-2004 (first entry)

XX

DE PRO polypeptide SEQ ID NO:2189.

XX

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;

KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX

OS Unidentified.

XX

XX WO2004041170-A2.

XX

XX 21-MAY-2004.

XX

XX 30-OCT-2003; 2003WO-US034312.

PF

XX

XX 01-NOV-2002; 2002US-0423394P.

PR

XX

XX (GETH ) GENENTECH INC.

PA

XX

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

PI Wu TD;

XX

XX WPI; 2004-419628/39.

DR

XX N-PSDB; ADP25010.

DR

XX

XX New PRO polypeptides and polynucleotides, useful for treating e.g.

PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated

PT renal disease, or demyelinating diseases of the central or peripheral

PT nervous system.

XX

XX Claim 7; SEQ ID NO 2189; 2940pp; English.

PS

XX

XX The invention relates to a novel isolated nucleic acid and the PRO

CC polypeptide encoded by it. A protein of the invention has

CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,

CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide

CC of the invention may have a use in gene therapy. The PRO polypeptide, its

CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous

CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,

CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary

CC disease, infectious or autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,

CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's

CC disease, an autoimmune or immune-mediated skin disease, a bullous skin

CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic

CC disease, asthma, allergic rhinitis, atopic dermatitis, food

CC hypersensitivity, urticaria, an immunologic disease of the lung,

CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity

CC pneumonia, a transplantation associated disease, graft rejection or  
 CC graft-versus-host disease. The present sequence represents a PRO protein  
 CC of the invention.  
 XX  
 SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;  
 Best Local Similarity 100.0%; Pred. NO. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 292 KVVFFA 297

RESULT 34  
 ADR97294  
 ID ADR97294 standard; protein; 925 AA.  
 XX

AC ADR97294;

XX 02-DEC-2004 (first entry)

XX Human RIG-I-DEAD/H box protein, an apoptosis related target Seq 2.

XX human; enzyme; apoptosis; cancer; inflammation; autoimmune;  
 KW neurodegenerative disorder; cytostatic; antiinflammatory;  
 KW immunosuppressive; neuroprotective; gene therapy; RIG-I-DEAD/H box.

XX Homo sapiens.

XX WO2004078783-A2.

XX 16-SEP-2004.

XX 05-MAR-2004; 2004WO-GB000957.

XX 07-MAR-2003; 2003GB-00005267.

XX (BIRX-) BIRX THERAPEUTICS LTD.

XX Murphy FJ, Sheehan DE, Keating KE, Hayes I, Seera L;

XX WPI; 2004-662402/64.

XX N-PSDB; ADR97293.

XX Identifying an agent that modulates the function of an apoptosis-  
 PT associated polypeptide, useful for diagnosing or treating e.g. cancer,  
 PT comprises comparing the binding of the polypeptide to the candidate agent  
 PT and to a control agent.

PS Claim 1; SEQ ID NO 2; 304pp; English.

XX This invention relates to novel agents that modulates the function of  
 CC human apoptosis-associated proteins specified within the specification.  
 CC Specifically, it refers to a method for the identification of target  
 CC genes whose expression is correlated with an early stage in the  
 CC regulation of apoptosis. The present invention describes a method of  
 CC contacting either candidate agents or control agents to the target genes  
 CC and assessing the difference of binding and inhibitory activity, where  
 CC the candidate agent is selected from a low molecular weight organic  
 CC molecule, an antibody or fragment thereof, an antisense oligonucleotide,  
 CC a small inhibitory dRNA, or a ribozyme. As such, the compositions and  
 CC methods are useful for diagnosing and treating diseases or conditions  
 CC associated with abnormal apoptosis in mammalian tissue, such as cancer,  
 CC inflammation, autoimmune or neurodegenerative disorders. Accordingly,  
 CC they exhibit cytostatic, antiinflammatory, immunosuppressive and  
 CC neuroprotective activities. These may also be used for drug screening  
 CC purposes and in gene therapy. This polypeptide sequence is a human target  
 CC protein, an enzyme associated with the regulation of apoptosis whose  
 CC expression is modulated by novel agents of the invention.

XX Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;  
 Best Local Similarity 100.0%; Pred. NO. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 292 KVVFFA 297

RESULT 35  
 ADY17516  
 ID ADY17516 standard; protein; 925 AA.  
 XX

AC ADY17516;

XX 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 3322.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
 KW Antiallergic; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH ) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX Claim 8; SEQ ID NO 3322; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO  
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,  
 CC composition, and method are useful for diagnosing and treating an immune  
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
 CC arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 925 AA;

Query Match 100.0%; Score 29; DB 9; Length 925;  
 Best Local Similarity 100.0%; Pred. NO. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 292 KVVFFA 297

RESULT 36  
 AEA23525  
 ID AEA23525 standard; protein; 925 AA.  
 XX

AC AEA23525;

XX 11-AUG-2005 (first entry)

XX

DE Human PRO polypeptide SEQ ID NO 67.  
 XX immune disorder; PRO; Antiinflammatory; Dermatological;  
 KW Immunosuppressive; Antirheumatic; Antiarthritic; Osteopathic;  
 KW Muscular-Gen.; Vasotropic; Antianemic; Antipsoriatic; Immunostimulant.  
 XX Homo sapiens.  
 XX WO2005051988-A2.  
 PN 09-JUN-2005.  
 PD 02-MAR-2004; 2004WO-US006460.  
 XX 03-MAR-2003; 2003US-0451884P.  
 XX (GETH ) GENENTECH INC.  
 XX Abbas A, Bodary S, Clark H, Schoenfeld J, Williams PM, Wood WI;  
 PI Wu TD;  
 XX WPI; 2005-417958/42.  
 DR N-PSDB; AEA23524.  
 XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, or  
 PT psoriasis.  
 XX Disclosure; SEQ ID NO 67; 966pp; English.  
 PS The invention relates to an isolated nucleic acid. The polypeptide,  
 CC compound or composition, and methods are useful for diagnosing and  
 CC treating an immune related disorder, e.g. systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,  
 CC spondyloarthropathies, systemic sclerosis, idiopathic inflammatory  
 CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
 CC autoimmune hemolytic anemia, autoimmune or immune-mediated skin diseases  
 CC including bullous skin diseases, erythema multiforme and contact  
 CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The  
 CC present sequence represents the amino acid sequence of a human PRO  
 CC polypeptide.  
 XX Sequence 925 AA;  
 SQ Query Match 100.0%; Score 29; DB 9; Length 925;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 DB 292 KVVFFA 297  
 |||||  
 RESULT 37  
 AAR77360  
 ID AAR77360 standard; protein; 1144 AA.  
 XX AAR77360;  
 AC 10-MAY-1996 (first entry)  
 DT Inducible nitrogen monoxide synthase.  
 DE nitrogen monoxide synthase; inducible; treatment; prevention;  
 KW vascular disease; restenosis.  
 XX Mus musculus.  
 XX DE4411402-A1.  
 PN 05-OCT-1995.  
 PD  
 XX

PF 31-MAR-1994; 94DE-04411402.  
 XX 31-MAR-1994; 94DE-04411402.  
 XX (SCHR/) SCHRADER J.  
 XX Schrader J, Goedecke A;  
 XX WPI; 1995-345550/45.  
 DR N-PSDB; AAQ94252.  
 XX Eukaryotic expression vector for nitrogen-mon:oxide synthase gene -  
 PT useful in the treatment and prevention of diseases of blood vessels by  
 PT gene therapy.  
 XX Claim 5; Fig 1; 28pp; German.  
 XX Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, and  
 CC is encoded by AAQ94252. iNOS is homodimer with a mol. wt. of 130 kDa per  
 CC subunit. The activity of iNOS is independent of calmodulin and cellular  
 CC calcium levels. Vectors contg. the DNA are used in the treatment or  
 CC prevention of vascular diseases, high blood pressure, arteriosclerosis,  
 CC stenosis or restenosis of blood vessels, esp. coronary vessels after  
 CC percutane transluminal coronary angioplasty. See AAR77363 and AAR77362  
 CC for endothelial and brain-derived NOS  
 XX Sequence 1144 AA;  
 SQ Query Match 100.0%; Score 29; DB 2; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 DB 514 KVVFFA 519  
 |||||  
 RESULT 38  
 AAW51246  
 ID AAW51246 standard; protein; 1144 AA.  
 XX AAW51246;  
 AC 25-MAR-2003 (revised)  
 DT 12-AUG-1998 (first entry)  
 XX Inducible nitric oxide synthase, long isoform.  
 DE Inducible nitric oxide synthase; iNOS; recombinant protein; cDNA library;  
 KW isoform.  
 XX Mus sp.  
 XX US5766909-A.  
 PN 16-JUN-1998.  
 PD 05-NOV-1993; 93US-00147812.  
 PF 04-FEB-1992; 92US-00841641.  
 PR (MERI ) MERCK & CO INC.  
 PA Mumford RA, Calaycay JR, Xie Q, Nathan CF;  
 PI WPI; 1998-361696/31.  
 DR N-PSDB; AAV07247.  
 XX DNA encoding inducible nitric oxide synthase proteins - useful for  
 PT producing recombinant proteins.  
 XX Claim 1; Col 25-32; 39pp; English.  
 PS

CC The invention relates to two DNA molecules encoding inducible nitric  
 CC oxide synthase (iNOS) proteins, where the DNA molecules comprise defined  
 CC sequences of 4041 and 4165 base pairs given in the specification and the  
 CC proteins have 1144 amino acids. Also claimed are expression vectors  
 CC containing the DNA molecules, and recombinant host cells containing the  
 CC vectors. The DNA molecules are useful for producing the recombinant  
 CC proteins. The present sequence represents inducible nitric oxide, long  
 CC isoform. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 1144 AA;  
 Query Match 100.0%; Score 29; DB 2; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 514 KVVFFA 519  
 RESULT 39  
 AAG64500  
 ID AAG64500 standard; protein; 1144 AA.  
 XX  
 AC AAG64500;  
 XX  
 DT 02-OCT-2001 (first entry)  
 XX  
 DE Mouse inducible nitric oxide synthase 2.  
 XX  
 KW Antisense oligonucleotide; inducible nitric oxide synthase;  
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;  
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;  
 KW 2'-O-methoxyethyl; phosphorothioate; mouse.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200152902-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 XX 15-JAN-2001; 2001WO-US001381.  
 XX  
 PF 24-JAN-2000; 2000US-00490208.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CP, Dean NM, Cowseert LM;  
 XX  
 DR WPI; 2001-465340/50.  
 DR N-PSDB; AAH47974.  
 XX  
 XX New antisense oligonucleotides for modulating the expression of inducible  
 PT nitric oxide synthase in cells or tissues, particularly useful for  
 PT treating e.g. immunological, cardiovascular or neurological disorders, or  
 PT ischemia.  
 XX  
 PS Example 17; Page 110-114; 144pp; English.  
 XX  
 CC The invention relates to antisense compounds, especially  
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible  
 CC nitric oxide synthase and which specifically hybridise to and modulate  
 CC expression of inducible nitric oxide synthase. The antisense compounds  
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,  
 CC neuroprotective, disorder and vasotropic activity. The antisense  
 CC oligonucleotides are useful for inhibiting the expression of inducible  
 CC nitric oxide synthase in cells or tissues. In particular, the antisense  
 CC oligonucleotides are useful for treating diseases or disorders associated  
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological  
 CC disorder, cardiovascular disorder, neurological disorder or  
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also  
 CC useful for research and diagnostics. The present sequence is that of  
 CC mouse inducible nitric oxide synthase

XX  
 SQ Sequence 1144 AA;  
 Query Match 100.0%; Score 29; DB 4; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 514 KVVFFA 519  
 RESULT 40  
 ABU79138  
 ID ABU79138 standard; protein; 1144 AA.  
 XX  
 AC ABU79138;  
 XX  
 DT 18-JUN-2003 (first entry)  
 XX  
 DE Inducible nitric oxide synthase protein.  
 XX  
 KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;  
 KW gene therapy; mammalian cell receptor; cytostatic;  
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;  
 KW tumouricidal immunocyte; antitumour.  
 XX  
 OS Unidentified.  
 XX  
 PN US2002177551-A1.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 30-MAY-2001; 2001US-00870759.  
 XX  
 PR 31-MAY-2000; 2000US-0208128P.  
 XX  
 PA (TERM/) TERMAN D S.  
 XX  
 PI Terman DS;  
 XX  
 DR WPI; 2003-361759/34.  
 DR N-PSDB; ACA64740.  
 XX  
 PT A mammalian cell receptor, useful in the treatment of cancer by binding  
 PT to tumor associated lipids where the binding induces anergy or apoptosis  
 PT in T cells and antigen presenting cells.  
 XX  
 PS Example 2; Page; 167pp; English.  
 XX  
 CC The invention relates to a mammalian cell receptor, useful in the  
 CC treatment of cancer, which binds to tumour associated lipids and induces  
 CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).  
 CC Also included are a mammalian cell useful in the treatment of cancer  
 CC where the receptor which binds tumour associated lipids and induces  
 CC cellular inactivation or death is deleted or functionally deactivated,  
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal  
 CC (by allowing tumour associated lipids to contact immunocytes in which  
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,  
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,  
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or  
 CC deleted), a construct useful in the treatment of cancer comprising a  
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell  
 CC useful in the treatment of cancer (where an adaptor protein which  
 CC inhibits T cell activation by tumour associated antigens is deleted or  
 CC functionally deactivated), a composition useful in the treatment of  
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing  
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by  
 CC allowing tumour associated lipids to contact immunocytes, in which  
 CC receptors for the lipids are inactivated or deleted to produce a  
 CC tumouricidal immunocyte population, and administering the tumouricidal  
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC  
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to

CC contact APCs, in which receptors for the tumour associated lipids are  
 CC inactivated or deleted to produce a tumouricidally activated population,  
 CC and administering APCs to the host), producing a tumouricidal T cell  
 CC population ex vivo in a mammal) by allowing a tumour associated lipids to  
 CC contact T cells, in which adaptor proteins, which inhibit T cell  
 CC activation by tumour associated antigens, are deleted or functionally  
 CC deactivated to produce a tumouricidal population of T cells, and  
 CC administering the tumouricidally activated T cells to the host, or  
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and  
 CC administering the tumouricidally activated T cells to the host), treating  
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which  
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)  
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a  
 CC tumour associated antigen to contact immunocytes in which adaptor  
 CC proteins which inhibit T cell activation by tumour associated antigens  
 CC are deleted or functionally deactivated) and producing (M7) a  
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a  
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The  
 CC receptors, methods and compositions are useful for treating cancers and  
 CC tumours. Bacterial superantigens are co-administered or administered as  
 CC fusion constructs with anti-tumour proteins or motifs. The present  
 CC sequence represents an anti-tumour protein which is co-administered with  
 CC or incorporated into a fusion construct with a superantigen. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format from the US patent  
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"  
 XX  
 SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 6; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 514 KVVFFA 519

## RESULT 41

ADP43404  
 ID ADF43404 standard; protein; 1144 AA.

XX  
 AC ADF43404;

DT 12-FEB-2004 (first entry)

XX  
 DE iNOS polypeptide seqid 124.

XX  
 KW receptor; lipid-based tumour associated antigen; cytostatic;  
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;  
 KW infectious disease; iNOS.

XX  
 OS Unidentified.

XX  
 PN US2003157113-A1.

XX  
 PD 21-AUG-2003.

XX  
 PF 28-DEC-2000; 2000US-00751708.

XX  
 PR 28-DEC-1999; 99US-0173371P.

XX  
 PA (TERM/) TERMAN D S.

XX  
 PI Terman DS;

XX  
 DR WPI; 2003-787326/74.

XX  
 DR N-PSDB; ADF43403.

XX  
 PT New receptor in a mammalian cell that inhibits regular activation by  
 PT receptors specific for lipid-based tumor associated antigens, useful for  
 PT treating a neoplastic disease or tumor, and infectious diseases.

XX

PS Example 3; SEQ ID NO 124; 151pp; English.

XX The invention describes a receptor in a mammalian cell that inhibits  
 CC regular activation by receptors specific for lipid-based tumour  
 CC associated antigen. The receptor has cytostatic and antimicrobial  
 CC properties and is suitable for use in gene therapy. The receptors,  
 CC methods and compositions are useful for treating a neoplastic disease or  
 CC tumour (cancer), and infectious diseases. This sequence represents iNOS  
 CC polypeptide, a cell surface moiety, the DNA of which can be transfected  
 CC into a cell with superantigen DNA to generate antitumour immunity.

XX  
 SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 7; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 Db 514 KVVFFA 519

## RESULT 42

ADP77432

ID ADF77432 standard; protein; 1144 AA.

XX  
 AC ADF77432;

DT 26-FEB-2004 (first entry)

XX  
 DE Mouse inducible nitric oxide synthase, iNOS.

XX  
 KW Mouse; inducible nitric oxide synthase; iNOS; cardiant; vasodilator;  
 KW cytostatic; gynaecological; restenotic response; angioplasty;  
 KW vasodilation; angina; cancer; cell death; premature labour; tumour;  
 KW nervous system; brain; erectile dysfunction; uterus; lung; vascular tone;  
 KW regional blood flow.

XX  
 OS Mus musculus.

XX  
 PN US6620616-B1.

XX  
 PD 16-SEP-2003.

XX  
 PF 13-SEP-2000; 2000US-00661258.

XX  
 PR 13-SEP-2000; 2000US-00661258.

XX  
 PA (CLEV-) CLEVELAND CLINIC FOUND.

XX  
 PI Stuehr DJ, Adak S;

XX  
 DR WPI; 2003-895427/82.

XX  
 PT New isolated polynucleotide encoding a variant of a corresponding wild-  
 PT type nitric oxide synthase, useful for reducing the restenotic response  
 PT after angioplasty, or for inhibiting the development or onset of  
 PT premature labor.

XX  
 PS Disclosure; SEQ ID NO 5; 35pp; English.

XX The invention relates to an isolated polynucleotide encoding a variant of  
 CC a corresponding wild-type nitric oxide synthase (NOS). The variant has  
 CC the tryptophan in the alpha 3 helix substituted by tyrosine or  
 CC phenylalanine. Also included are a nucleic acid construct comprising the  
 CC nucleotide sequence that encodes a variant of a corresponding wild-type  
 CC nitric oxide synthase and a promoter operably linked to the encoding  
 CC sequence of the variant and a transformed cell comprising the construct,  
 CC where the cell expresses the nitric oxide synthase variant. The variant  
 CC has an in vitro enzymatic activity that is greater than the in vitro  
 CC enzymatic activity of the corresponding wild-type nitric oxide synthase.  
 CC The variant can preferably be of a corresponding wild-type endothelial  
 CC nitric oxide synthase (eNOS), neuronal nitric oxide synthase (nNOS), or



inducible nitric oxide synthase (iNOS). The polynucleotides are useful for reducing the restenotic response after angioplasty, or related interventional procedures, or to enhance the vasodilation response in treating angina, for anticancer therapy to promote cell death, and for inhibiting the development or onset of premature labour. The polynucleotides are useful to achieve or augment expression of NOS variant proteins or polypeptides in vivo to increase NOS production in target tissue, tumour tissue, tissue of the nervous system, including brain, penis (e.g. in erectile dysfunction) and uterine tissue, and lung tissue. NOS is useful for maintaining vascular tone and regulating regional blood flow. The present sequence is wild-type mouse iNOS.

Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 7; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
DB 514 KVVFFA 519

#### RESULT 43

ADJ76212  
ID ADJ76212 standard; protein; 1144 AA.

AC ADJ76212;

DT 20-MAY-2004 (first entry)

DE Marker gene related amino acid sequence SEQ ID NO:1464.

XX bronchial asthma; chronic obstructive pulmonary disease;  
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
KW gene therapy; marker.

XX Mus musculus.

XX EPI394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by  
PT comparing the expression level of a marker gene in a biological sample  
PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.

XX Claim 16; SEQ ID NO 1464; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic  
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
CC genes (S1) whose expression levels increase when respiratory epithelial  
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
CC whose expression levels decrease when respiratory epithelial cells are  
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for  
CC testing for bronchial asthma or chronic obstructive pulmonary disease;

CC (2) a kit for screening for a candidate compound for a therapeutic agent  
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
CC an animal model for bronchial asthma or chronic obstructive pulmonary  
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
CC method for producing an animal model for bronchial asthma or chronic  
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
CC a marker gene or an antisense nucleic acid corresponding to a portion of  
CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
CC expression of the gene through an RNAi effect or an antibody recognising  
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
CC probe has been immobilised to assay a marker gene. (I) has respiratory  
CC and antiasthmatic activities, and can be used in gene therapy. The method  
CC is useful for testing for or screening for a therapeutic agent for  
CC bronchial asthma or chronic obstructive pulmonary disease. The present  
CC sequence is used in the exemplification of the present invention.

XX Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 8; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|||||  
DB 514 KVVFFA 519

#### RESULT 44

ADJ76136  
ID ADJ76136 standard; protein; 1144 AA.

XX AC ADJ76136;

DT 20-MAY-2004 (first entry)

DE Marker gene related amino acid sequence SEQ ID NO:1388.

XX bronchial asthma; chronic obstructive pulmonary disease;

XX respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
KW gene therapy; marker.

XX Mus musculus.

XX EPI394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by  
PT comparing the expression level of a marker gene in a biological sample  
PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.

XX Claim 16; SEQ ID NO 1388; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic



CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
 CC genes (S1) whose expression levels increase when respiratory epithelial  
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
 CC whose expression levels decrease when respiratory epithelial cells are  
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for  
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
 CC (2) a kit for screening for a candidate compound for a therapeutic agent  
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
 CC an animal model for bronchial asthma or chronic obstructive pulmonary  
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
 CC method for producing an animal model for bronchial asthma or chronic  
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
 CC a marker gene or an antisense nucleic acid corresponding to a portion of  
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
 CC expression of the gene through an RNAi effect or an antibody recognising  
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
 CC probe has been immobilised to assay a marker gene. (I) has respiratory  
 CC and antiasthmatic activities, and can be used in gene therapy. The method  
 CC is useful for testing for or screening for a therapeutic agent for  
 CC bronchial asthma or chronic obstructive pulmonary disease. The present  
 CC sequence is used in the exemplification of the present invention.

XX  
 SQ Sequence 1144 AA;  
 Query Match 100.0%; Score 29; DB 8; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0;

QY 1 KVVFFA 6  
 |||||  
 DB 514 KVVFFA 519

RESULT 45  
 AEA03075  
 ID AEA03075 standard; protein; 1144 AA.

AC AEA03075;

DT 28-JUL-2005 (first entry)

DE VEGF amino acid sequence SEQ ID NO:101.

KW tumor; neoplasm; gene therapy; immunotherapy; cytostatic;  
 KW vascular endothelial cell growth factor.

OS Unidentified.

PN US2005112141-A1.

PD 26-MAY-2005.

PF 08-SEP-2004; 2004US-00937758.

PR 30-AUG-2000; 2000US-00650884.

PA (TERM/) TERMAN D S.

PI Terman DS;

DR WPI; 2005-394926/40.

DR N-PGDB; AEA03074.

XX New composition for treating a tumor or neoplastic disease in a subject  
 PT comprises conjugates comprising superantigen polypeptides or nucleic  
 PT acids with other molecules that produce a tumoricidal response.

PS Example 3; SEQ ID NO 101; 125pp; English.

XX The invention relates to a composition for treating a tumor or neoplastic  
 CC disease in a subject. Also described: (1) a mammalian cell comprising an

CC exogenous nucleic acid encoding a superantigen expressed in the cell,  
 CC which cell also produces or expresses all alpha-anomers of  
 CC monoglycosylceramide or diglycosylceramide, where expression of the  
 CC superantigen and the mono- or diglycosylceramide is capable of eliciting  
 CC an antitumor immune response in a mammal into which the cell is  
 CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)  
 CC preparing a population of immunotherapeutic T or natural killer T (NKT)  
 CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an  
 CC apoptotic cell preparation or lysate useful for treating a tumor or  
 CC neoplastic disease in a subject, comprising a cell population that has  
 CC been transfected with naked DNA encoding a superantigen, and treated to  
 CC undergo apoptosis or lysis; and (5) a cell that has ingested or been  
 CC transfected with the above apoptotic preparation or lysate, thus,  
 CC rendering the cell effective in presenting material expressed from  
 CC transfecting nucleic acid or material ingested to the immune system of a  
 CC mammal to elicit an anti-tumor immune response. The composition and  
 CC methods are useful for treating tumors or neoplastic diseases. The  
 CC present sequence represents a VEGF protein sequence, which is used in an  
 CC example from the present invention. Note - The sequence data for this  
 CC patent is not represented in the printed specification, but was obtained  
 CC in electronic format directly from the USPTO web site.

XX Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 9; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |||||  
 DB 514 KVVFFA 519

RESULT 46

AAB48483  
 ID AAB48483 standard; peptide; 6 AA.

AC AAB48483;

DT 02-MAR-2001 (first entry)

DE Antifibrillogenic peptide #10.

KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.

OS Homo sapiens.

PN Key Location/Qualifiers

FT Modified-site 6 /note= "C-terminal amide"

XX WO200068263-A2.

PN 16-NOV-2000.

PF 04-MAY-2000; 2000WO-CA000515.

PR 05-MAY-1999; 99US-0132592P.

PA (NEUR-) NEUROCHEM INC.

PI Chalifour R, Gervais P, Gupta A;

XX WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein.

CC Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:||||  
 Db 1 KIVFFA 6

RESULT 47  
 AAB48474  
 ID AAB48474 standard; peptide; 6 AA.

AC AAB48474;  
 XX  
 DT 02-MAR-2001 (first entry)  
 DE Antifibrillogenic peptide #1.

XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.

XX Homo sapiens.  
 XX WO200068263-A2.  
 XX 16-NOV-2000.

XX 04-MAY-2000; 2000WO-CA000515.  
 XX 05-MAY-1999; 99US-0132592P.

XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Gervais F, Gupta A;

XX WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein

CC Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6  
 |:||||  
 Db 1 KIVFFA 6

RESULT 48  
 AAB82623

ID AAB82623 standard; peptide; 6 AA.

AC AAB82623;

DT 02-OCT-2001 (first entry)

DE All-D peptide used in Alzheimer's disease vaccine.

KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
 KW therapy; antigen.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 1..6 /note= "all D-form residues"

PT WO200139796-A2.

PN 07-JUN-2001.

XX 29-NOV-2000; 2000WO-CA001413.

XX 29-NOV-1999; 99US-0168594P.

XX 28-NOV-2000; 2000US-00724842.

XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Hebert L, Kong X, Gervais F;

XX WPI; 2001-441458/47.

XX Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
 PT which elicits production of antibodies to prevent fibrillogenesis and  
 PT associated cellular toxicity.

XX Disclosure; Page 10; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for  
 CC preparing vaccines for preventing or treating Alzheimer's disease and  
 CC other amyloid related disorders in humans. It is based on a portion of  
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
 CC inserting 1 or more amino acid residues, or by substituting 1 or more  
 CC amino acid residues with other amino acid residues or non-amino acid  
 CC fragments. Vaccines of the invention are produced using 'non-self'  
 CC peptides synthesised from the unnatural D-configuration amino acids to  
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
 CC aggregated to be operative or immunogenic. They preferably interact with  
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic  
 CC fragments, protein conjugates, immunogenic derivative peptides and  
 CC immunogenic peptidomimetics. Examples include all-D peptides  
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
 CC prion protein related disorders, or systemic amyloidosis associated with  
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CC	amyloidosis found in long-term haemodialysis patients
XX	
SQ	Sequence 6 AA;
	Query Match 96.6%; Score 28; DB 4; Length 6;
	Best Local Similarity 83.3%; Pred. No. 2e-06;
	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KVVFFA 6
DB	1 KIVFFA 6
	1:
	2:
RESULT 50	
AAU96819	AAU96819 standard; peptide; 6 AA.
XX	
AC	AAU96819;
XX	
DT	30-JUL-2002 (first entry)
XX	
DE	Amyloid targeting peptide #9.
XX	
KW	Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
KW	transmissible cerebral amyloidosis; transmissible virus dementia;
KW	scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
KW	bovine spongiform encephalopathy; inflammation associated amyloid;
KW	primary amyloidosis; feline spongiform encephalopathy;
KW	Alzheimer's disease; prion-mediated disease; blood-brain barrier;
KW	dialysis-related amyloidosis; light chain-related amyloidosis;
KW	cerebral amyloid angiopathy.
XX	
OS	Synthetic.
XX	
PH	Key Location/Qualifiers
FT	Misc-difference 1..6 /note= "Preferably D-form residue"
FT	Modified-site 6
FT	/note= "Ala is amidated"
XX	
PN	WQ200207781-A2.
XX	
PD	31-JAN-2002.
XX	
PF	25-JUL-2001; 2001WO-CA001071.
XX	
PR	25-JUL-2000; 2000US-0220808P.
PR	24-JUL-2001; 2001US-00915092.
XX	
PA	(NEUR-) NEUROCHEM INC.
XX	
PI	Gervais F, Kong X, Chalifour R, Migneault D;
XX	
DR	WPI; 2002-371447/40.
XX	
PT	New amyloid-targeting imaging agents useful for in vivo imaging amyloid
PT	plaques and/or for the treatment of amyloidosis disorders.
XX	
PS	Claim 49; Page 21; 57pp; English.
XX	
CC	The invention relates to an amyloid-targeting imaging agent comprising an
CC	amyloid targeting moiety, a linker moiety and a labelling moiety. The
CC	agent is of general formula A t-(A 1 n k) z-A 1 a b (1) where z = 0 - 1;
CC	A t = an amyloid targeting moiety; A 1 n k = a linker moiety; and A 1 a b
CC	= a labelling moiety. Also included are imaging amyloid deposition or
CC	diagnosing an amyloid-related condition in a patient involving
CC	administering (1) to the patient, and ultrasound imaging (1) in the
CC	patient to determine the presence of amyloid or amyloid-related condition
CC	; and a kit for preparing a radiopharmaceutical preparation comprising
CC	instructions for the preparation and use of the radiopharmaceutical in
CC	the imaging of amyloid or an amyloid-related condition. The agents are
CC	used for imaging amyloid deposition and for diagnosing an amyloid related

CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible  
 CC cerebral amyloidosis (transmissible virus dementias), familial CJD,  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention  
 XX  
 XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |:||||  
 Db 1 KIVFFA 6

RESULT 51  
 AAU96811  
 ID AAU96811 standard; peptide; 6 AA.

XX AC AAU96811;

XX DT 30-JUL-2002 (first entry)

XX DE Amyloid targeting peptide #1.

XX KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; kuru; CJD;  
 KW transmissible cerebral amyloidosis; transmissible virus dementias;  
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
 KW bovine spongiform encephalopathy; inflammation associated amyloid;  
 KW primary amyloidosis; feline spongiform encephalopathy;  
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
 KW dialysis-related amyloidosis; light chain-related amyloidosis;  
 KW cerebral amyloid angiopathy.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Misc-difference 1. .6

FT /note= "Preferably D-form residue"

XX PN WO200207781-A2.

XX PD 31-JAN-2002.

XX PF 25-JUL-2001; 2001WO-CA001071.

XX PR 25-JUL-2000; 2000US-0220808P.

XX FR 24-JUL-2001; 2001US-00915092.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Gervais F, Kong X, Chalfour R, Migneault D;

XX DR WPI; 2002-371447/40.

XX PT New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
 XX plaques and/or for the treatment of amyloidosis disorders.

XX PS Claim 49; Page 21; 57pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent comprising an  
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The  
 CC agent is of general formula A<sub>t</sub>-(A<sub>1</sub>)<sub>n</sub>(A<sub>2</sub>)<sub>k</sub>-A<sub>1</sub>-A<sub>2</sub>-A<sub>3</sub> where z = 0 - 1;  
 CC A<sub>t</sub> = an amyloid targeting moiety; A<sub>1</sub>, A<sub>2</sub>, A<sub>3</sub> = a linker moiety; and A<sub>1</sub>, A<sub>2</sub>, A<sub>3</sub>  
 CC = a labelling moiety. Also included are imaging amyloid deposition or

CC diagnosing an amyloid-related condition in a patient involving  
 CC administering (I) to the patient, and ultrasound imaging (I) in the  
 CC patient to determine the presence of amyloid or amyloid-related condition  
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising  
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and  
 CC instructions for the preparation and use of the radiopharmaceutical in  
 CC the imaging of amyloid or an amyloid-related condition. The agents are  
 CC used for imaging amyloid deposition and for diagnosing an amyloid related  
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible  
 CC scrapie, transmissible mink encephalopathy, bovine spongiform  
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,  
 CC primary amyloidosis, Alzheimer's disease, prion-mediated diseases,  
 CC cerebral amyloidosis, feline spongiform encephalopathy, non-transmissible  
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral  
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain  
 CC barrier and are capable of binding specifically to amyloid plaques. The  
 CC present sequence is a peptide forming the amyloid targeting moiety of the  
 CC agent of the invention  
 XX  
 XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |:||||  
 Db 1 KIVFFA 6

RESULT 52

AAU11657  
 ID AAU11657 standard; peptide; 6 AA.

XX AC AAU11657;

XX DT 09-APR-2002 (first entry)

XX DE Peptide #10, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.

XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 KW CAA; nontropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 6 /note= "C-terminal amide"

XX PN WO200185093-A2.

XX PD 15-NOV-2001.

XX PF 23-DEC-2000; 2000WO-IB002078.

XX PR 23-DEC-1999; 99US-0171877P.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Green AM, Gervais F;

XX DR WPI; 2002-075222/10.

XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
 XX disease comprises contacting blood vessel wall cell with amyloid-beta 40  
 XX inhibitor.

XX PS Disclosure; Page 10; 68pp; English.

XX CC The present invention relates to a new method of inhibiting cerebral  
 XX amyloid angiopathy. The new method of the invention involves contacting a

CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
 CC The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)  
 XX  
 SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWVFFA 6  
 Db 1 KIVFFA 6

RESULT 53

AAU11648  
 ID AAU11648 standard; peptide; 6 AA.

AC AAU11648;

XX 09-APR-2002 (first entry)

XX Peptide #1, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

OS Synthetic.

XX WO200185093-A2.

XX 15-NOV-2001.

XX 22-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's  
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40  
 PT inhibitor.

PS Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting a  
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral amyloid  
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral  
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.  
 CC The present sequence represents one of a group of peptides (AAU11648-  
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a  
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor  
 CC was used in the invention to treat a disease state characterised by  
 CC cerebral amyloid angiopathy (CAA)

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KWVFFA 6  
 Db 1 KIVFFA 6

RESULT 54

AAE35446  
 ID AAE35446 standard; peptide; 6 AA.

XX AAE35446;

XX 17-JUN-2003 (first entry)

XX Abeta peptide #17.

XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotrophic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 1..6

FT /note= "D-form residues"

FT Modified-site 6

FT /note= "C-terminal amide"

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.

XX Prevention and/or treatment of an amyloid-related disease e.g.

XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.

XX Claim 1; Page 59; 44pp; English.

XX The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of including  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 | : | | |  
 Db 1 KIVFFA 6

RESULT 55  
 AAE35438  
 ID AAE35438 standard; peptide; 6 AA.

AC AAE35438;

DT 17-JUN-2003 (first entry)

DE Abeta peptide #9.

XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;  
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;  
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;  
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;  
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;  
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;  
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 1. .6 /note= "D-form residues"

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.

XX Prevention and/or treatment of an amyloid-related disease e.g.

XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.

XX Claim 1; Page 58; 44pp; English.

XX The invention relates to a method for prevention and/or treatment of an  
 CC amyloid-related disease which comprises administration of an all-D -  
 CC amyloid-beta peptide. The method is used for preventing and/or treating  
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid  
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and  
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from  
 CC the mammal; and reducing or inhibiting the formation of plaques. It is  
 CC also used for treating AA (reactive) amyloid diseases including  
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic  
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,  
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's  
 CC disease. AA deposits are also produced as a result of chronic microbial  
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus  
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).  
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits  
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung  
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The  
 CC present sequence is an Abeta peptide used to illustrate the method of the  
 CC invention

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 6; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 | : | | |  
 Db 1 KIVFFA 6

RESULT 56

ADQ37322

ID ADQ37322 standard; peptide; 6 AA.

XX ADQ37322;

XX 07-OCT-2004 (first entry)

XX Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antichyroid; vasotropic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular dementia;  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 6 /note= "amidated"

XX WO2004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/S2.

XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 CC that prevents or treats amyloid-beta related disease and second agent  
 CC that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 69; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,

CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators' and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0;

QY 1 KVVFFA 6  
 |:||||  
 Db 1 KIVFFA 6

RESULT 57

ADQ37270  
 ID ADQ37270 standard; peptide; 6 AA.

AC ADQ37270;

DT 07-OCT-2004 (first entry)

DE Vaccine antigen amyloid-beta related amino acid sequence.

KW amyloid-beta; amyloid-beta related disease;  
 KW amyloid-beta fibril formation; immune response; neurotropic;  
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
 KW antithyroid; vasotonic; cardiovascular; tranquilliser; uropathic;  
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
 KW cardiant; antidepressant; endocrine; hypnotic;  
 KW amyloid-beta fibril formation modulator; immune system modulator;  
 KW Alzheimer's disease; mild cognitive impairment;  
 KW mild-to-moderate cognitive impairment; vascular  
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
 KW senile dementia; Down's syndrome; inclusion body myositis;  
 KW age-related macular degeneration; hypothyroidism;  
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
 KW behavioural dysfunction; neurological condition; psychological condition;  
 KW vaccine antigen.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 1..6 /note= "D-form residues"

FT Modified-site 6

/note= "amidated"

FT WO2004058239-A1.

PN 15-JUL-2004.

PD 24-DEC-2003; 2003WO-CA002021.

PF 24-DEC-2002; 2002US-0436379P.

PR 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent  
 PT that prevents or treats amyloid-beta related disease and second agent  
 PT that is either a peptide or peptidomimetic or an immune system modulator.  
 XX Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
 CC modulates amyloid-beta fibril formation or induces a prophylactic or  
 CC therapeutic immune response against amyloid-beta fibril formation; or  
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
 CC fibril formation. Also described is a kit comprising (C). (C) have  
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
 CC ophthalmological, antithyroid, vasotonic, cardiovascular, tranquilliser,  
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
 CC and can be used as amyloid-beta fibril formation modulators, and as  
 CC immune system modulators. (C) can be used for preventing or treating an  
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
 CC Down's syndrome, inclusion body myositis, age-related macular  
 CC degeneration, or a condition associated with Alzheimer's disease  
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
 CC field deficits, incoordination, gait disturbance, transient ischaemic  
 CC attack or stroke, transient alertness, attention deficit, frequent falls,  
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
 CC damage), or a psychological condition (e.g. depression, delusions,  
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
 CC having amyloid-beta deposits. The present sequence represents a peptide  
 CC that can be used as a vaccine antigen in the exemplification of the  
 CC present invention.

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
 |:||||

Db 1 KIVFFA 6



RESULT 58  
ADQ37313  
ID ADQ37313 standard; peptide; 6 AA.  
XX  
AC ADQ37313;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Antifibrillogenic amyloidosis inhibiting peptide.  
XX  
KW amyloid-beta; amyloid-beta related disease;  
KW amyloid-beta fibril formation; immune response; nootropic;  
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;  
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
KW cardiant; antidepressant; endocrine; hypnotic;  
KW amyloid-beta fibril formation modulator; immune system modulator;  
KW Alzheimer's disease; mild cognitive impairment;  
KW mild-to-moderate cognitive impairment; vascular dementia;  
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
KW senile dementia; Down's syndrome; inclusion body myositis;  
KW age-related macular degeneration; hypothyroidism;  
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
KW behavioural dysfunction; neurological condition; psychological condition;  
KW vaccine antigen.  
XX  
OS Synthetic.  
XX  
PN WO2004058239-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 24-DEC-2003; 2003WO-CA002021.  
XX  
PR 24-DEC-2002; 2002US-0436379P.  
PR 23-JUN-2003; 2003US-0482214P.  
XX  
XX (NEUR-) NEUROCHEM INT LTD.  
XX  
PI Gervais F, Bellini F;  
XX  
XX WPI; 2004-543342/52.  
XX  
XX Composition for treating e.g. Alzheimer's disease comprises first agent  
PT that prevents or treats amyloid-beta related disease and second agent  
PT that is either a peptide or peptidomimetic or an immune system modulator.  
XX  
PS Disclosure; Page 69; 143pp; English.  
XX  
CC The present invention describes compositions (C) comprising: (a) a first  
CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
CC modulates amyloid-beta fibril formation or induces a prophylactic or  
CC therapeutic immune response against amyloid-beta fibril formation; or  
CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
CC fibril formation. Also described is a kit comprising (C). (C) have  
CC nootropic, neuroprotective, cerebroprotective, haemostatic,  
CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,  
CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,  
CC and can be used as amyloid-beta fibril formation modulators, and as  
CC immune system modulators. (C) can be used for preventing or treating an  
CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
CC Down's syndrome, inclusion body myositis, age-related macular  
CC degeneration, or a condition associated with Alzheimer's disease  
CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia

CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
CC field deficits, incoordination, gait disturbance, transient ischaemic  
CC attack or stroke, transient alertness, attention deficit, frequent falls,  
CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
CC damage), or a psychological condition (e.g. depression, delusions,  
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
CC excessive guilt)) in a subject e.g. human having a genomic mutation in an  
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
CC having amyloid-beta deposits. The present sequence represents a peptide  
CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide  
CC in the exemplification of the present invention.  
XX  
XX Sequence 6 AA;  
SQ  
Query Match 96.6%; Score 28; DB 8; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
DB 1 KIVFFA 6  
|:||||  
RESULT 59  
ADQ37262  
ID ADQ37262 standard; peptide; 6 AA.  
XX  
AC ADQ37262;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Vaccine antigen amyloid-beta related amino acid sequence.  
XX  
KW amyloid-beta; amyloid-beta related disease;  
KW amyloid-beta fibril formation; immune response; nootropic;  
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;  
KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;  
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;  
KW cardiant; antidepressant; endocrine; hypnotic;  
KW amyloid-beta fibril formation modulator; immune system modulator;  
KW Alzheimer's disease; mild cognitive impairment;  
KW mild-to-moderate cognitive impairment; vascular dementia;  
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;  
KW senile dementia; Down's syndrome; inclusion body myositis;  
KW age-related macular degeneration; hypothyroidism;  
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;  
KW behavioural dysfunction; neurological condition; psychological condition;  
KW vaccine antigen.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1. .6  
FT /note= "D-form residues"  
XX  
XX WO2004058239-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 24-DEC-2003; 2003WO-CA002021.  
XX  
PR 24-DEC-2002; 2002US-0436379P.  
PR 23-JUN-2003; 2003US-0482214P.  
XX  
XX (NEUR-) NEUROCHEM INT LTD.  
XX  
XX Gervais F, Bellini F;  
XX  
XX WPI; 2004-543342/52.  
XX



PT Composition for treating e.g. Alzheimer's disease comprises first agent  
PT that prevents or treats amyloid-beta related disease and second agent  
XX that is either a peptide or peptidomimetic or an immune system modulator.

PS Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first  
CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)  
CC a second agent (a2) that is: (i) a peptide or peptidomimetic that  
CC modulates amyloid-beta fibril formation or induces a prophylactic or  
CC therapeutic immune response against amyloid-beta fibril formation; or  
CC (ii) an immune system modulator that prevents or inhibits amyloid-beta  
CC fibril formation. Also described is a kit comprising (C). (C) have  
CC neurotropic, neuroprotective, cerebroprotective, haemostatic,  
CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,  
CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,  
CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,  
CC and can be used as amyloid-beta fibril formation modulators, and as  
CC immune system modulators. (C) can be used for preventing or treating an  
CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic  
CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,  
CC mild-to-moderate cognitive impairment, vascular dementia, cerebral  
CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,  
CC Down's syndrome, inclusion body myositis, age-related macular  
CC degeneration, or a condition associated with Alzheimer's disease  
CC (including hypothyroidism, cerebrovascular disease, cardiovascular  
CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,  
CC aggression, or incontinence), a neurological condition (e.g. Huntington's  
CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,  
CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia  
CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual  
CC field deficits, incoordination, gait disturbance, transient ischaemic  
CC attack or stroke, transient alertness, attention deficit, frequent falls,  
CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural  
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic  
CC damage), or a psychological condition (e.g. depression, delusions,  
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep  
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal  
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or  
CC excessive guilt) in a subject e.g. human having a genomic mutation in an  
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;  
CC having amyloid-beta deposits. The present sequence represents a peptide  
CC that can be used as a vaccine antigen in the exemplification of the  
XX present invention.

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 1 KIVFFA 6

RESULT 60

ADY37921  
ID ADY37921 standard; peptide; 6 AA.

XX

AC ADY37921;

XX 19-MAY-2005 (first entry)

DT

DE Amyloid-targeting peptide, SEQ ID NO:1, for use in imaging agent.

XX

KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
KW transmissible spongiform encephalopathy; scrapie; BSE;  
KW Alzheimer's disease; neurological disease; amyloidosis;  
KW non-insulin dependent diabetes; metabolic disorder.

OS Synthetic.

XX

PN US2005048000-A1.

XX

PD 03-MAR-2005.

XX

PF 03-DEC-2003; 2003US-00728028.

XX

PR 25-JUL-2000; 2000US-0220808P.

XX

PR 24-JUL-2001; 2001US-00915092.

XX

PR 29-JAN-2003; 2003US-0443291P.

XX

PA (NEUR-) NEUROCHEM INT LTD.

XX

PI Gervais F, Kong X, Chalifour R, Migneault D;

XX

PI WPI; 2005-212201/22.

XX

XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-

XX related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform

XX encephalopathy, primary amyloidosis or Alzheimer's disease.

XX

PS Disclosure; SEQ ID NO 1; 34pp; English.

XX

CC The invention relates to an amyloid-targeting imaging agent. The imaging

CC agent comprises an amyloid targeting moiety (such as a peptide) joined to

CC the blood-brain barrier. The invention also relates to a kit for

CC preparing a radiopharmaceutical preparation from the imaging agent and a

CC method for diagnosing an amyloid-related condition in a patient. The

CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-

CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,

CC transmissible cerebral amyloidosis (also known as transmissible virus

CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,

CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,

CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,

CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-

CC mediated diseases, dialysis-related amyloidosis, light chain-related

CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a

CC patient. The agent does not exhibit excessive toxicity or irritation,

CC does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence

CC prevention of the undesirable effects of such disorders. Sequences

CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as

CC the amyloid-targeting moiety in an imaging agent of the invention.

XX

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
|:||||  
Db 1 KIVFFA 6

RESULT 61

ADY37929  
ID ADY37929 standard; peptide; 6 AA.

XX

AC ADY37929;

XX 19-MAY-2005 (first entry)

DT

DE Amyloid-targeting peptide, SEQ ID NO:9, for use in imaging agent.

XX

KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;  
KW transmissible spongiform encephalopathy; scrapie; BSE;  
KW Alzheimer's disease; neurological disease; amyloidosis;  
KW non-insulin dependent diabetes; metabolic disorder.

OS Synthetic.

XX



XX 21-DEC-2004.  
 XX 10-JUL-2001; 2001US-00902540.  
 XX 10-JUL-2000; 2000US-0217883P.  
 XX (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;  
 XX WPI; 2005-028716/03.  
 XX New substantially purified Myxococcus xanthus nucleic acid molecule  
 encoding a nitrite reductase, useful for determining gene expression,  
 identifying mutations in a gene of interest, and for constructing  
 mutations in a gene of interest.  
 XX Example 2; SEQ ID NO 13513; 25pp; English.  
 XX The invention relates to a substantially purified nucleic acid molecule  
 encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a  
 recombinant DNA construct for expression of a nitrite reductase gene in a  
 plant cell, and a plant cell comprising the recombinant DNA construct.  
 XX The nucleic acid is useful for determining gene expression, identifying  
 mutations in a gene of interest, and for constructing mutations in a gene  
 of interest. Sequences given in records for SEQ IDs 9692-16825 represent  
 a group of 7134 Myxococcus xanthus proteins and peptides. Note: The  
 sequence data for this patent did not form part of the printed from USPTO  
 specification, but was obtained in electronic format directly from USPTO  
 XX Sequence 123 AA;  
 Query Match 96.6%; Score 28; DB 9; Length 123;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 52 KVIFFA 57  
 RESULT 64  
 ADM16726  
 ID ADM16726 standard; protein; 393 AA.  
 XX ADM16726;  
 XX 17-JUN-2004 (first entry)  
 XX PERL-P7-G8 protein.  
 XX Phlebotomus ariasi; Phlebotomus perniciosus; Vaccine;  
 XX Leishmania infection.  
 XX Phlebotomus perniciosus.  
 XX WO2004027041-A2.  
 XX 01-APR-2004.  
 XX 18-SEP-2003; 2003WO-US029833.  
 XX 19-SEP-2002; 2002US-0412327P.  
 XX 12-NOV-2002; 2002US-0425852P.  
 XX (MERI-) MERIAL LTD.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;  
 Audonnet J, Milward F;  
 WPI; 2004-295410/27.  
 XX 01-APR-2004.  
 XX 18-SEP-2003; 2003WO-US029833.  
 XX 19-SEP-2002; 2002US-0412327P.  
 XX 12-NOV-2002; 2002US-0425852P.  
 XX (MERI-) MERIAL LTD.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;  
 Audonnet J, Milward F;  
 WPI; 2004-295410/27.

DR N-PSDB; ADM16727.  
 XX New substantially purified salivary Phlebotomus ariasi or Phlebotomus  
 PT perniciosus polypeptide, useful for inhibiting, treating or preventing  
 PT Leishmania infection in a subject.  
 XX Claim 40; SEQ ID NO 49; 200pp; English.  
 XX The present invention relates to a substantially purified salivary  
 CC Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The  
 CC composition comprising the polypeptide or the nucleic acid encoding the  
 CC polypeptide is useful for manufacture of a medicament. The polypeptides  
 CC and nucleic acids are useful for inducing an immune response to a P.  
 CC ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a  
 CC symptom of a Leishmania infection or preventing a Leishmania infection in  
 CC a subject. The present sequence represents a purified Phlebotomus ariasi  
 XX protein.  
 XX Sequence 393 AA;  
 Query Match 96.6%; Score 28; DB 8; Length 393;  
 Best Local Similarity 83.3%; Pred. No. 4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 299 KVIFFA 304  
 RESULT 65  
 ADM16684  
 ID ADM16684 standard; protein; 393 AA.  
 XX ADM16684;  
 XX 17-JUN-2004 (first entry)  
 XX PRL-P4-D6 protein.  
 XX Phlebotomus ariasi; Phlebotomus perniciosus; Vaccine;  
 XX Leishmania infection.  
 XX Phlebotomus ariasi.  
 XX WO2004027041-A2.  
 XX 01-APR-2004.  
 XX 18-SEP-2003; 2003WO-US029833.  
 XX 19-SEP-2002; 2002US-0412327P.  
 XX 12-NOV-2002; 2002US-0425852P.  
 XX (MERI-) MERIAL LTD.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;  
 Audonnet J, Milward F;  
 WPI; 2004-295410/27.  
 XX N-PSDB; ADM16685.  
 XX New substantially purified salivary Phlebotomus ariasi or Phlebotomus  
 PT perniciosus polypeptide, useful for inhibiting, treating or preventing  
 PT Leishmania infection in a subject.  
 XX Claim 1; SEQ ID NO 7; 200pp; English.  
 XX The present invention relates to a substantially purified salivary  
 CC Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The  
 CC composition comprising the polypeptide or the nucleic acid encoding the  
 CC polypeptide is useful for manufacture of a medicament. The polypeptides  
 CC and nucleic acids are useful for inducing an immune response to a P.

CC ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a  
CC symptom of a Leishmania infection or preventing a Leishmania infection in  
CC a subject. The present sequence represents a purified Phlebotomus ariasi  
CC protein.

XX Sequence 393 AA;

Query Match 96.6%; Score 28; DB 8; Length 393;  
Best Local Similarity 83.3%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
||:||||  
Db 298 KVIFFA 303

RESULT 66

ADO43456  
ID ADO43456 standard; protein; 399 AA.

XX ADO43456;

XX 29-JUL-2004 (first entry)

XX Lutzomyia longipalpis (sand fly) salivary protein LJM11.

XX LJM11; sand fly; leishmaniasis; diagnosis; vaccine; genetic immunisation.  
XX Lutzomyia longipalpis.

PH Key Location/Qualifiers  
FT Peptide 1..24  
/label= Signal\_peptide  
FT Protein 25..399  
/label= Mature\_protein

XX WO2004039958-A2.

XX 13-MAY-2004.

XX 29-OCT-2003; 2003WO-US034453.

XX 29-OCT-2002; 2002US-0422303P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX (PESQ-) CENT PESQUISAS GONCALO MONIZ.

XX Valenzuela JG, Ribeiro JMC, Barral A, Netto M, Brodekyn C;  
PI Gomes R;

XX WPI; 2004-376184/35.

XX N-PSDB; ADO43457.

XX Novel salivary Lutzomyia longipalpis polypeptide, useful for inhibiting  
PT symptom of Leishmania infection or preventing Leishmania infection in  
FT subjects.

XX Claim 2; SEQ ID NO 63; 145pp; English.

XX The present sequence is the protein sequence of LJM11, a Lutzomyia  
CC longipalpis (New World sand fly) salivary polypeptide. The invention  
CC provides substantially purified L. longipalpis polypeptides and the  
CC polynucleotides encoding them, as well as vectors, host cells, antibodies  
CC and pharmaceutical compositions comprising the polypeptides or  
CC polynucleotides. A claimed method for inducing an immune response to L  
CC longipalpis in a subject involves administering a L. longipalpis salivary  
CC polypeptide (or its variant or immunogenic fragment) or a polynucleotide  
CC encoding it. The immune response is a T-cell or B-cell response, and the  
CC subject is preferably a dog or a human. A claimed method for inhibiting a  
CC symptom of a Leishmania infection or preventing a Leishmania infection in  
CC a subject comprises administering a L. longipalpis salivary protein or  
CC polynucleotide. A claimed method of diagnosing Leishmania infection  
CC comprises contacting a solid substrate comprising at least 3, 6 or 10 L.

CC longipalpis salivary polypeptides with a sample from the subject and  
CC detecting binding of a component of the sample to at least one of the  
CC polypeptides.

XX Sequence 399 AA;

Query Match 96.6%; Score 28; DB 8; Length 399;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
||:||||  
Db 305 KVIFFA 310

RESULT 67

ABB61977

ID ABB61977 standard; protein; 564 AA.

XX ABB61977;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 12723.

XX Drosophila; developmental biology; cell signalling; insecticide;  
XX pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL06080.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.

XX Disclosure; SEQ ID NO 12723; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at fcp.wipo.int/pub/published\_pct\_sequences

XX Sequence 564 AA;

Query Match 93.1%; Score 27; DB 4; Length 564;  
Best Local Similarity 66.7%; Pred. No. 9.9e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6  
||:||||  
Db 53 KIIFFA 58

KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;  
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;  
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;  
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9628471-A1.  
 XX  
 PD 19-SEP-1996.  
 XX  
 PF 14-MAR-1996; 96WO-US003492.  
 XX  
 PR 14-MAR-1995; 95US-00404831.  
 PR 07-JUN-1995; 95US-00475579.  
 PR 27-OCT-1995; 95US-00548998.  
 XX  
 XX (PHAR-) PHARM PEPTIDES INC.  
 XX  
 PI Findeis MA, Benjamin H, Garnick MB, Geftter ML, Hundal A;  
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S;  
 PI Kubasek W, Chin J, Lee J, Kelley M,  
 XX WPI; 1996-433762/43.  
 DR  
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic  
 PT protein coupled (in)directly to at least 1 modifying gp., useful in  
 PT treatment of Alzheimer's disease.  
 XX  
 XX Claim 16; Page 91; 106pp; English.  
 XX  
 CC AAW02310-W02332 represent the peptide portions of the beta-amyloid  
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4  
 CC kilodalton peptide that is the major protein component of amyloid  
 CC plaques. Amyloid plaques are present both in the brain lesions, and in  
 CC the walls of cerebral blood vessels in Alzheimer's disease patients. The  
 CC amyloid modulators of the invention comprise an amyloidogenic protein or  
 CC peptide (such as this sequence) coupled directly or indirectly to at  
 CC least one modifying group. The modifying group is preferably a cyclic,  
 CC heterocyclic, or polycyclic group, such as decaalin, a cholanyl group, a  
 CC biotin containing group, or a fluorescein containing group. These  
 CC compounds then modulate the aggregation of these sequences to natural  
 CC amyloid proteins or peptides when contacted with the natural  
 CC amyloidogenic proteins or peptides. The modulator compounds can be used  
 CC in the treatment of disorders associated with amyloidosis, such as  
 CC familial amyloid polynuropathy, familial amyloid cardiomyopathy,  
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,  
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset  
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid  
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage  
 CC and other types of amyloidosis. The modulators are also useful for the  
 CC treatment of disorders associated with beta-amyloidosis, especially  
 CC Alzheimer's disease  
 XX  
 SQ Sequence 6 AA;  
 Query Match 89.7%; Score 26; DB 2; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1 KLVFFA 6  
 RESULT 70  
 AAW89378  
 ID AAW89378 standard; peptide; 6 AA.  
 XX  
 AC AAW89378;  
 XX  
 XX 02-MAR-1999 (first entry)  
 DT  
 XX

KW ABB68472 standard; protein; 1443 AA.  
 AC ABB68472;  
 XX  
 XX 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 32208.  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 XX (PEKE ) PE CORP NY.  
 PA  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 XX WPI; 2001-856860/75.  
 DR N-PSDB; ABL12575.  
 XX  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Disclosure; SEQ ID NO 32208; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIFO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1443 AA;  
 Query Match 93.1%; Score 27; DB 4; Length 1443;  
 Best Local Similarity 66.7%; Pred. No. 2.5e+03; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KVVFFA 6  
 Db 1204 KLIFFA 1209  
 RESULT 69  
 AAW02314  
 ID AAW02314 standard; peptide; 6 AA.  
 XX  
 AC AAW02314;  
 XX  
 XX 02-MAY-1997 (first entry)  
 DT  
 XX Beta-amyloid modulator peptide #5.  
 DE  
 XX Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;  
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;  
 KW familial amyloid polynuropathy; familial amyloid cardiomyopathy;  
 KW

DE Beta-amyloid peptide derivative A-beta-16-21.  
 XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;  
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;  
 KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;  
 KW Creutzfeldt-Jakob disease; bap.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX US5854204-A.  
 XX 29-DEC-1998.  
 XX  
 XX 14-MAR-1996; 96US-00612785.  
 XX  
 XX 14-MAR-1995; 95US-00404831.  
 PR 07-JUN-1995; 95US-00475579.  
 PR 27-OCT-1995; 95US-00548998.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX  
 XX Hundal A, Geffer ML, Kasman L, Musso G, Molineaux S, Benjamin H;  
 PI Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;  
 PI Garnick WB, Kubasek W, Signer ER;  
 XX  
 XX WPI; 1999-094964/08.  
 XX  
 XX New peptide(s) derived from beta-amyloid peptide that inhibit amyloid  
 PT aggregation - and neurotoxicity, specifically for treatment and  
 PT prevention of Alzheimer's disease.  
 XX  
 XX Example 12; Col 64; 52pp; English.  
 XX  
 XX The present invention describes beta-amyloid peptide (bap) derivatives.  
 CC The bap derivatives inhibit aggregation of amyloidogenic proteins and  
 CC peptides, specifically bap, and their neurotoxicity, so are useful for  
 CC treating and preventing any disease involving amyloidosis, specifically  
 CC Alzheimer's disease but also Down's syndrome, familial amyloid  
 CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and  
 CC Creutzfeldt-Jakob disease. The bap derivatives are also used to diagnose  
 CC these diseases, in vitro or in vivo, by detecting binding of bap to  
 CC labelled bap derivatives. Some bap derivatives inhibit bap aggregation  
 CC even when bap is present in molar excess. The present sequence represents  
 CC a bap derivative  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 89.7%; Score 26; DB 2; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVVFFA 6  
 Db 1 KLVFFA 6  
 RESULT 71  
 AAB48484  
 ID AAB48484 standard; peptide; 6 AA.  
 XX  
 AC AAB48484;  
 XX  
 XX 02-MAR-2001 (first entry)  
 DT  
 XX Antifibrillogenic peptide #11.  
 DE  
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX

FH Key Location/Qualifiers  
 FT Modified-site 6 /note= "C-terminal amide"  
 XX  
 XX WO200068263-A2.  
 PN 16-NOV-2000.  
 XX  
 XX 04-MAY-2000; 2000WO-CA000515.  
 PF  
 XX 05-MAY-1999; 99US-0132592P.  
 PR  
 XX (NEUR-) NEUROCHEM INC.  
 PA  
 XX Chalifour R, Gervais F, Gupta A;  
 PI  
 XX WPI; 2001-031852/04.  
 DR  
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic.  
 XX  
 XX Claim 7; Page 25; 46pp; English.  
 PS  
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
 CC binding region and the prot-prot interaction region of the human amyloid  
 CC protein  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 89.7%; Score 26; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KVVFFA 6  
 Db 1 KLVFFA 6  
 RESULT 72  
 AAB48476  
 ID AAB48476 standard; peptide; 6 AA.  
 XX  
 AC AAB48476;  
 XX  
 XX 02-MAR-2001 (first entry)  
 DT  
 XX Antifibrillogenic peptide #3.  
 DE  
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200068263-A2.  
 PN  
 XX 16-NOV-2000.  
 PD  
 XX 04-MAY-2000; 2000WO-CA000515.  
 PF  
 XX 05-MAY-1999; 99US-0132592P.  
 PR  
 XX (NEUR-) NEUROCHEM INC.  
 PA  
 XX Chalifour R, Gervais F, Gupta A;  
 PI  
 XX WPI; 2001-031852/04.  
 DR  
 XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
PT its isomer or peptidomimetic.  
XX  
XX  
PS Claim 7; Page 25; 46pp; English.  
XX  
CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore  
CC useful for treating amyloidosis disorders such as Alzheimer's disease.  
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan  
CC binding region and the prot-prot interaction region of the human amyloid  
CC protein  
XX  
XX Sequence 6 AA;  
SQ  
Query Match 89.7%; Score 26; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
Db 1 KLVFFA 6  
|:|||||  
1 KLVFFA 6

RESULT 73  
AAB82632  
ID AAB82632 standard; peptide; 6 AA.  
XX  
AC AAB82632;  
XX  
DT 02-OCT-2001 (first entry)  
XX  
DE All-D peptide used in Alzheimer's disease vaccine.  
XX  
KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;  
KW therapy; antigen.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..6  
FT /note= "all D-form residues"  
FT Modified-site 6  
FT /note= "C-terminal amide"  
XX  
XX WO200139796-A2.  
XX  
PD 07-JUN-2001.  
XX  
XX 29-NOV-2000; 2000WO-CA001413.  
XX  
XX 29-NOV-1999; 99US-0168594P.  
XX  
XX 28-NOV-2000; 2000US-00724842.  
XX  
XX (NEUR-) NEUROCHEM INC.  
XX  
XX Chalfour R, Hebert L, Kong X, Gervais F;  
XX  
XX WPI; 2001-441458/47.  
XX  
XX Preventing/treating amyloid-related disease, especially Alzheimer's  
PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,  
PT which elicits production of antibodies to prevent fibrillogenesis and  
PT associated cellular toxicity.  
XX  
XX Disclosure; Page 11; 31pp; English.  
XX  
XX The present sequence is that of an all-D peptide suitable for use for  
CC preparing vaccines for preventing or treating Alzheimer's disease and  
CC other amyloid related disorders in humans. It is based on a portion of  
CC amyloid-beta peptide (see AAB82622), and may be modified by removing or  
XX inserting 1 or more amino acid residues, or by substituting 1 or more

CC amino acid residues with other amino acid residues or non-amino acid  
CC fragments. Vaccines of the invention are produced using 'non-self'  
CC peptides synthesised from the unnatural D-configuration amino acids to  
CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be  
CC aggregated to be operative or immunogenic. They preferably interact with  
CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or  
CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic  
CC fragments, protein conjugates, immunogenic derivative peptides and  
CC immunogenic peptidomimetics. Examples include all-D peptides  
CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and  
CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given  
CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,  
CC preventing fibrillogenesis and associated cellular toxicity. The amyloid  
CC related diseases may be localised amyloidosis, e.g. diabetes type II,  
CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,  
CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and  
CC prion protein related disorders, or systemic amyloidosis associated with  
CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.  
CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic  
CC amyloidosis found in long-term haemodialysis patients. The present all-D  
CC peptide was demonstrated to elicit antibody production in rabbits, and  
CC provided greater anti-fibrillogenic activity than its all-L equivalent  
XX  
XX Sequence 6 AA;  
SQ  
Query Match 89.7%; Score 26; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVVFFA 6  
Db 1 KLVFFA 6  
|:|||||  
1 KLVFFA 6

RESULT 74  
ABG71009  
ID ABG71009 standard; peptide; 6 AA.  
XX  
XX AC ABG71009;  
XX  
DT 05-DEC-2002 (first entry)  
XX  
DE Long form beta-amyloid protein fragment #6.  
XX  
KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;  
KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;  
KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;  
KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;  
KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;  
KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;  
KW macroglobulinaemia-associated amyloidosis; reactive amyloidosis;  
KW primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;  
KW hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;  
KW hereditary non-neuropathic systemic amyloidosis;  
KW familial Mediterranean Fever.  
XX  
XX Homo sapiens.  
XX  
XX US2002098173-A1.  
XX  
XX 25-JUL-2002.  
XX  
XX 04-OCT-2001; 2001US-00972475.  
XX  
XX 14-MAR-1995; 95US-00404831.  
XX  
XX 07-JUN-1995; 95US-00475579.  
XX  
XX 27-OCT-1995; 95US-00548998.  
XX  
XX 14-MAR-1996; 96US-00617267.  
XX  
XX (PRAE-) PRAECIS PHARM INC.  
XX  
XX Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;  
XX Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;



XX WPI; 2002-697709/75.  
 XX  
 XX Amyloid modulator useful for treating a disorder associated with  
 PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment  
 PT coupled to a modifying group.  
 XX  
 XX Example 12; Page 35; 41pp; English.  
 PS  
 XX  
 CC The invention describes an amyloid modulator comprising an amyloidogenic  
 CC protein and/or peptide fragment coupled to a modifying group so that the  
 CC compound modulates the aggregation of natural amyloid proteins or  
 CC peptides. The modulator is used for treating a disorder associated with  
 CC amyloidosis e.g. familial amyloid polynuropathy (Portuguese, Japanese  
 CC and Swedish types), familial amyloid cardiomyopathy (Danish type),  
 CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine  
 CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset  
 CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated  
 CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or  
 CC macroglobulinaemia-associated amyloidosis, primary localised cutaneous  
 CC nodular amyloidosis associated with Sjogren's syndrome, reactive  
 CC (secondary) amyloidosis, familial Mediterranean Fever and familial  
 CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),  
 CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,  
 CC amyloidosis associated with long term haemodialysis, hereditary non-  
 CC neuropathic systemic amyloidosis (familial amyloid polynuropathy III),  
 CC familial amyloidosis of Finnish type, amyloidosis associated with  
 CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary  
 CC renal amyloidosis and lysozyme-associated hereditary systemic  
 CC amyloidosis. The compound is capable of altering and inhibiting beta-  
 CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins  
 CC or peptides when contacted with a molar excess amount of natural beta-APs  
 CC relative to the modulator. This sequence represents a fragment of the  
 CC long form of beta-amyloid used in the creation of an amyloid modulator  
 XX  
 SQ Sequence 6 AA;  
 Query Match 89.7%; Score 26; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFA 6  
 Db |:|:|:|  
 1 KLVFFA 6  
 RESULT 75  
 ABB05157  
 ID ABB05157 standard; peptide, 6 AA.  
 XX  
 AC ABB05157;  
 XX  
 DT 02-APR-2002 (first entry)  
 XX  
 DE Beta amyloid peptide (16-21) SEQ ID NO:9.  
 XX  
 KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;  
 KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;  
 KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;  
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;  
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;  
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;  
 KW hereditary cerebral haemorrhage; familial amyloid polynuropathy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX US6319498-B1.  
 XX  
 XX 20-NOV-2001.  
 XX  
 XX 14-MAR-1996; 96US-00617267.  
 XX

PR 14-MAR-1995; 95US-00404831.  
 PR 07-JUN-1995; 95US-00475579.  
 PR 27-OCT-1995; 95US-00548998.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX  
 PI Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;  
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;  
 XX  
 DR WPI; 2002-146668/19.  
 XX  
 XX Amyloid modulator compound useful for treatment of an amyloidogenic  
 PT disease such as Alzheimer's disease comprises an aggregation core domain  
 PT and a modifying group attached to it.  
 XX  
 PS Disclosure; Col 18; 54pp; English.  
 XX  
 CC The present invention describes an amyloid modulator compound (I)  
 CC comprising an aggregation core domain and a modifying group attached to  
 CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,  
 CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic  
 CC and auditory activities, and can be used as a natural amyloid aggregation  
 CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide  
 CC (beta-AP). (I) are used in the manufacture of a medicament for the  
 CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's  
 CC disease and other clinical occurrences of beta amyloid deposition such as  
 CC Down's syndrome individuals and in patients with hereditary cerebral  
 CC haemorrhage with amyloidosis, and for treating a disorder associated with  
 CC amyloidosis such as familial amyloid polynuropathy. (I) reduces the  
 CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)  
 CC not only reduces the formation of neurotoxic aggregates but also have the  
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The  
 CC present sequence represents a beta-AP peptide, which is used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 6 AA;  
 Query Match 89.7%; Score 26; DB 5; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVFFA 6  
 Db |:|:|:|  
 1 KLVFFA 6  
 Search completed: December 29, 2005, 17:33:37  
 Job time : 82.7742 secs



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds  
(without alignments)  
54.137 Million cell updates/sec

Title: US-10-009-122-7  
Perfect score: 29  
Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	143	2	Q91Y69 MESAU
2	29	100.0	162	2	Q9N284 BOVIN
3	29	100.0	248	2	Q9BGL4 SHEEP
4	29	100.0	261	1	Y1086 HAEIN
5	29	100.0	261	2	Q4QLX2 HAE18
6	29	100.0	277	2	Q73KX6 TREDE
7	29	100.0	314	2	Q9M716 ARATH
8	29	100.0	381	2	Q5LIA8 GEOKA
9	29	100.0	389	2	Q8KHB6 CLODI
10	29	100.0	469	2	Q8S807 ARATH
11	29	100.0	632	2	Q9N1P6 CANFA
12	29	100.0	654	2	Q6U789 MELGA
13	29	100.0	660	1	MMP2 HUMAN
14	29	100.0	660	2	Q5IY21 TUPGB
15	29	100.0	661	2	Q95J44 PIG
16	29	100.0	661	2	Q9GLS5 BOVIN
17	29	100.0	662	1	MMP2 MOUSE
18	29	100.0	662	1	MMP2 RABIT
19	29	100.0	662	1	MMP2 RAT
20	29	100.0	662	2	Q6GMN9 RAT
21	29	100.0	663	1	MMP2 CHICK
22	29	100.0	767	2	Q8KTV1 CLODI
23	29	100.0	770	2	Q7XXG3 ORISA
24	29	100.0	840	2	Q6QK33 ORISA
25	29	100.0	842	2	Q60HB5 ORISA
26	29	100.0	842	2	Q69DS7 ORISA
27	29	100.0	945	2	Q9N175 SHEEP
28	29	100.0	1147	1	NOS2 RAT
29	29	100.0	1147	2	Q8XST6 RAT
30	29	100.0	1147	2	Q9QW28 NMURI
31	29	100.0	1147	2	Q9R0W4 RAT

32	28	96.6	118	2	Q8Y1S2 RALSO
33	28	96.6	169	2	Q8U1S9 AGRT5
34	28	96.6	283	2	Q19334 CAEL
35	28	96.6	305	2	Q8EM92 OCEIH
36	28	96.6	355	2	Q6LJY6 PHOPR
37	28	96.6	1044	2	Q8XIN5 CLOPE
38	26	89.7	85	2	Q19641 CAEL
39	26	89.7	99	2	Q731J0 WOLPM
40	26	89.7	109	2	Q8XQ19 RALSO
41	26	89.7	126	2	Q6G347 BARHE
42	26	89.7	131	2	Q6C1M8 YARLI
43	26	89.7	137	2	Q6G346 BARHE
44	26	89.7	137	2	Q5SKK3 THE8
45	26	89.7	142	2	Q4JC95 SULAC
46	26	89.7	149	2	Q5WU01 LEGPL
47	26	89.7	149	2	Q5X274 LEGPA
48	26	89.7	149	2	Q5ZSR4 LEGPH
49	26	89.7	150	2	Q51314 GNOSO
50	26	89.7	156	1	GUAD BACSU
51	26	89.7	156	2	Q5WB80 BACSK
52	26	89.7	166	2	Q59317 PYRHO
53	26	89.7	185	2	Q67590 AQUAE
54	26	89.7	191	1	CSRPI CHICK
55	26	89.7	191	1	CSRPI COTJA
56	26	89.7	229	2	Q9RR88 DEIRA
57	26	89.7	232	2	Q67QU1 SYMTH
58	26	89.7	233	2	Q527F8 MAGGR
59	26	89.7	233	2	Q30760 RHOSH
60	26	89.7	235	2	Q9N2Y5 CAEL
61	26	89.7	266	2	Q5UEW2 9PROT
62	26	89.7	268	2	Q5GU79 XANOR
63	26	89.7	276	2	Q7QS35 GIALA
64	26	89.7	285	2	Q48777 ARATH
65	26	89.7	290	2	Q5A5P9 CANAL
66	26	89.7	296	2	Q751V7 ORISA
67	26	89.7	299	1	VG12 ICHV1
68	26	89.7	318	2	Q8GX90 ARATH
69	26	89.7	321	2	Q6ASCI DESPS
70	26	89.7	340	2	Q9EZ99 ZYMWO
71	26	89.7	348	1	CYSA METCA
72	26	89.7	352	2	Q83MJ3 SHIFL
73	26	89.7	352	2	Q72FT5 DESVH
74	26	89.7	383	2	Q6M190 DBEBA
75	26	89.7	390	2	Q4HML6 CAMLA
76	26	89.7	403	2	Q4WJL6 ASFPU
77	26	89.7	421	1	YIHN ECOLI
78	26	89.7	421	2	Q8FEG3 ECOL6
79	26	89.7	421	2	Q8X8P3 ECOS7
80	26	89.7	426	2	Q895U4 CLOTE
81	26	89.7	426	2	Q84QAB ORISA
82	26	89.7	428	2	Q4KEQ1 PSBP5
83	26	89.7	432	2	Q6L6X3 9VIRU
84	26	89.7	432	2	Q6L6X5 9VIRU
85	26	89.7	432	2	Q6L6X5 9VIRU
86	26	89.7	432	2	Q5YF80 9VIRU
87	26	89.7	433	2	Q68Y86 9VIRU
88	26	89.7	453	2	Q6GVF2 9VIRU
89	26	89.7	453	2	Q6GVF3 9VIRU
90	26	89.7	453	2	Q6GVF4 9VIRU
91	26	89.7	453	2	Q6GVF6 9VIRU
92	26	89.7	453	2	Q6GVF7 9VIRU
93	26	89.7	453	2	Q6GVF8 9VIRU
94	26	89.7	453	2	Q6GVF9 9VIRU
95	26	89.7	453	2	Q6GVG0 9VIRU
96	26	89.7	453	2	Q6GVG1 9VIRU
97	26	89.7	453	2	Q6GVG2 9VIRU
98	26	89.7	453	2	Q6GVG3 9VIRU
99	26	89.7	453	2	Q6PNE1 9VIRU
100	26	89.7	453	2	Q6QNG1 9VIRU
101	26	89.7	453	2	Q6QNG4 9VIRU
102	26	89.7	453	2	Q6QNG5 9VIRU
103	26	89.7	453	2	Q6QNG6 9VIRU
104	26	89.7	453	2	Q6QNG6 9VIRU

Q8Y1S2	ralstonia s
Q8U1S9	agrobacteri
Q19334	caenorhabdi
Q8EM92	caenorhabdi
Q6LJY6	photobacter
Q8XIN5	clostridium
Q19641	caenorhabdi
Q731J0	wolbachia p
Q8XQ19	ralstonia s
Q6G347	bartonella
Q6C1M8	yarrowella l
Q6G346	bartonella
Q5SKK3	thermus the
Q4JC95	lulolobus
Q5WU01	legionella
Q5X274	legionella
Q5ZSR4	legionella
Q51314	nostoc sp.
Q34598	bacillus su
Q5WB80	bacillus cl
Q59317	pyrococcus
Q67590	aquifex aeo
P67966	gallus gall
P67967	coturnix co
Q9RR88	deinococcus
Q67QU1	syntrophobacte
Q527F8	magnaporthe
Q30760	rhodospir
Q9N2Y5	caenorhabdi
Q5UEW2	uncultured
Q5GU79	xanthomonas
Q7Q835	giardia lam
Q48777	arabidopsis
Q5A5P9	candida alb
Q751V7	oryza sativ
Q00165	ictaluriid h
Q8GX90	arabidopsis
Q6ASCI	desulfotale
Q9EZ99	zymomonas m
Q609Q1	methylococc
Q83MJ3	shigella fl
Q72FT5	desulfowibr
Q6M190	bdellovibri
Q4HML6	campylobact
Q4WJL6	aspergillus
P32135	escherichia
Q8FEG3	escherichia
Q8X8P3	escherichia
Q895U4	clostridium
Q84QAB	oryza sativ
Q4KEQ1	pseudomonas
Q6L6X3	red sea bre
Q6L6X5	rock break
Q6L6X5	sea bass ir
Q75PQ4	turbot irid
Q5YF80	rock bream
Q88Y86	olive floun
Q6GVF2	korean flou
Q6GVF3	korean flou
Q6GVF4	korean flou
Q6GVF6	korean flou
Q6GVF7	korean flou
Q6GVF8	korean flou
Q6GVF9	korean flou
Q6GVG0	korean flou
Q6GVG1	korean flou
Q6GVG2	korean flou
Q6GVG3	korean flou
Q6PNE1	turbot redd
Q6QNG1	rock bream
Q6QNG4	rock bream
Q6QNG5	rock bream
Q6QNG6	rock bream

105	26	89.7	453	2	Q6QNG7_9VIRU	Q6qng7	rock	breem	178	25	86.2	46	2	Q81W20_BACAN	Q81w20	bacillus	a	
106	26	89.7	453	2	Q6QNG8_9VIRU	Q6qng8	rock	breem	179	25	86.2	54	2	Q4Z1B9_PLABE	Q4z1b9	plasmidium		
107	26	89.7	453	2	Q6QNH0_9VIRU	Q6qnh0	rock	breem	180	25	86.2	61	2	Q72A11_DESVH	Q72a11	desulfobivr		
108	26	89.7	453	2	Q6QNH1_9VIRU	Q6qnh1	rock	breem	181	25	86.2	72	2	Q7Y541_BPR69	Q7y541	bacterioph		
109	26	89.7	453	2	Q7T3Y6_9VIRU	Q7t3y6	dwarf	goura	182	25	86.2	75	2	Q4KA43_PSEF5	Q4ka43	pseudomonas		
110	26	89.7	453	2	Q7T3Y7_9VIRU	Q7t3y7	african	lam	183	25	86.2	76	2	Q6MKJ3_BDEBA	Q6mkj3	bdellovibr		
111	26	89.7	453	2	Q7T3Z1_RSIV	Q7t3z1	red	sea	bre	184	25	86.2	76	2	Q7QD77_DESVH	Q7qd77	desulfobivr	
112	26	89.7	453	2	Q8OM45_RSIV	Q8om45	red	sea	bre	185	25	86.2	95	2	Q5LDD7_BACFN	Q5ldj7	bacteroides	
113	26	89.7	453	2	Q8V5D9_9VIRU	Q8v5d9	infectious		186	25	86.2	95	2	Q64UL9_BACFR	Q64ul9	bacteroides		
114	26	89.7	453	2	Q516L1_9VIRU	Q516l1	rock	breem	187	25	86.2	100	2	Q8YM06_ANASP	Q8ym06	anabaena	sp	
115	26	89.7	453	2	Q516L2_9VIRU	Q516l2	rock	breem	188	25	86.2	107	2	Q4U9W4_THEAN	Q4u9w4	theileria	a	
116	26	89.7	453	2	Q7T2P6_9VIRU	Q7t2p6	sea	baas	ir	189	25	86.2	109	2	Q6S0T2_ORISA	Q6s0t2	oryza	sativ
117	26	89.7	453	2	Q7T3Y4_9VIRU	Q7t3y4	grouper	sle	190	25	86.2	119	2	Q60VP6_9CHLO	Q60vp6	pseudendocl		
118	26	89.7	453	2	Q4KSF0_9VIRU	Q4ksf0	orange-spot		191	25	86.2	120	1	COP1_STAAR	P03861	staphylococ		
119	26	89.7	457	1	TRME_LITSIN	Q926u7	listeria	in	192	25	86.2	122	2	Q7QD79_ANOGA	Q7qd79	anopheles	g	
120	26	89.7	458	2	Q4TRD0_9SPHN	Q4trd0	erythroba	ct	193	25	86.2	122	2	Q4YZC4_PLABE	Q4yzc4	plasmidium		
121	26	89.7	464	1	COAT_IRV1	P18162	tipula	irid	194	25	86.2	128	2	Q4RIS1_TETNG	Q4ris1	tetraodon	n	
122	26	89.7	465	2	Q4U3U9_9VIRU	Q4usu9	trichoplusi		195	25	86.2	129	2	Q4M0F9_9BURK	Q4m0f9	burkholderi		
123	26	89.7	467	1	COAT_IRV6	Q05915	chilo	iride	196	25	86.2	132	2	Q4S455_BACSU	Q4s455	bacillus	su	
124	26	89.7	468	2	Q83LY5_SHIFL	Q83ly5	shigella	fl	197	25	86.2	134	1	ACPS_ZYMO	Q5nl87	zymomonas	m	
125	26	89.7	472	1	COAT_IRV22	P22166	simulium	ir	198	25	86.2	141	2	Q5ERC9_CARAU	Q95vd6	sulfolobus		
126	26	89.7	479	2	Q9RFD8_RHOSH	Q9rfd8	rhodobacter		199	25	86.2	141	2	Q5ERC9_CARAU	Q5erc9	carassius	a	
127	26	89.7	479	2	Q9Z5E2_RHOSH	Q9z5e2	rhodobacter		200	25	86.2	141	2	Q4SJV9_TETNG	Q4sjv9	tetraodon	n	
128	26	89.7	483	2	Q5FQ43_GLUOX	Q5fq43	gluconoba	ct	201	25	86.2	144	2	Q61G33_CAEBR	Q61g33	caenorhabd		
129	26	89.7	487	2	Q8BTV9_MOUSE	Q8btv9	mus	musculu	202	25	86.2	144	2	Q9LA12_PASMU	Q9la12	pasteurella		
130	26	89.7	494	2	Q6NT77_HUMAN	Q6nt77	homo	sapien	203	25	86.2	144	2	Q9CPF9_PASMU	Q9cpf9	pasteurella		
131	26	89.7	496	2	Q6C9A3_YARLI	Q6c9a3	yarrowia	li	204	25	86.2	152	2	Q7W079_BORPE	Q7w079	bordetella		
132	26	89.7	496	2	Q8D2N2_WIGRI	Q8d2n2	wiggleswort		205	25	86.2	160	2	Q84L47_MIRJA	Q84l47	mirabilis	j	
133	26	89.7	498	2	Q5YZV4_NOCFA	Q5yzv4	nocardia	fa	206	25	86.2	167	2	Q4UDQ7_THEAN	Q4udq7	theileria	a	
134	26	89.7	504	2	Q4H3G7_CIOIN	Q4h3g7	ciona	intes	207	25	86.2	167	2	Q965S0_CAEBL	Q965s0	caenorhabd		
135	26	89.7	525	2	Q5FVY8_XENTR	Q5fvy8	xenopus	tro	208	25	86.2	172	2	Q4N5T6_THEPA	Q4n5t6	theileria	p	
136	26	89.7	539	2	Q5B5V3_EMENI	Q5b5v3	aspergillus		209	25	86.2	172	2	Q92K27_RHIME	Q92k27	rhizobium	m	
137	26	89.7	547	2	Q4TC12_TETNG	Q4tc12	tetraodon	n	210	25	86.2	174	2	Q680L9_ARATH	Q680l9	arabidopsis	s	
138	26	89.7	555	2	Q9P103_HUMAN	Q9p103	homo	sapien	211	25	86.2	174	2	Q8L9P9_ARATH	Q8l9p9	arabidopsis	s	
139	26	89.7	555	2	Q8NCA4_HUMAN	Q8nc44	homo	sapien	212	25	86.2	186	1	GLI9_ORISA	P29835	oryza	sativ	
140	26	89.7	555	2	Q8BXN9_MOUSE	Q8bxn9	mus	musculu	213	25	86.2	186	2	P93414_ORISA	P93414	oryza	sativ	
141	26	89.7	556	2	Q8R2P9_MOUSE	Q8r2p9	mus	musculu	214	25	86.2	190	2	Q6MJF8_BDEBA	Q6mjf8	bdellovibr		
142	26	89.7	558	2	Q8BU98_MOUSE	Q8bu98	mus	musculu	215	25	86.2	191	1	Y1137_METJA	Q59537	methanococ		
143	26	89.7	559	2	Q7NSY8_CHRVO	Q7nsy8	chromoba	ct	216	25	86.2	192	2	Q4FMI1_9RICK	Q4fmi1	candidatus		
144	26	89.7	564	2	Q8NBN3_HUMAN	Q8nbn3	homo	sapien	217	25	86.2	199	2	Q4UMD0_RICFE	Q4umd0	rickettsia		
145	26	89.7	634	2	Q7RYI1_NEUCR	Q7ryi1	neurospora		218	25	86.2	202	2	Q7SESO_NEUCR	Q7seso	neurospora		
146	26	89.7	646	2	Q5FS65_GLUOX	Q5fs65	gluconoba	ct	219	25	86.2	202	2	Q25798_HELPU	Q25798	helicoba	ct	
147	26	89.7	647	2	Q8WU27_HUMAN	Q8wu27	homo	sapien	220	25	86.2	206	2	Q67T36_SYMTN	Q67t36	symbioba	ct	
148	26	89.7	679	2	Q5YY78_NOCFA	Q5yy78	nocardia	fa	221	25	86.2	209	2	Q4FV94_9GAMM	Q4fv94	psychoba	ct	
149	26	89.7	715	2	Q5PCX6_SALPA	Q5pcx6	salmonella		222	25	86.2	209	2	Q8YMX5_ANASP	Q8ymx5	anabaena	sp	
150	26	89.7	715	2	Q824Z0_SALTI	Q824z0	salmonella		223	25	86.2	210	2	Q5F654_NEIG1	Q5f654	neisseria	g	
151	26	89.7	728	2	Q7NBR7_MYCGA	Q7nbr7	mycoplasma		224	25	86.2	210	2	Q9JSP2_NEIMA	Q9jsp2	neisseria	m	
152	26	89.7	733	2	Q8KTI9_MYCSY	Q8kti9	mycoplasma		225	25	86.2	210	2	Q9K184_NEIMA	Q9k184	neisseria	m	
153	26	89.7	742	2	Q8KTJ1_MYCSY	Q8ktj1	mycoplasma		226	25	86.2	212	2	Q57AX8_BRUAB	Q57ax8	brucella	ab	
154	26	89.7	743	2	Q8KTJ0_MYCSY	Q8ktj0	mycoplasma		227	25	86.2	212	2	Q8FYG0_BRUSU	Q8fyg0	brucella	su	
155	26	89.7	844	2	Q6UE32_9BURK	Q6ue32	burkholderi		228	25	86.2	212	2	Q9L6H7_BRUME	Q9l6h7	brucella	me	
156	26	89.7	939	2	Q6AK45_DESPS	Q6ak45	desulfotale		229	25	86.2	214	2	Q92LJ7_RHIME	Q92lj7	rhizobium	m	
157	26	89.7	960	2	Q418E7_GIBZE	Q418e7	gibberella		230	25	86.2	215	2	Q5Z1S9_MAGGR	Q5z1s9	magnaporthe		
158	26	89.7	1041	2	Q5LD76_BACFN	Q5ld76	bacteroides		231	25	86.2	220	2	Q8T3Z2_DROME	Q8t3z2	drosophila		
159	26	89.7	1041	2	Q64U98_BACFR	Q64u98	bacteroides		232	25	86.2	226	1	Y209_METTH	Q82311	methanoba	ct	
160	26	89.7	1041	2	Q8A9Y5_BACTN	Q8a9y5	bacteroides		233	25	86.2	229	2	Q5AXR0_EMENI	Q5axr0	aspergillus		
161	26	89.7	1055	2	Q94887_HUMAN	Q94887	homo	sapien	234	25	86.2	229	2	Q4WVZ8_ASPFU	Q4wvz8	aspergillus		
162	26	89.7	1065	2	Q91V88_MOUSE	Q91v88	mus	musculu	235	25	86.2	231	2	Q8C6Y8_MOUSE	Q8c6y8	mus	musculu	
163	26	89.7	1139	1	SRBP2_CRIGR	Q60429	cricetulus		236	25	86.2	234	2	Q5JEG7_PYRKO	Q5jeg7	pyrococcus		
164	26	89.7	1411	2	Q73Y53_MYCPA	Q73y53	mycobacteri		237	25	86.2	234	2	Q8U3K3_PYRFO	Q8u3k3	pyrococcus		
165	26	89.7	1701	2	Q61164_PLAYO	Q61164	plasmidium		238	25	86.2	240	2	Q6NUA9_XENLA	Q6nu9a	xenopus	lae	
166	26	89.7	1701	2	Q7RC08_PLAYO	Q7rc08	plasmidium		239	25	86.2	246	2	Q9V9U6_DROME	Q9v9u6	drosophila		
167	26	89.7	1723	2	Q8WRD0_PLABE	Q8wrd0	plasmidium		240	25	86.2	246	2	Q6SPZ1_9BACT	Q6sfz1	uncultured		
168	26	89.7	1769	2	Q4YQJ3_PLABE	Q4yqj3	plasmidium		241	25	86.2	246	2	Q73NMG_TREDE	Q73nm6	treponema	d	
169	26	89.7	1869	2	Q997D0_5COMO	Q997d0	broad	bean	242	25	86.2	247	2	Q92K30_HELPU	Q92k30	helicoba	ct	
170	26	89.7	2297	1	MOX11_SCHPO	Q09854	schizosacch		243	25	86.2	249	2	Q4NHD7_9NICC	Q4nhd7	arthrobact		
171	26	89.7	2601	2	Q4YQB7_PLABE	Q4yqb7	plasmidium		244	25	86.2	251	2	Q7N2P7_PHOLL	Q7n2p7	photothabu		
172	26	89.7	3888	2	Q51X35_MAGGR	Q51x35	magnaporthe		245	25	86.2	252	2	Q7NUJ0_CHRVO	Q7nuj0	chromoba	ct	
173	26	89.7	4212	2	Q4V2I8_BURMA	Q4v2i8	burkholderi		246	25	86.2	253	2	Q9Z1I1_ACICA	Q9z1i1	acinetoba	ct	
174	26	89.7	5935	2	Q63LK8_BURPS	Q63lk8	burkholderi		247	25	86.2	255						

251 25 86.2 260 2 P94512\_BACSU  
 252 25 86.2 263 2 Q92VA5\_RHIME  
 253 25 86.2 268 1 TRUA\_TREDE  
 254 25 86.2 268 2 Q84148\_MIRJA  
 255 25 86.2 268 2 Q5ZJP4\_CHICK  
 256 25 86.2 270 2 Q4WER8\_ASPPU  
 257 25 86.2 271 2 Q65GA6\_BACLD  
 258 25 86.2 276 2 Q6BVF3\_PARTE  
 259 25 86.2 276 2 Q940Q3\_ARATH  
 260 25 86.2 276 2 Q62RR1\_BACLD  
 261 25 86.2 282 1 PNMT\_HUMAN  
 262 25 86.2 282 2 Q6FHD9\_HUMAN  
 263 25 86.2 285 2 Q9KMB5\_VIBCH  
 264 25 86.2 291 2 Q87JJ8\_VIBPA  
 265 25 86.2 293 2 Q9ZAF0\_9ZZZ  
 266 25 86.2 293 2 Q9KY30\_STRCO  
 267 25 86.2 295 2 Q8D6E6\_VIBVY  
 268 25 86.2 295 2 Q7MD99\_VIBVY  
 269 25 86.2 297 2 Q8PID6\_XANAC  
 270 25 86.2 298 2 Q97VK7\_SULSO  
 271 25 86.2 299 2 Q5NTR3\_9BACT  
 272 25 86.2 300 2 Q4ZTF5\_PSESY  
 273 25 86.2 300 2 Q80B08\_9POXV  
 274 25 86.2 302 2 Q7AGM6\_ECO57  
 275 25 86.2 303 2 Q9CLP3\_PASMU  
 276 25 86.2 303 2 Q6TVN6\_9POXV  
 277 25 86.2 303 2 Q6TW16\_9POXV  
 278 25 86.2 307 2 Q6TVA4\_9POXV  
 279 25 86.2 313 2 Q71KR8\_KLEFL  
 280 25 86.2 317 2 Q4QEH6\_LEIMA  
 281 25 86.2 321 2 Q9WZB8\_THEMEA  
 282 25 86.2 322 1 OR1J1\_HUMAN  
 283 25 86.2 323 2 Q8X9H6\_ECO57  
 284 25 86.2 324 2 Q4IFV0\_GIBZE  
 285 25 86.2 325 2 Q4TJG6\_9SPHN  
 286 25 86.2 326 1 PELA\_EMENI  
 287 25 86.2 326 2 Q5BFP9\_EMENI  
 288 25 86.2 327 2 Q6FKK4\_CANGA  
 289 25 86.2 327 2 Q7W5S8\_BORPA  
 290 25 86.2 327 2 Q7WDB5\_BORBP  
 291 25 86.2 327 2 Q7VZ12\_BORPE  
 292 25 86.2 331 2 Q4HS16\_CAMUP  
 293 25 86.2 331 2 Q821X4\_CHLCV  
 294 25 86.2 331 2 Q9Z6V0\_CHLPN  
 295 25 86.2 332 2 Q9YCL2\_AERPE  
 296 25 86.2 332 2 Q5L571\_CHLAB  
 297 25 86.2 334 2 Q6LH05\_PHOPR  
 298 25 86.2 337 2 Q4M1D9\_BURK  
 299 25 86.2 340 1 YRU3\_CABEL  
 300 25 86.2 340 2 Q63KW3\_BURPS

## ALIGNMENTS

RESULT 1  
 Q91Y69 MESAU  
 ID Q91Y69 MESAU PRELIMINARY; PRT; 143 AA.  
 AC Q91Y69  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Matrix metalloproteinase-2 (Fragment).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Cricetinae; Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Tracheal surface;  
 RA Ko K.H., Shin C.Y., Lee W.J., Yoo B.K., Ryu J.R., Park K.H.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF260254; RAKS1635.1; -; mRNA.  
 DR HSSP; P08253; 1CK7.  
 DR MEROPS; M10.004; -.  
 DR InterPro; IPR000585; Hemopexin.  
 DR Pfam; PF00045; Hemopexin; 3.  
 DR SMART; SM00120; HX; 3.  
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN\_1.  
 FT NON\_TER 1 143 143  
 SQ SEQUENCE 143 AA; 16316 MW; 1B4310F9E6A023EF CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFPA 6  
 |||||  
 DB 21 KAVFFPA 26  
 RESULT 2  
 Q9N284 BOVIN  
 ID Q9N284 BOVIN PRELIMINARY; PRT; 162 AA.  
 AC Q9N284  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE MMP-2 (Fragment).  
 GN Name=bmmp-2;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Rutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sato T., Hirata M., Ito A., Hashizume K.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB043994; BAA96387.1; -; mRNA.  
 DR HSSP; P08253; 1CK7.  
 DR MEROPS; M10.003; -.  
 DR InterPro; IPR000585; Hemopexin.  
 DR Pfam; PF00045; Hemopexin; 3.  
 DR SMART; SM00120; HX; 3.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 162 AA; 18351 MW; B8898B49E5E5326A CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFPA 6  
 |||||  
 DB 33 KAVFFPA 38  
 RESULT 3  
 Q9BGL4 SHEEP  
 ID Q9BGL4 SHEEP PRELIMINARY; PRT; 248 AA.  
 AC Q9BGL4  
 DT 01-JUN-2001 (TRENBLrel. 17, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Gelatinase A (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Ovary;

```

RX MEDLINE-21858324; PubMed=11870075;
RA Riche W.A., Smith G.W., Smith M.F.;
RT "Matrix metalloproteinase expression and activity following
RT prostaglandin F(2 alpha)-induced luteolysis.";
RL Biol. Reprod. 66:685-691(2002).
DR EMBL; AF267159; AAGS9847.1; -; mRNA.
DR HSP; P08253; IGMD.
DR MEROPS; M10.003; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00045; Hemopexin; 3.
DR Pfam; PF00413; Peptidase M10; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00120; HX; 3.
DR SMART; SM00235; ZMHC; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 248
FT NON_TER 248
SQ SEQUENCE 248 AA; 28034 MW; 56F421C2D6DC133E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 184 KAVFFA 189

RESULT 4
Y1086_HAEIN
ID Y1086_HAEIN STANDARD; PRT; 261 AA.
AC F45030;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein H1086.
GN OrderedLocusNames=H1086;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Spruyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.I., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."
RL Science 269:496-512(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: Belongs to the DUF140 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

```

---

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U32788; AAC22742.1; -; Genomic_DNA.
DR PIR; D64166; D64166.
DR TIGR; H11086; -.
DR InterPro; IPR003453; DUF140.
DR Pfam; PF02405; DUF140; 1.
DR TIGRFAMs; TIGR00056; DUF140; 1.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 13
FT TRANSMEM 33
FT TRANSMEM 50
FT TRANSMEM 70
FT TRANSMEM 90
FT TRANSMEM 110
FT TRANSMEM 148
FT TRANSMEM 168
FT TRANSMEM 199
FT TRANSMEM 219
FT TRANSMEM 239
FT TRANSMEM 259
SQ SEQUENCE 261 AA; 28015 MW; 4BC3695F247A6BF6 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 205 KAVFFA 210

RESULT 5
Q4OLK2_HAB18
ID Q4OLK2_HAB18 PRELIMINARY; PRT; 261 AA.
AC Q4OLK2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Conserved ABC-type transport system protein, permease component.
GN OrderedLocusNames=NT11249;
OS Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
RN [1]
NUCLEOTIDE SEQUENCE.
RP PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RX Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakalez L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20."
RL J. Bacteriol. 187:4627-4636(2005).
DR EMBL; CF000057; AAX88095.1; -; Genomic_DNA.
DR InterPro; IPR003453; DUF140.
DR Pfam; PF02405; DUF140; 1.
DR TIGRFAMs; TIGR00056; DUF140; 1.
KW Complete proteome.
SQ SEQUENCE 261 AA; 28075 MW; 0EB1BEEDD2FA133A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 205 KAVFFA 210

RESULT 6
Q73KX6_TREDE
ID Q73KX6_TREDE PRELIMINARY; PRT; 277 AA.
AC Q73KX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

```

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Amino acid ABC transporter, amino acid-binding protein, putative.  
 GN OrderedLocuNames=TDE2091;  
 OS Treponema denticola.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
 OX NCBI\_TaxID=158;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 35405 / DSM 14222;  
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;  
 RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.P.,  
 RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,  
 RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,  
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,  
 RA Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,  
 RA Shatman S., McLeod M.P., Smajs J.K., Pal S., Amin A.,  
 RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,  
 RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.,  
 RT "Comparison of the genome of the oral pathogen Treponema denticola  
 with other spirochete genomes."  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).  
 DR EMBL; AE017253; AAS12611.1; -; Genomic\_DNA.  
 DR TIGR; TDE2091; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.  
 DR GO; GO:0005215; F:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001311; SBP\_glu receptor.  
 DR InterPro; IPR001638; SBP\_bac\_3.  
 DR Pfam; PF00497; SBP\_bac\_3; 1.  
 DR SMART; SM0062; PBPB; 1.  
 DR PROSITE; PS01039; SBP\_BACTERIAL\_3; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 277 AA; 31013 MW; AC9F1BC5DB10A16E CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 8 KAVFFA 13  
 RESULT 7  
 ID Q9WY6\_ARATH PRELIMINARY; PRT; 314 AA.  
 AC Q9WY6;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE F3222.6 protein.  
 GN Name=F3222.6;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosidia II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,  
 RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uterback T.R.,  
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC023912; AAF63818.1; -; Genomic\_DNA.  
 DR InterPro; IPR002575; APH-trans.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR Pfam; PF01636; APH; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN\_1.  
 SQ SEQUENCE 314 AA; 34938 MW; BE31A6DFA610A5DB CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 314;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 282 KAVFFA 287  
 RESULT 8  
 ID QSLIA8\_GEOKA PRELIMINARY; PRT; 381 AA.  
 AC QSLIA8;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Proton/sodium antiporter.  
 GN OrderedLocuNames=GK0987;  
 OS Geobacillus kaustophilus.  
 OC Bacteria; Firmicutes; Bacillales; Geobacillus.  
 OX NCBI\_TaxID=1462;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HTA426;  
 RX PubMed=15576355; DOI=10.1093/nar/gkh970;  
 RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,  
 RA Matsui S., Uchiyama I.;  
 RT "Thermoadaptation trait revealed by the genome sequence of  
 thermophilic Geobacillus kaustophilus.";  
 RL Nucleic Acids Res. 32:6292-6303 (2004).  
 DR EMBL; BA000043; BAD75272.1; -; Genomic DNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0015299; F:olute:hydrogen antiporter activity; IEA.  
 DR GO; GO:0006885; P:regulation of pH; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR006153; Na\_H Exchanger; 1.  
 DR Pfam; PF00999; Na\_H Exchanger; 1.  
 KW Complete proteome; Transmembrane; Transport.  
 SQ SEQUENCE 381 AA; 39481 MW; AE3EA4252A7B367B CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 381;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 179 KAVFFA 184  
 RESULT 9  
 ID Q8KHB6\_CLODI PRELIMINARY; PRT; 389 AA.  
 AC Q8KHB6;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE S-layer protein variable domain SlpA (Fragment).  
 GN Name=slpA;  
 OS Clostridium difficile.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OX NCBI\_TaxID=1496;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 43597, 90-111, and 93-136;  
 RX MEDLINE=22083941; PubMed=12089261;  
 RX DOI=10.1128/JCM.40.7.2452-2458.2002;  
 RA Karjalainen T., Saumier N., Barc M.C., Delmee M., Collignon A.;  
 RT "Clostridium difficile genotyping based on slpA variable region in S-  
 layer gene sequence: an alternative to serotyping.";  
 RL J. Clin. Microbiol. 40:2452-2458 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 43597, 90-111, and 93-136;

```

RA Karjalainen T.K., Saunier N.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458880; AAM75944.1; -; Genomic DNA.
DR EMBL; AF458881; AAM75945.1; -; Genomic DNA.
DR EMBL; AF458882; AAM75946.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 389
SQ SEQUENCE 389 AA; 41788 MW; C5ED8F4901C18F8C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 340 KAVFFA 345

RESULT 10
Q8S9Q7 ARATH PRELIMINARY; PRT; 469 AA.
AC Q8S9Q7_21, Created
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative selenium-binding protein (Pentatricopeptide repeat-containing protein).
DE ORFNames=At2g34370;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]_TaxID=3702;
RP NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Karlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Underwood B.A., Xiao Y., Moskal W., Monaghan E., Wang W., Redman J.,
RA Wu H.C., Uterback T., Town C.D.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004481; AAM14949.1; -; Genomic_DNA.
DR EMBL; DQ056566; AAY78716.1; -; mRNA.
DR FIR; T02325; T02325.
DR GO; GO:0005488; F.binding; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF01535; PPR; 4.
DR TIGRFAMs; TIGR00756; PPR; 3.
KW Repeat.
SQ SEQUENCE 469 AA; 53856 MW; FB698FC9C0238437 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 213 KAVFFA 218

RESULT 11
Q9N1P6 CANFA PRELIMINARY; PRT; 632 AA.
AC Q9N1P6_1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

```

```

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase-2 (Fragment).
GN Name=MMP-2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]_TaxID=9615;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=fibrosarcoma;
RA Jahic H., Paria B., Balkin R., Baxendale V., Fang Y., Kitchell B.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177217; AAF67517.1; -; mRNA.
DR HSSP; P08253; 1GXD.
DR MEROPS; M10.003; -.
DR Ensembl; ENSCAFG00000009421; Canis familiaris.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HK; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 632 AA; 70991 MW; D8AE895497E129F3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 632;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 503 KAVFFA 508

RESULT 12
Q6U7G9 MELGA PRELIMINARY; PRT; 654 AA.
AC Q6U7G9_1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gelatinase A.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Monsonego Ornan E., Tong A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY376899; AAO98971.1; -; mRNA.
DR HSSP; P08254; 1B3D.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

```

```

DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2_3.
DR Pfam; PF00045; Hemopexin; 3.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTPYPII.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2_3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN 2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 654 AA; 73956 MW; F9B0755F76B6F8DD CRC64;

Query Match 100.0%; Score 29; DB 2; Length 654;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
   |||||
DB 533 KAVFFPA 538

RESULT 13
MMP2_HUMAN STANDARD; PRT; 660 AA.
AC P08253;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A) (TBE-
DE 1).
GN Name=MMP2; Synonyms=CLG4A;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE OF 19-660, AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=88198218; PubMed=2834383;
RA Collier I.E., Wilhelm S.M., Eisen A.Z., Marmer B.L., Grant G.A.,
RA Seltzer J.L., Kronberger A., He C., Bauer B.A., Goldberg G.I.;
RT "H-ras oncogene-transformed human bronchial epithelial cells (TBE-1)
RT secrete a single metalloprotease capable of degrading basement
RT membrane collagen.";
RL J. Biol. Chem. 263:6579-6587 (1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91236162; PubMed=1851724;
RA Collier I.E., Bruns G.A.P., Goldberg G.I., Gerhard D.S.;
RT "On the structure and chromosome location of the 72- and 92-kDa human
RT type IV collagenase genes.";
RL Genomics 9:429-434 (1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90293047; PubMed=2162831;
RA Huhtala P., Chow L.T., Tryggvason K.;
RT "Structure of the human type IV collagenase gene.";
RL J. Biol. Chem. 265:11077-11082 (1990).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-447 AND LEU-621.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Chambers S.W., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;

```

```

RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RN Submitted (AUG-2004) to the EMBL/GenBank/DBSJ databases.
RP [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Pange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 1-51.
RX MEDLINE=90228972; PubMed=2158484;
RA Huhtala P., Eddy R.L., Fan Y.S., Byers M.G., Shows T.B.,
RA Tryggvason K.;
RT "Completion of the primary structure of the human type IV collagenase
RT preproenzyme and assignment of the gene (CLG4) to the q21 region of
RT chromosome 16.";
RN Genomics 6:554-559 (1990).
RN [7]
RP ENZYME REGULATION.
RX PubMed=11179305; DOI=10.1128/IAI.69.3.1402-1408.2001;
RA Gusman H., Travis J., Helmerhorst E.J., Potempa J., Troxler R.F.,
RA Oppenheim F.G.;
RT "Salivary histatin 5 is an inhibitor of both host and bacterial
RT enzymes implicated in periodontal disease.";
RL Infect. Immun. 69:1402-1408 (2001).
RN [8]
RP PROCESSING OF KISS1.
RX MEDLINE=22761370; PubMed=12879005; DOI=10.1038/sj.onc.1206542;
RA Takino T., Koshikawa N., Miyamori H., Tanaka M., Sasaki T., Okada Y.,
RA Saiki M., Sato H.;
RT "Cleavage of metastasis suppressor gene product KISS-1
RT protein/metastatin by matrix metalloproteinases.";
RN Oncogene 22:4617-4626 (2003).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 443-660.
RX MEDLINE=96069777; PubMed=7583664;
RA Libson A.M., Gittis A.G., Collier I.E., Marmer B.L., Goldberg G.I.,
RA Lattman E.B.;
RT "Crystal structure of the haemopexin-like C-terminal domain of
RT gelatinase A.";
RN Nat. Struct. Biol. 2:938-942 (1995).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 458-660.
RX MEDLINE=96140723; PubMed=8549817; DOI=10.1016/0014-5793(95)01435-7;
RA Gohlke U., Gomis-Rueth F.-X., Crabbe T., Murphy G., Docherty A.J.,
RA Bode W.;
RT "The C-terminal (haemopexin-like) domain structure of human gelatinase
RT A (MMP2): structural implications for its function.";
RL FEBS Lett. 378:126-130 (1996).
RN CC -1- FUNCTION: in addition to gelatin and collagens, it cleaves KISS1
RN at a Gly|-Leu bond.
RN CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
RN IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly|-
RN Ile-Ala-Gly-Gln.

```



CC -|- COFACTOR: Binds 4 calcium ions per subunit.  
 CC -|- COFACTOR: Binds 2 zinc ions per subunit.  
 CC -|- ENZYME REGULATION: Inhibited by histatin-3 1/24 (histatin-5).  
 CC -|- SUBUNIT: Ligand for integrin alpha-V/beta-3.  
 CC -|- TISSUE SPECIFICITY: Produced by normal skin fibroblasts.  
 CC -|- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-MMP3).  
 CC -|- SIMILARITY: Belongs to the peptidase M10A family.  
 CC -|- SIMILARITY: Contains 3 fibronectin type-II domains.  
 CC -|- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC -----  
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: J03210; AAA35701.1; -; mRNA.  
 CC EMBL: M33789; AAA52027.1; -; Genomic DNA.  
 CC EMBL: M55593; AAA52028.1; -; Genomic DNA.  
 CC EMBL: M58552; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55582; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55583; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55584; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55585; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55586; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55587; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55588; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55589; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55590; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55591; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: M55592; AAA52028.1; JOINED; Genomic DNA.  
 CC EMBL: AY738117; AAU10089.1; -; Genomic DNA.  
 CC EMBL: BC002576; AAH02576.1; -; mRNA.  
 CC PIR: A28153; A28153.  
 CC PDB: 1CK7; X-ray; A=30-660.  
 CC PDB: 1CKW; NMR; A=278-336.  
 CC PDB: 1EAK; X-ray; A/B/C/D=32-452.  
 CC PDB: 1GEN; X-ray; @=443-660.  
 CC PDB: 1GXD; X-ray; A/B=30-660.  
 CC PDB: 1HOV; NMR; A=110-214.  
 CC PDB: 1U7M; NMR; A=337-394.  
 CC PDB: 1KS0; NMR; A=223-282.  
 CC PDB: 1Q1B; X-ray; A=115-216.  
 CC PDB: 1RTG; X-ray; @=451-660.  
 CC MEROPS: M10\_003; -.  
 CC Ensembl: ENSG00000087245; Homo sapiens.  
 CC HGNC: HGNC:7166; MMP2.  
 CC H-invDB: HIX0013041; -.  
 CC MIM: 120360; -.  
 CC GO: GO:0005615; C:extracellular space; TAS.  
 CC GO: GO:0004228; F:gelatinase A activity; TAS.  
 CC GO: GO:0008270; F:zinc ion binding; TAS.  
 CC GO: GO:0006508; P:proteolysis and peptidolysis; TAS.  
 CC InterPro: IPR000562; FN\_type2\_col\_bd.  
 CC InterPro: IPR000585; Hemopexin.  
 CC InterPro: IPR001818; Pept\_M10A\_M12B.  
 CC InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 CC InterPro: IPR006026; Peptidase\_M.  
 CC Pfam: PF00040; fn2; 3.  
 CC Pfam: PF00045; Hemopexin; 4.  
 CC Pfam: PF00413; Peptidase\_M10; 1.  
 CC Pfam: PF03933; Peptidase\_M10\_N; 1.  
 CC PRINTS: PR00013; FNTYPEII.  
 CC PRINTS: PR00138; MATRXIN.  
 CC ProDom: PD000995; FN\_Type\_II; 3.  
 CC SMART: SM00059; FN2; 3.  
 CC SMART: PF00040; fn2; 3.  
 CC Pfam: PF00045; Hemopexin; 4.  
 CC Pfam: PF00413; Peptidase\_M10; 1.  
 CC Pfam: PF03933; Peptidase\_M10\_N; 1.  
 CC PRINTS: PR00013; FNTYPEII.  
 CC PRINTS: PR00138; MATRXIN.  
 CC ProDom: PD000995; FN\_Type\_II; 3.  
 CC SMART: SM00059; FN2; 3.  
 CC SMART: SM00120; HX; 4.  
 CC SMART: SM00235; ZnMG; 1.  
 CC PROSITE: PS00546; CYSTEINE\_SWITCH; 1.  
 CC PROSITE: PS00023; FN2\_1; 2.  
 CC PROSITE: PS51092; FN2\_2; 3.  
 CC PROSITE: PS00024; HEMOPEXIN; 1.  
 CC KX Calcium; Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc.  
 CC SQ SEQUENCE 660 AA; 73871 MW; FCTEB8481091C5ED CRC64;

DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW 3D-structure; Calcium; Collagen degradation;  
 KW Direct protein sequencing; Extracellular matrix; Glycoprotein;  
 KW Hydrolase; Metal-binding; Metalloprotease; Polymorphism; Protease;  
 KW Repeat; Signal; Zinc; Zymogen.  
 FT SIGNAL; 1 29 Potential.  
 FT PROPEP 30 109 Activation peptide.  
 FT CHAIN 110 660 72 kDa type IV collagenase.  
 FT DOMAIN 228 276 Fibronectin type-II 1.  
 FT DOMAIN 286 334 Fibronectin type-II 2.  
 FT DOMAIN 344 392 Fibronectin type-II 3.  
 FT DOMAIN 466 660 Hemopexin-like.  
 FT REGION 110 221 Collagenase-like 1.  
 Query Match 100.0%; Score 29; DB 1; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 3.le+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KAVFFA 6  
 Db 531 KAVFFA 536  
 RESULT 14  
 Q51Y21\_TUPGB  
 ID Q51Y21\_TUPGB PRELIMINARY; PRT; 660 AA.  
 AC Q51Y21;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Matrix metalloproteinase 2.  
 OS Tupaia glis belangeri (Common tree shrew).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupia.  
 OC NCBI\_TaxID=37347;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15621657; DOI=10.1080/10425170400012925;  
 RA Kenning M.S., Gentile A., McBrien N.A.;  
 RT "Expression and cDNA sequence of matrix metalloproteinase-2 (MMP-2) in  
 FT a mammalian model of human disease processes: Tupaia belangeri.";  
 RL DNA Seq. 15:332-337(2004).  
 DR EMBL; AY600958; AAU44903.1; -; mRNA.  
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000562; FN\_type2\_col\_bd.  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR006026; Peptidase\_M.  
 DR Pfam; PF00040; fn2; 3.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase\_M10; 1.  
 DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
 DR PRINTS; PR00013; FNTYPEII.  
 DR PRINTS; PR00138; MATRXIN.  
 DR ProDom; PD000995; FN\_Type\_II; 3.  
 DR SMART; SM00059; FN2; 3.  
 DR SMART; SM00120; HX; 4.  
 DR SMART; SM00235; ZnMG; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00023; FN2\_1; 2.  
 DR PROSITE; PS51092; FN2\_2; 3.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 KW Calcium; Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc.  
 SQ SEQUENCE 660 AA; 73871 MW; FCTEB8481091C5ED CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 3.le+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 KAVFFA 6
DB      531 KAVFFA 536

RESULT 15
Q95JA4_FIG
ID      Q95JA4_FIG PRELIMINARY; PRT; 661 AA.
AC      Q95JA4;
DT      01-DEC-2001 (T-EMBLrel. 19, Created)
DT      01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT      01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE      Gelatinase A.
GN      Name=MMP-2;
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC      Sus.
NCBI_TaxID=9823;
RN      [1]
NUCLEOTIDE SEQUENCE.
RC      TISSUE=Tooth enamel organ;
RX      MEDLINE=21480581; PubMed=11597028;
RA      Caron C., Xue J., Sun X., Simmer J.P., Bartlett J.D.;
RT      "Gelatinase A (MMP-2) in developing tooth tissues and amelogenin
RT      hydrolysis.";
RL      J. Dent. Res. 80:1660-1664(2001).
DR      EMBL; AF295805; AAK97133.1; -; mRNA.
DR      HSSP; P08253; IGXD.
DR      MEROPS; M10.003; -.
DR      GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR      GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR000562; FN_Type_II.
DR      InterPro; IPR000585; Hemopexin.
DR      InterPro; IPR006026; Peptidase M.
DR      InterPro; IPR001818; Pept M10A_M12B.
DR      InterPro; IPR006025; Pept_M_Zn_BS.
DR      Pfam; PF00040; fn2; 3.
DR      Pfam; PF00045; Hemopexin; 4.
DR      Pfam; PF00413; Peptidase M10; 1.
DR      PRINTS; PR00133; FNTYPEII.
DR      PRINTS; PR00138; MATRXIN.
DR      ProDom; PD000995; FN_Type_II; 3.
DR      SMART; SM00120; HX; 4.
DR      SMART; SM00235; ZnMC; 1.
DR      PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR      PROSITE; PS00023; FIBRONECTIN_2; 3.
DR      PROSITE; PS00024; HEMOPEXIN; 1.
DR      PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ      SEQUENCE 661 AA; 73669 MW; 41CD448BD72D2CC2 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      532 KAVFFA 537

RESULT 16
Q9GLE5_BOVIN
ID      Q9GLE5_BOVIN PRELIMINARY; PRT; 661 AA.
AC      Q9GLE5;
DT      01-MAR-2001 (T-EMBLrel. 16, Created)
DT      01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT      01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE      Matrix metalloproteinase 2.
OS      Bos taurus (Bovine).

```

```

OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC      Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN      [1]
NUCLEOTIDE SEQUENCE.
RA      Yan L., Zhang B., Teang P., Fang J., Yu Y., Ingber D.E., Moses M.A.;
RL      Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF290428; AAG28169.1; -; mRNA.
DR      HSSP; P08253; IGXD.
DR      MEROPS; M10.003; -.
DR      GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR      GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR000562; FN_Type_II.
DR      InterPro; IPR000585; Hemopexin.
DR      InterPro; IPR006026; Peptidase M.
DR      InterPro; IPR001818; Pept M10A_M12B.
DR      InterPro; IPR006025; Pept_M_Zn_BS.
DR      Pfam; PF00040; fn2; 3.
DR      Pfam; PF00045; Hemopexin; 4.
DR      Pfam; PF00413; Peptidase M10; 1.
DR      PRINTS; PR00133; FNTYPEII.
DR      PRINTS; PR00138; MATRXIN.
DR      ProDom; PD000995; FN_Type_II; 3.
DR      SMART; SM00059; FN2; 3.
DR      SMART; SM00120; HX; 4.
DR      SMART; SM00235; ZnMC; 1.
DR      PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR      PROSITE; PS00023; FIBRONECTIN_2; 3.
DR      PROSITE; PS00024; HEMOPEXIN; 1.
DR      PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW      Metalloprotease; Protease.
SQ      SEQUENCE 661 AA; 73776 MW; 90545F7645E5F84D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      532 KAVFFA 537

RESULT 17
MMP2_MOUSE
ID      MMP2_MOUSE STANDARD; PRT; 662 AA.
AC      P33434;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE      gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN      Name=Mmp2;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN      [1]
NUCLEOTIDE SEQUENCE.
RA      Reponen P., Sahlberg C., Huhtala P., Hurskainen T., Thesleff I.,
RA      Tryggvason K.;
RT      "Molecular cloning of murine 72-kDa type IV collagenase and its
RT      expression during mouse development.";
RL      J. Biol. Chem. 267:7856-7862(1992).
RN      [2]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC      STRAIN=C57BL/6; TISSUE=Brain;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

```

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RN DEVELOPMENTAL STAGE.  
RC TISSUE=Embryo;  
RX PubMed=274464;  
RA Brenner C.A., Adler R.R., Rappolee D.A., Pedersen R.A., Werb Z.;  
RT "Genes for extracellular-matrix-degrading metalloproteinases and their  
RT inhibitor, TIMP, are expressed during early mammalian development.";  
RL Genes Dev. 3:848-859(1989).  
CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types  
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-  
CC Ile-Ala-Gly-Gln.  
CC -!- COFACTOR: Binds 4 calcium ions per subunit (By similarity).  
CC -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).  
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.  
CC -!- DEVELOPMENTAL STAGE: Present in unfertilized eggs and at the  
CC zygote and cleavage stages. Levels increase at the blastocyst  
CC stage and with endoderm differentiation.  
CC -!- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-  
CC MMP3) (By similarity).  
CC -!- SIMILARITY: Belongs to the peptidase M10A family.  
CC -!- SIMILARITY: Contains 3 fibronectin type-II domains.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; M84324; AAA39338.1; -; mRNA.  
CC EMBL; BC070430; AAH70430.1; -; mRNA.  
CC PIR; A42496; A42496.  
CC HSSP; P08253; 1RTG.  
CC MEROPS; M10.003; -.  
CC DR Ensembl; ENSMUSG00000031740; Mus musculus.  
CC DR MGI; MGI:97009; Mmp2.  
CC DR GO; GO:0005615; C:extracellular space; TAS.  
CC DR InterPro; IPR000562; FN type2 col\_bd.  
CC DR InterPro; IPR000585; Hemopexin.  
CC DR InterPro; IPR001818; Pept\_M10A\_M12B.  
CC DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
CC DR InterPro; IPR006026; Peptidase\_M.  
CC DR Pfam; PF00040; fn2; 3.  
CC DR Pfam; PF00045; Hemopexin; 4.  
CC DR Pfam; PF00413; Peptidase\_M10; 1.  
CC DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
CC DR PRINTS; PR00013; FNTYPEII.  
CC DR PRINTS; PR00138; MATRILIX.  
CC DR ProDom; PD000995; FN Type\_II; 3.  
CC DR SMART; SM00059; FN2; 3.  
CC DR SMART; SM00120; HX; 4.  
CC DR SMART; SM00235; ZnMc; 1.  
CC DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
CC DR PROSITE; PS00023; FN2\_1; 3.

DR PROSITE; PS51092; FN2\_2; 3.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;  
KW Hydrolase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;  
KW Zinc; Zymogen.  
FT SIGNAL 1 29 Potential.  
FT PROPEP 30 109 Activation peptide.  
FT CHAIN 110 662 72 kDa type IV collagenase.  
FT DOWAIN 228 276 Fibronectin type-II 1.  
FT DOWAIN 286 334 Fibronectin type-II 2.  
FT DOWAIN 344 392 Fibronectin type-II 3.  
FT DOWAIN 410 662 Hemopexin-like.  
FT REGION 110 221 Collagenase-like 1.  
FT REGION 222 396 Collagen-binding.  
FT REGION 397 467 Collagenase-like 2.  
FT ACT\_SITE 404 404 By similarity.  
FT METAL 134 134 Calcium 1 (By similarity).  
FT METAL 168 168 Calcium 2 (By similarity).  
FT METAL 178 178 Zinc 1 (By similarity).  
FT METAL 180 180 Zinc 1 (By similarity).  
FT METAL 185 185 Calcium 3 (By similarity).  
FT METAL 186 186 Calcium 3 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 193 193 Zinc 1 (By similarity).  
FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 204 204 Calcium 2 (By similarity).  
FT METAL 206 206 Zinc 1 (By similarity).  
FT METAL 208 208 Calcium 3 (By similarity).  
FT METAL 209 209 Calcium 1 (By similarity).  
FT METAL 211 211 Calcium 3 (By similarity).  
FT METAL 403 403 Zinc 2 (catalytic) (By similarity).  
FT METAL 407 407 Zinc 2 (catalytic) (By similarity).  
FT METAL 413 413 Zinc 2 (catalytic) (By similarity).  
FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 523 523 Calcium 4 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 620 620 Calcium 4 (via carbonyl oxygen) (By  
FT similarity).  
FT SITE 102 102 Cysteine switch (Potential).  
FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 644 644 N-linked (GlcNAc...) (Potential).  
FT DISULFID 471 562 By similarity.  
SQ SEQUENCE 662 AA; 74102 MW; C630A7DBDB272F02 CRC64;  
Query Match 100.0%; Score 29; DB 1; Length 662;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0;  
QY 1 KAVFFA 6  
DB 533 KAVFFA 538  
RESULT 18  
MMP2\_RABIT STANDARD; PRT; 662 AA.  
ID MMP2\_RABIT STANDARD; PRT; 662 AA.  
AC P50757;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa  
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).  
GN Name=MMP2;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;

FT	METAL	193	Zinc 1 (By similarity).
FT	METAL	200	Calcium 2 (via carbonyl oxygen) (By similarity).
FT	METAL	202	Calcium 2 (via carbonyl oxygen) (By similarity).
FT	METAL	204	Calcium 2 (By similarity).
FT	METAL	206	Zinc 1 (By similarity).
FT	METAL	208	Calcium 3 (By similarity).
FT	METAL	209	Calcium 1 (By similarity).
FT	METAL	211	Calcium 3 (By similarity).
FT	METAL	403	Zinc 2 (catalytic) (By similarity).
FT	METAL	407	Zinc 2 (catalytic) (By similarity).
FT	METAL	413	Zinc 2 (catalytic) (By similarity).
FT	METAL	478	Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL	523	Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL	571	Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL	620	Calcium 4 (via carbonyl oxygen) (By similarity).
FT	STTS	102	Cysteine switch (Potential).
FT	CARBOHYD	575	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD	644	N-linked (GLNAC. . .) (Potential).
FT	DISULFID	471	By similarity.
SQ	SEQUENCE	662 AA; 73803 MW; 1CC246B270B440C8 CRC64;	

Query Match 100.0%; Score 29; DB 1; Length 662;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY	1	KAVFFFA 6
DB	533	KAVFFFA 538

RESULT 19  
MMP2 RAT STANDARD; PRT; 662 AA.  
AC P33436; P97581;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 12-FEB-2005 (Rel. 48, Last annotation update)  
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa  
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).  
DE Names=Mmp2;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93249363; PubMed=7916617;  
RA Marti H.P., McNeil L., Davies M., Martin J., Lovett D.H.;  
RA "Homology cloning of rat 72 kDa type IV collagenase: cytokine and  
RA second-messenger inducibility in glomerular mesangial cells.";  
RA Biochem. J. 291:441-446(1993).  
RL [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Skin;  
RA Okada A., Basset P.;  
RA "The cloning of the cDNA encoding rat gelatinase A from a rat skin  
RA round cDNA library.";  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types  
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-  
CC Ile-Ala-Gly-Gln.  
CC -1- COPACITOR: Binds 4 calcium ions per subunit (By similarity).  
CC -1- COPACITOR: Binds 2 zinc ions per subunit (By similarity).  
CC -1- SUBUNIT: Ligand for integrin alpha-v/beta-3.  
CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-MMP3) (By similarity).  
CC

CC -!- SIMILARITY: Belongs to the peptidase M10A family.  
 CC -!- SIMILARITY: Contains 3 fibronectin type-II domains.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X71466; CAA50593.1; -; mRNA.  
 CC EMBL; U65656; AAB41692.1; -; mRNA.  
 CC PIR; S34780; S34780.  
 CC HSSP; P08253; 1RTG.  
 CC MEROPS; M10.003; -.  
 CC RGD; 621316; Mmp2.  
 CC GO; GO:0004228; F.gelatinase A activity; IDA.  
 CC GO; GO:0008237; F.metalloproteinase activity; TAS.  
 CC InterPro; IPR000562; FN\_type2\_col\_bd.  
 CC InterPro; IPR000585; Hemopexin.  
 CC InterPro; IPR001818; Pept\_M10A\_M12B.  
 CC InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 CC InterPro; IPR006026; Peptidase\_M.  
 CC Pfam; PF00040; fn2; 3.  
 CC Pfam; PF00045; Hemopexin; 4.  
 CC Pfam; PF00413; Peptidase M10; 1.  
 CC Pfam; PF03933; Peptidase M10\_N; 1.  
 CC PRINTS; PR00013; FNTYPEII.  
 CC PRINTS; PR00138; MATPIXIN.  
 CC ProDom; PD000995; FN\_Type\_II; 3.  
 CC SMART; SM00059; FN2; 3.  
 CC SMART; SM00120; HX; 4.  
 CC SMART; SM00235; ZnMc; 1.  
 CC PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 CC PROSITE; PS00023; FN2\_1; 3.  
 CC PROSITE; PS10922; FN2\_2; 3.  
 CC PROSITE; PS00024; HEMOPEXIN; 1.  
 CC PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 CC Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;  
 KW Hydrolase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;  
 KW Zinc; Zymogen.  
 FT SIGNAL 1 29 Potential.  
 FT PROPEP 30 109 Activation peptide.  
 FT CHAIN 110 662 72 kDa type IV collagenase.  
 FT DOMAIN 228 276 Fibronectin type-II 1.  
 FT DOMAIN 286 334 Fibronectin type-II 2.  
 FT DOMAIN 344 392 Fibronectin type-II 3.  
 FT DOMAIN 468 662 Hemopexin-like.  
 FT REGION 110 221 Collagenase-like 1.  
 FT REGION 222 396 Collagen-binding.  
 FT REGION 397 457 Collagenase-like 2.  
 FT ACT\_SITE 404 404 By similarity.  
 FT METAL 134 134 Calcium 1 (By similarity).  
 FT METAL 168 168 Calcium 2 (By similarity).  
 FT METAL 178 178 Zinc 1 (By similarity).  
 FT METAL 180 180 Zinc 1 (By similarity).  
 FT METAL 185 185 Calcium 3 (By similarity).  
 FT METAL 186 186 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 193 193 Zinc 1 (By similarity).  
 FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 204 204 Calcium 2 (By similarity).  
 FT METAL 206 206 Zinc 1 (By similarity).  
 FT METAL 208 208 Calcium 3 (By similarity).  
 FT METAL 209 209 Calcium 1 (By similarity).  
 FT METAL 211 211 Calcium 3 (By similarity).  
 FT METAL 403 403 Zinc 2 (catalytic) (By similarity).  
 FT METAL 407 407 Zinc 2 (catalytic) (By similarity).  
 FT METAL 413 413 Zinc 2 (catalytic) (By similarity).  
 FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By similarity).

FT METAL 523 523 similarity).  
 FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT METAL 620 620 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT SITE 102 102 Cysteine switch (Potential).  
 FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 644 644 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 471 662 By similarity.  
 FT CONFLICT 42 42 A -> S (in Ref. 2).  
 FT CONFLICT 286 286 A -> G (in Ref. 2).  
 FT CONFLICT 369 369 N -> S (in Ref. 2).  
 FT CONFLICT 435 435 H -> N (in Ref. 2).  
 FT CONFLICT 586 586 A -> S (in Ref. 2).  
 SQ SEQUENCE 662 AA; 74182 MW; 7496B34B0A21884B CRC64;  
 Query Match 100.0%; Score 29; DB 1; Length 662;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 DB 533 KAVFFA 538  
 RESULT 20  
 Q6GMW9 RAT PRELIMINARY; PRT; 662 AA.  
 ID Q6GMW9 RAT PRELIMINARY;  
 AC Q6GMW9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Mmp2 protein.  
 GN Name=Mmp2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC074013; AA074013.1; -; mRNA.  
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.  
 DR GO; GO:0004222; P:metalloendopeptidase activity; IEA.

```

DR GO; GO:0008270; P:zinc ion binding; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_type2_col_bd.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; ENTYPRII.
DR PRINTS; PR00138; MATRIKIN.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FN2_1; 3.
DR PROSITE; PS1092; FN2_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Collagen degradation; Direct protein sequencing;
KW Extracellular matrix; Hydrolase; Metal-binding; Metalloprotease;
KW Protease; Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 26
FT PROPEP 27 106 Activation peptide.
FT CHAIN 107 663 72 kDa type IV collagenase.
FT DOMAIN 225 273 Fibronectin type-II 1.
FT DOMAIN 283 331 Fibronectin type-II 2.
FT DOMAIN 341 389 Fibronectin type-II 3.
FT DOMAIN 469 663 Hemopexin-like.
FT REGION 107 218 Collagenase-like 1.
FT REGION 219 393 Collagen-binding.
FT REGION 394 468 Collagenase-like 2.
FT ACT_SITE 401 401 By similarity.
FT METAL 131 131 Calcium 1 (By similarity).
FT METAL 165 165 Calcium 2 (By similarity).
FT METAL 175 175 Zinc 1 (By similarity).
FT METAL 177 177 Zinc 1 (By similarity).
FT METAL 182 182 Calcium 3 (By similarity).
FT METAL 183 183 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 190 190 Zinc 1 (By similarity).
FT METAL 197 197 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 199 199 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 201 201 Calcium 2 (By similarity).
FT METAL 203 203 Zinc 1 (By similarity).
FT METAL 205 205 Calcium 3 (By similarity).
FT METAL 206 206 Calcium 1 (By similarity).
FT METAL 208 208 Calcium 3 (By similarity).
FT METAL 400 400 Zinc 2 (catalytic) (By similarity).
FT METAL 404 404 Zinc 2 (catalytic) (By similarity).
FT METAL 410 410 Zinc 2 (catalytic) (By similarity).
FT METAL 479 479 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 524 524 Calcium 4 (via carbonyl oxygen) (By similarity).

CC MMP3) (By similarity).
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -1- SIMILARITY: Contains 3 fibronectin type-II domains.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U07775; AAA19596.1; -; mRNA.
DR PIR; S46492; S46492.
DR HSSP; P08253; 1Q1B.
DR MEROPS; M10.003; -.
DR Ensembl; ENSGALG00000003580; Gallus gallus.
DR InterPro; IPR000562; FN_type2_col_bd.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; ENTYPRII.
DR PRINTS; PR00138; MATRIKIN.
DR PRODOM; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FN2_1; 3.
DR PROSITE; PS1092; FN2_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Collagen degradation; Direct protein sequencing;
KW Extracellular matrix; Hydrolase; Metal-binding; Metalloprotease;
KW Protease; Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 26
FT PROPEP 27 106 Activation peptide.
FT CHAIN 107 663 72 kDa type IV collagenase.
FT DOMAIN 225 273 Fibronectin type-II 1.
FT DOMAIN 283 331 Fibronectin type-II 2.
FT DOMAIN 341 389 Fibronectin type-II 3.
FT DOMAIN 469 663 Hemopexin-like.
FT REGION 107 218 Collagenase-like 1.
FT REGION 219 393 Collagen-binding.
FT REGION 394 468 Collagenase-like 2.
FT ACT_SITE 401 401 By similarity.
FT METAL 131 131 Calcium 1 (By similarity).
FT METAL 165 165 Calcium 2 (By similarity).
FT METAL 175 175 Zinc 1 (By similarity).
FT METAL 177 177 Zinc 1 (By similarity).
FT METAL 182 182 Calcium 3 (By similarity).
FT METAL 183 183 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 190 190 Zinc 1 (By similarity).
FT METAL 197 197 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 199 199 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 201 201 Calcium 2 (By similarity).
FT METAL 203 203 Zinc 1 (By similarity).
FT METAL 205 205 Calcium 3 (By similarity).
FT METAL 206 206 Calcium 1 (By similarity).
FT METAL 208 208 Calcium 3 (By similarity).
FT METAL 400 400 Zinc 2 (catalytic) (By similarity).
FT METAL 404 404 Zinc 2 (catalytic) (By similarity).
FT METAL 410 410 Zinc 2 (catalytic) (By similarity).
FT METAL 479 479 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 524 524 Calcium 4 (via carbonyl oxygen) (By similarity).

Query March 100.0%; Score 29; DB 2; Length 662;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
DB 533 KAVFFA 538

RESULT 21
MMP2 CHICK
ID _MMP2 CHICK STANDARD; PRT; 663 AA.
AC Q90611;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN Name=MMP2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBITaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=94280397; PubMed=8010954;
RA Aimes R.T., French D.L., Quigley J.P.;
RT "Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from
RT chicken embryo fibroblasts using gene family PCR: expression of the
RT gelatinase increases upon malignant transformation.";
RL Biochem. J. 300:729-736(1994).
[2]
RN [2]
RP PROTEIN SEQUENCE OF 27-41 AND 107-122.
RX MEDLINE=91161603; PubMed=1848240;
RA Chen J.-M., Aimes R.T., Ward G.R., Youngleib G.L., Quigley J.P.;
RT "Isolation and characterization of a 70-kDa metalloprotease
RT (gelatinase) that is elevated in Rous sarcoma virus-transformed
RT chicken embryo fibroblasts.";
RL J. Biol. Chem. 266:5113-5121(1991).
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-
CC Ile-Ala-Gly-Gln.
CC -1- COPACITOR: Binds 4 calcium ions per subunit (By similarity).
CC -1- COPACITOR: Binds 2 zinc ions per subunit (By similarity).
CC -1- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -1- TISSUE SPECIFICITY: Produced by normal skin fibroblasts.
CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-

```

```

FT METAL 572 572 similarity).
FT METAL 621 621 Calcium 4 (via carbonyl oxygen) (By
FT METAL 621 621 Calcium 4 (via carbonyl oxygen) (By
FT SITE 99 99 Cysteine switch (Potential).
FT DISULFID 472 663 By similarity.
FT CONFLICT 40 40 P -> Q (in Ref. 2).
FT CONFLICT 116 116 W -> T (in Ref. 2).
FT CONFLICT 122 122 T -> I (in Ref. 2).
SQ SEQUENCE 663 AA; 74941 MW; 8D6FDA4E67C3EBCA CRC64;

Query Match 100.0%; Score 29; DB 1; Length 663;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 534 KAVFFA 539

RESULT 22
Q8KTW1_CLODI PRELIMINARY; PRT; 767 AA.
AC Q8KTW1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface layer protein A.
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RX MEDLINE=22077258; PubMed=12081960;
RX DOI=10.1128/JB.184.14.3886-3897.2002;
RA Calabi E., Fairweather N.;
RT "Patterns of sequence conservation in the S-layer proteins and related
sequences in Clostridium difficile."
RL J. Bacteriol. 184:3886-3897(2002).
DR EMBL; AF478571; AAM46790.1; -; Genomic_DNA.
DR InterPro; IPR007253; CW_binding_2.
DR Pfam; PF04122; CW_binding_2; 3.
SQ SEQUENCE 767 AA; 81461 MW; 7280626184495D70 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 767;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 358 KAVFFA 363

RESULT 23
Q7XX63_ORYSA PRELIMINARY; PRT; 770 AA.
AC Q7XX63;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNBa0052P16.14 protein.
GN Name=OSJNBa0052P16.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12447439; DOI=10.1038/nature01183;

```

```

RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4."
RL Nature 420:316-320(2002).
DR EMBL; AL662936; CAD39717.1; -; Genomic_DNA.
DR Gramene; Q7XX63; -;
DR GO; GO:0016829; P:lyase activity; IEA.
DR GO; GO:0000287; P:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 2.
SQ SEQUENCE 770 AA; 86360 MW; 6CFAB6855D904EE1 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 555 KAVFFA 560

RESULT 24
Q66QH3_ORYSA PRELIMINARY; PRT; 840 AA.
AC Q66QH3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Syn-pinara-7,15-diene synthase.
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15299118; DOI=10.1104/pp.104.045971;
RX Wilderman P.R., Xu M., Jin Y., Coates R.M., Peters R.J.;
RT "Identification of syn-pinara-7,15-diene synthase reveals functional
clustering of terpene synthases involved in rice
phytoalexin/allelochemical biosynthesis."
RL Plant Physiol. 135:2098-2105(2004).
DR EMBL; AY616862; AAU05906.1; -; mRNA.
DR Gramene; Q66QH3; -;
DR GO; GO:0016829; P:lyase activity; IEA.
DR GO; GO:0000287; P:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
SQ SEQUENCE 840 AA; 94757 MW; B0ECC89323C86ASE CRC64;

Query Match 100.0%; Score 29; DB 2; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 625 KAVFFA 630

```



```
RESULT 25
Q60HB5_ORYZA
ID Q60HB5_ORYSA PRELIMINARY; PRT; 842 AA.
AC Q60HB5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 9b-plmara-7,15-diene synthase.
GN Name=OsK54;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1538982; DOI=10.1271/bbb.68.2001;
RA Oikawa K., Kanno Y., Motegi A., Kenmoku H., Yamane H., Mitsuhashi W.,
RA Oikawa H., Toshihima H., Itoh H., Matsuo M., Sasea T., Toyomasu T.;
RT "Diterpene cyclases responsible for the biosynthesis of phytoalexins,
RT monilactones A, B, and oryzalexins A-F in rice.";
RL Biosci. Biotechnol. Biochem. 68:2001-2006(2004).
DR EMBL; AB126934; BAD54751.1; -; mRNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:000287; F:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synthase C.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth_C; 1.
SQ SEQUENCE 842 AA; 94568 MW; 928F88F8FCC35497 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 627 KAVFFA 632

RESULT 26
Q69DS7_ORYSA
ID Q69DS7_ORYSA PRELIMINARY; PRT; 842 AA.
AC Q69DS7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Ent-kaurene synthase like-4.
GN Name=OsK54;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15668792; DOI=10.1007/s00299-004-0896-6;
RA Margis-Pinheiro M., Zhou X.R., Zhu Q.H., Dennis E.S., Upadhyaya N.M.;
RT "Isolation and characterization of a Ds-tagged rice (Oryza sativa L.)
RT GA-responsive dwarf mutant defective in an early step of the
RT gibberellin biosynthesis pathway.";
RL Plant Cell Rep. 23:819-833(2005).
DR EMBL; AY347880; AAQ72563.1; -; mRNA.
DR Gramene; Q69DS7; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synthase C.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.

Query Match 100.0%; Score 29; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 627 KAVFFA 632

RESULT 27
Q9N175_SHEEP
ID Q9N175_SHEEP PRELIMINARY; PRT; 945 AA.
AC Q9N175;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21168784; PubMed=12181148;
RA Merhosh J.L., Baker R.S., Clark K.E.;
RT "Estrogen increases iNOS expression in the ovine coronary artery.";
RL Am. J. Physiol. Heart Circ. Physiol. 283:H1169-H1180(2002).
DR EMBL; AF223942; AAF34710.1; -; mRNA.
DR HSSP; P35228; INSI.
DR SNR; Q9N175; 1-326.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005516; P:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; PAD binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR008254; Flav_nitox synth.
DR InterPro; IPR001709; FPN_Cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Ox-red_FAD/NAD(P).
DR Pfam; PF00667; FAD binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; PFNCR.
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 945 945
SQ SEQUENCE 945 AA; 108001 MW; 9A5ACFD40440A74F CRC64;

Query Match 100.0%; Score 29; DB 2; Length 945;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 344 KAVFFA 349

RESULT 28
NOS2_RAT
```



ID NOS2 RAT STANDARD; PRT; 1147 AA.  
AC Q06518; Q03765; Q03766; Q060591; Q060604; P97774; Q63267; Q64005;  
AC Q64558;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)  
DE (Inducible NOS) (iNOS).  
DE Name=Nos2;  
GN Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Vascular smooth muscle;  
RX MEDLINE=931191721; PubMed=7680561;  
RA Nunokawa Y., Ishida N., Tanaka S.;  
RT "Cloning of inducible nitric oxide synthase in rat vascular smooth  
muscle cells.";  
RL Biochem. Biophys. Res. Commun. 191:89-94(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Pancreatic islets;  
RX MEDLINE=95309542; PubMed=7540573;  
RA Karlsen A.E., Andersen H.U., Viessing H., Larsen P.M., Fey S.J.,  
RA Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,  
RA Mandrup-Poulsen T., Boel E., Nerup J.;  
RT "Cloning and expression of cytokine-inducible nitric oxide synthase  
cDNA from rat islets of Langerhans.";  
RL Diabetes 44:753-758(1995).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Astocytes;  
RX MEDLINE=94231594; PubMed=7513765;  
RA Galea E., Reis D.J., Feinstein D.L.;  
RT "Cloning and expression of inducible nitric oxide synthase from rat  
astrocytes.";  
RL J. Neurosci. Res. 37:406-414(1994).  
RN [4]  
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=94039059; PubMed=7693462;  
RA Adachi H., Iida S., Oguchi S., Ohehima H., Suzuki H., Nagasaki K.,  
RA Kawasaki H., Sugimura T., Esumi H.;  
RT "Molecular cloning of a cDNA encoding an inducible calmodulin-  
dependent nitric-oxide synthase from rat liver and its expression in  
COS 1 cells.";  
RL Eur. J. Biochem. 217:37-43(1993).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Hepatocyte;  
RX MEDLINE=93221515; PubMed=7682072;  
RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;  
RT "Hepatocytes and macrophages express an identical cytokine inducible  
nitric oxide synthase gene.";  
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Aorta;  
RX MEDLINE=94325351; PubMed=7519448; DOI=10.1016/0167-4781(94)90196-1;  
RA Geng Y.J., Almqvist M., Hansson G.K.;  
RT "cDNA cloning and expression of inducible nitric oxide synthase from  
rat vascular smooth muscle cells.";  
RL Biochim. Biophys. Acta 1218:421-424(1994).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RA Kosuga K., Yui Y., Hattori R., Sase K., Bizawa H., Aoyama T.,  
RA Inoue R., Sasayama S.;  
RT "Cloning of an inducible nitric oxide synthase from rat  
polymorphonuclear neutrophils.";  
RL Endothelium 2:217-221(1994).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97070590; PubMed=8913516;  
RA Teutemshita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,  
RA Futaki S., Niwa M.;  
RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,  
lung, and uterus.";  
RL Biol. Pharm. Bull. 19:1374-1376(1996).  
RN [9]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99066690; PubMed=9851365; DOI=10.1006/niox.1998.0184;  
RA Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S.,  
RA Schuler G., Hambrecht R.;  
RT "Complete coding sequence of inducible nitric oxide synthase from  
human heart and skeletal muscle of patients with chronic heart  
failure.";  
RL Nitric Oxide 2:242-249(1998).  
RN [10]  
RP NUCLEOTIDE SEQUENCE OF 426-788.  
RC STRAIN=Dahl/Rapp salt sensitive strain; TISSUE=Vascular smooth muscle;  
RX MEDLINE=98195092; PubMed=9535415;  
RA Chen P.Y., Gladish R.D., Sanders P.W.;  
RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp  
salt-sensitive rats.";  
RL Hypertension 31:918-924(1998).  
RN [11]  
RP NUCLEOTIDE SEQUENCE OF 509-740.  
RC STRAIN=Wistar; TISSUE=Renal glomerulus;  
RA Saura M., Zaragoza C., Martinez-Balme R., Perez-Sala D., Lamas S.;  
RT "Advances in the studies of NO synthesis regulation in mesangial  
cells.";  
RL Nephrologia 16:35-39(1996).  
RN [12]  
RP NUCLEOTIDE SEQUENCE OF 479-655.  
RC STRAIN=Sprague-Dawley; TISSUE=Renal glomerulus;  
RX MEDLINE=94276509; PubMed=7516453;  
RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,  
RA Klahr S.;  
RT "Location of an inducible nitric oxide synthase mRNA in the normal  
kidney.";  
RL Kidney Int. 45:998-1005(1994).  
RN [13]  
RP NUCLEOTIDE SEQUENCE OF 420-479.  
RC TISSUE=Myocardium;  
RA Michel T., Balligand J.-L.;  
RT "Isolation and characterization of iNOS from rat cardiocytes.";  
Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule  
with diverse functions throughout the body.  
CC -!- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline +  
nitric oxide + n NADP(+).  
CC -!- COFACTOR: Heme.  
CC -!- COFACTOR: FAD. Binds 1 mole of FAD.  
CC -!- COFACTOR: FMN. Binds 1 mole of FMN.  
CC -!- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric  
form of the enzyme.  
CC -!- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin  
inhibits expression and function of this enzyme and effects may be  
exerted at the level of translational/posttranslational  
modification and directly on the catalytic activity (by  
similarity).  
CC -!- SUBUNIT: Homodimer. Binds SLC9A3R1 (By similarity).  
CC -!- TISSUE SPECIFICITY: In normal kidney, expressed primarily in the  
medullary thick ascending limb, with minor amounts in the  
medullary collecting duct and vasa recta bundle.  
CC -!- INDUCTION: By interferon gamma and lipopolysaccharides (LPS).  
CC -!- SIMILARITY: Belongs to the NOS family.  
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.  
CC -!- CAUTION: Ref.9 sequence was originally thought to originate from  
human but appears to be from rat.  
-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC -----  
 DR EMBL; D14051; BAA03138.1; -; mRNA.  
 DR EMBL; U26686; AAAS5861.1; -; mRNA.  
 DR EMBL; U03699; AAC13747.1; -; mRNA.  
 DR EMBL; D12520; BAA02090.1; -; mRNA.  
 DR EMBL; L12562; AAA41720.1; -; mRNA.  
 DR EMBL; X76881; BAA54208.1; -; mRNA.  
 DR EMBL; D44591; BAA07994.1; -; mRNA.  
 DR EMBL; D83661; BAA12035.1; -; mRNA.  
 DR EMBL; AF049656; AAC83553.1; -; mRNA.  
 DR EMBL; AF051164; AAC83554.1; -; mRNA.  
 DR EMBL; AF006619; AAC16401.1; -; mRNA.  
 DR EMBL; AF006620; AAC16402.1; -; mRNA.  
 DR EMBL; U48829; AAB18620.1; -; mRNA.  
 DR EMBL; S71597; AAB31028.2; -; mRNA.  
 DR EMBL; L36063; AAC02242.1; -; mRNA.  
 DR PIR; I53165; I53165.  
 DR PIR; I56575; I56575.  
 DR PIR; JC5027; JC5027.  
 DR PIR; S38253; S38253.  
 DR PIR; S47647; S47647.  
 DR HSP; P29477; INOS.  
 DR SMR; Q6518; 80-499.  
 DR Ensembl; ENSRNOG0000011023; Rattus norvegicus.  
 DR RGD; 3185; Nos2.  
 DR GO; GO:0005829; C:cytosol; ISS.  
 DR GO; GO:0005516; F:calmodulin binding; ISS.  
 DR GO; GO:0008603; F:cAMP-dependent protein kinase regulator act. .; IDA.  
 DR GO; GO:0020037; F:heme binding; ISS.  
 DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.  
 DR GO; GO:0042742; P:defense response to bacteria; ISS.  
 DR GO; GO:0007199; P:G-protein signaling, coupled to cGMP nucleo. .; IDA.  
 DR GO; GO:0006954; P:inflammatory response; ISS.  
 DR GO; GO:0006809; P:nitric oxide biosynthesis; TAS.  
 DR GO; GO:0007165; P:signal transduction; IDA.  
 DR GO; GO:0006801; P:superoxide metabolism; ISS.  
 DR InterPro; IPR003097; FAD bd.  
 DR InterPro; IPR008254; Flav nitox synth.  
 DR InterPro; IPR001094; Flavodoxin like.  
 DR InterPro; IPR001709; FPN\_cyt\_redctse.  
 DR InterPro; IPR004030; NO\_synthase.  
 DR InterPro; IPR012144; NOS.  
 DR InterPro; IPR001433; Oxred FAD NAD bd.  
 DR PANTHER; PTHR19386; NO synthase; 1.  
 DR Pfam; PF00667; FAD binding\_1; 1.  
 DR Pfam; PF00258; Flavodoxin\_1; 1.  
 DR Pfam; PF02898; NO synthase; 1.  
 DR PIRSF; PIRSF000333; NOS; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; PFNCR.

Query Match 100.0%; Score 29; DB 1; Length 1147;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||  
 Db 517 KAVFFA 522

## RESULT 29

Q6XS76 RAT PRELIMINARY; PRT; 1147 AA.  
 AC Q6XS76;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Inducible nitric oxide synthase (Fragment).  
 GN Name=Nos2;

OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Aortic smooth muscle;  
 RA Cui Z., Tuladhar R., Hart S., Marber M., Pearson J., Baydoun A.R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY211532; AAP43670.1; -; mRNA.  
 DR HSP; P29477; IJWK.  
 DR SMR; Q6XS76; 80-499.  
 DR GO; GO:0005516; F:calmodulin binding; IEA.  
 DR GO; GO:0005489; F:electron transporter activity; IEA.  
 DR GO; GO:0010181; F:FMN binding; IEA.  
 DR GO; GO:0004517; F:nitric-oxide synthase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006809; P:nitric oxide biosynthesis; IEA.  
 DR InterPro; IPR003097; FAD binding.  
 DR InterPro; IPR001094; Flavodoxin like.  
 DR InterPro; IPR008254; Flav nitox synth.  
 DR InterPro; IPR001709; FPN\_cyt\_redctse.  
 DR InterPro; IPR012144; NOS.  
 DR InterPro; IPR004030; NO\_synthase.  
 DR InterPro; IPR001433; Oxred FAD/NAD(P).  
 DR Pfam; PF00667; FAD binding\_1; 1.  
 DR Pfam; PF00258; Flavodoxin\_1; 1.  
 DR Pfam; PF00175; NAD binding\_1; 1.  
 DR Pfam; PF02898; NO synthase; 1.  
 DR PIRSF; PIRSF000333; NOS; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; PFNCR.  
 DR PROSITE; PS05902; FLAVODOXIN LIKE; 1.  
 DR PROSITE; PS60001; NOS; UNKNOWN\_1.  
 FT NON TER 1147 1147  
 SQ SEQUENCE 1147 AA; 130673 MW; 204484P2231D9ECA CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 1147;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KAVFFA 6  
 |||||  
 Db 517 KAVFFA 522  
 RESULT 30  
 Q9QW28 9MURI PRELIMINARY; PRT; 1147 AA.  
 AC Q9QW28;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cytokine inducible nitric oxide synthase, iNOS.  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93221515; PubMed=7682072;  
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;  
 RT "Hepatocytes and macrophages express an identical cytokine inducible  
 RT nitric oxide synthase gene";  
 RL Biochem. Biophys. Res. Commun. 191:767-774 (1993).  
 DR HSP; P29477; INOS.  
 DR SMR; Q9QW28; 80-499.  
 DR GO; GO:0005829; C:cytosol; ISS.  
 DR GO; GO:0005516; F:calmodulin binding; ISS.  
 DR GO; GO:0020037; F:heme binding; ISS.

```

DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. . .; ISS.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF00333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN_1.
SQ SEQUENCE 1147 AA; 136625 MW; 2CABP983E56F651A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. NO. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPFA 6
Db 517 KAVPFA 522

RESULT 31
Q9R0W4_RAT PRELIMINARY; PRT; 1147 AA.
AC Q9R0W4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Name=iNOS;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=9326503; PubMed=10395902; DOI=10.1016/S0378-1119(99)00196-1;
RX Keinanen R.A., Vartiainen N., Koistinaho J.;
RA "Molecular cloning and characterization of the rat inducible nitric
RT oxide synthase (iNOS) gene.";
RL Gene 234:297-305(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=864711;
RA Iwashina M., Hirata Y., Imai T., Sato K., Marumo F.;
RT "Molecular cloning of endothelial, inducible nitric oxide synthase
RT gene from rat aortic endothelial cell.";
RL Eur. J. Biochem. 237:668-673(1996).
DR EMBL; AJ230462; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230463; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230465; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230464; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230467; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230469; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230471; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230473; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230475; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230484; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230483; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230482; CAB46089.1; JOINED; Genomic DNA.

```

```

DR EMBL; AJ230481; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230480; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230479; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230478; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230477; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230476; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230487; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230486; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230485; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230474; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230472; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230470; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230468; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230466; CAB46089.1; JOINED; Genomic DNA.
DR PIR; JC5028; JC5028.
DR PIR; JC5029; JC5029.
DR PIR; S65440; S65440.
DR HSP; P29477; INOS.
DR SMR; Q9R0W4; 80-499.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD bd.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR PIRSF; PIRSF00333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN_1.
SQ SEQUENCE 1147 AA; 130614 MW; E76B3F8407D54CF6 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. NO. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPFA 6
Db 517 KAVPFA 522

RESULT 32
Q8Y1S2_RALSO PRELIMINARY; PRT; 118 AA.
AC Q8Y1S2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE PROBABLE SIGNAL PEPTIDE PROTEIN.
GN OrderedLocustNames=RSC0617; ORFNames=RS01518;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,

```

```

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646060; CAD14147.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 118 AA; 12054 MW; 955D9DEA2C16CF42 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 118;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 8 KAIFFA 13

RESULT 33
Q8UI59 AGRT5
ID Q8UI59 AGRT5 PRELIMINARY; PRT; 169 AA.
AC Q8UI59;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Atu0441.
GN OrderedLocuNames=Atu0441;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OC NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
RA Neester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AB009014; AAL41460.1; -; Genomic_DNA.
DR PIR; AF2630; AF2630.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 169 AA; 19428 MW; FDBBB0BAC5D38EB CRC64;

Query Match 96.6%; Score 28; DB 2; Length 169;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 114 KAIFFA 119

RESULT 34
Q19334 CAEEL
ID Q19334 CAEEL PRELIMINARY; PRT; 283 AA.
AC Q19334; Q21599;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein M79.2.
GN ORFNames=M79.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

```

```

OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z50857; CAA90720.1; -; Genomic_DNA.
DR EMBL; Z50806; CAA90692.1; -; Genomic_DNA.
DR EMBL; Z50806; CAA90720.1; JOINED; Genomic_DNA.
DR EMBL; Z50857; CAA90692.1; JOINED; Genomic_DNA.
DR PIR; T20734; T20734.
DR Ensemble; M79.2; Caenorhabditis elegans.
DR WormBase; WBGene00010902; M79.2.
DR WormPep; M79.2; CR03507.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 283 AA; 32582 MW; 51638B43CB266860 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 157 KAIFFA 162

RESULT 35
Q8EM92 OCEIH
ID Q8EM92 OCEIH PRELIMINARY; PRT; 305 AA.
AC Q8EM92;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical conserved protein.
GN OrderedLocuNames=OB2966;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OC NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC14922.1; -; Genomic_DNA.
DR InterPro; IPR003507; Peptidase U61.
DR Pfam; PF02016; Peptidase U61.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 305 AA; 33528 MW; 6A7F3E282B2B5580 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 305;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 75 KAIFFA 80

RESULT 36
Q6LJY6 PHOPR
ID Q6LJY6 PHOPR PRELIMINARY; PRT; 355 AA.
AC Q6LJY6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

```

DE Hypothetical protein.
GN OrderedLocusNames=PBPRB0521;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro P.M., Cestaro A., Malacrida G., Simonati B., Camata N.,
RA Romualdi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis.";
RL Science 307:1459-1461(2005).
DR EMBL; CR378676; CAG22394.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 355 AA; 40056 MW; 6A3C866307079447 CRC64;
    Query Match      96.6%; Score 28; DB 2; Length 355;
    Best Local Similarity 83.3%; Pred. No. 3e+02;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 316 KAIFFA 321

RESULT 37
QBXINS CLOPE
ID QBXINS_CLOPE PRELIMINARY; PRT; 1044 AA.
AC QBXINS;
DT 01-WAR-2002 (TReMBLrel. 20, Created)
DT 01-WAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-WAR-2004 (TReMBLrel. 26, Last annotation update)
DE Alpha-mannosidase.
GN OrderedLocusNames=CPR2080;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; BA000016; BAB81786.1; -; Genomic DNA.
DR GO; GO:0004559; F:alpha-mannosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006013; P:mannose metabolism; IEA.
DR InterPro; IPR000602; Glyco_hydro_38.
DR InterPro; IPR011682; Glyco_hydro_38C.
DR Pfam; PF01074; Glyco_hydro_38; 1.
DR Pfam; PF07748; Glyco_hydro_38C; 1.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 1044 AA; 121432 MW; 3CABB79447D42B6F CRC64;
    Query Match      96.6%; Score 28; DB 2; Length 1044;
    Best Local Similarity 83.3%; Pred. No. 8.1e+02;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 666 KAIFFA 671

RESULT 38
Q19641_CABEL

```

```

ID Q19641 CABEL PRELIMINARY; PRT; 85 AA.
AC Q19641;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein F20D12.5.
GN ORFNames=F20D12.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SIMILARITY: Contains 1 LIM zinc-binding domain.
DR EMBL; U40933; AAL27241.1; -; Genomic_DNA.
DR HSSP; P04006; LIML.
DR SMR; Q19641; 2-77.
DR Ensembl; F20D12.5; Caenorhabditis elegans.
DR WormBase; WBGene00017644; F20D12.5.
DR WormPep; F20D12.5; CE29767.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001781; LIM_zn_bd.
DR Pfam; PF00412; LIM; 1.
DR ProDom; PD000094; LIM; 1.
DR SMART; SM00132; LIM; 1.
DR PROSITE; PS00023; LIM DOMAIN 2; 1.
KW Complete proteome; Hypothetical protein; LIM domain; Metal-binding;
KW Zinc.
SQ SEQUENCE 85 AA; 9479 MW; 83B93440C82AE849 CRC64;
    Query Match      89.7%; Score 26; DB 2; Length 85;
    Best Local Similarity 83.3%; Pred. No. 2.5e+02;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 9 KAVYFA 14

RESULT 39
Q731J0_WOLPM
ID Q731J0_WOLPM PRELIMINARY; PRT; 99 AA.
AC Q731J0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Oxidoreductase, putative.
GN OrderedLocusNames=WD0173;
OS Wolbachia pipientis wMel.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachieae; Wolbachia.
OX NCBI_TaxID=66077;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15024419; DOI=10.1371/journal.pbio.0020069;
RA Wu M., Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,
RA Brownlie J.C., McGraw E.A., Martin W., Esser C., Almadinejad N.,
RA Wigand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA Durkin A.S., Kolonay J.P., Nelson W.C., Mohamoud Y., Lee P.,
RA Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,
RA Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.;
RT "Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
RT a streamlined genome overrun by mobile genetic elements.";
RL PLOS Biol. 2:327-341(2004).
DR EMBL; AE017256; AAS13922.1; -; Genomic_DNA.
DR TIGR; WD0173; -.

```

```

RX PubMed:15210978, DOI=10.1073/pnas.0305659101;
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scala B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
RD EMBL; EX897699; CAP27754.1; -, Genomic_DNA.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 126 AA; 14027 MW; 7A632D838151PFAE CRC64;

Query Match      89.7%; Score 26; DB 2; Length 126;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 34 RAVFFA 39
      :|||||

RESULT 42
Q6C1M8 YARLI PRELIMINARY; PRT; 131 AA.
AC Q6C1M8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Similar to w|NCU06209.1 Neurospora crassa NCU06209. 1 hypothetical
DE protein.
GN OrderedLocusNames=YAL10F14905g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OC NCBI_TaxID=4952;
RL [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed:15229592; DOI=10.1038/nature02579;
RX Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekaita F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RL "Genome evolution in yeasts.";
RT Nature 430:35-44(2004).
RD ENBL; CR382132; CAG78243.1; -, Genomic_DNA.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 131 AA; 14843 MW; 5D7F9328DBC87E19 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 131;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 126 KAVFFS 131
      :|||||

RESULT 43
Q6G346 BARHE PRELIMINARY; PRT; 131 AA.
AC Q6G346;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

```

```

DE Hypothetical protein.
GN OrderedLocusNames=BH09620;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 49882 / Houston 1;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scala B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF27755.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 131 AA; 14730 MW; 48D91F115B667439 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 131;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 34 KAVFFA 39

RESULT 44
QSKK3 THET8
ID Q5SKK3_THET8 PRELIMINARY; PRT; 137 AA.
AC Q5SKK3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein TTHA0640.
GN OrderedLocusNames=TTHA0640;
OS Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=300852;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HB8;
RA Masui R., Kurokawa K., Nakagawa N., Tokunaga F., Koyama Y.,
RA Shibata T., Oshima T., Yokoyama S., Yasunaga T., Kuramitsu S.;
RT "Complete genome sequence of Thermus thermophilus HB8.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008226; BAD70463.1; -; Genomic_DNA.
DR InterPro; IPR007842; HEPN.
DR Pfam; PF05168; HEPN; 1.
DR PROSITE; PS0910; HEPN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 137 AA; 15304 MW; 37D01C6D9C3287FA CRC64;

Query Match 89.7%; Score 26; DB 2; Length 137;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 43 KAVFFA 48

RESULT 45
QAJC95 SULAC
ID QAJC95_SULAC PRELIMINARY; PRT; 142 AA.
AC QAJC95;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Conserved membrane protein.

```

```

GN OrderedLocusNames=Saci_0164;
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
RX PubMed=1595215; DOI=10.1128/JB.187.14.4992-4999.2005;
RA Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarinsson E.,
RA Greve B., Awaryez M., Zibat A., Klenk H.-P., Garrett R.A.;
RT "The genome of Sulfolobus acidocaldarius, a model organism of the
RT Crenarchaeota.";
RL J. Bacteriol. 187:4992-4999(2005).
DR EMBL; CP000077; AAY79584.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 142 AA; 16221 MW; 5B92483FA7F864C4 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 142;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 82 KSVFFA 87

RESULT 46
QSWU01 LEGPL
ID Q5WU01_LEGPL PRELIMINARY; PRT; 149 AA.
AC Q5WU01;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lp12372;
OC Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch P., Kunst P.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR628337; CAH16612.1; -; Genomic_DNA.
DR Legioli; lp12372; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16274 MW; F698CECF32B0837 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 37 KSVFFA 42

RESULT 47
Q5X274 LEGPA
ID Q5X274_LEGPA PRELIMINARY; PRT; 149 AA.
AC Q5X274;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lp2519;
OS Legionella pneumophila (strain Paris).

```



OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Legionellaceae; Legionella.

OX NCBI\_TaxID=297246;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,  
 RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,  
 RA Etienne J., Glaser P., Buchrieser C.;  
 RT "Evidence in the Legionella pneumophila genome for exploitation of  
 RT host cell functions and high genome plasticity.";  
 RL Nat. Genet. 36:1165-1173(2004).  
 DR EMBL; CR28336; CAH13672.1; -; Genomic\_DNA.  
 DR Legionellist; lpp2519; -.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 149 AA; 16323 MW; 8489CE2861AD3D5A CRC64;

Query Match 89.7%; Score 26; DB 2; Length 149;  
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

DB 37 KSVFFA 42

RESULT 48

Q5ZSR4 LEGPH

ID Q5ZSR4 LEGPH PRELIMINARY; PRT; 149 AA.

AC Q5ZSR4

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE Hypothetical protein.

GN OrderedLocuNames=lpq2453;

OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /

ATCC 33152).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;

OC Legionellaceae; Legionella.

OX NCBI\_TaxID=272624;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15448271; DOI=10.1126/science.1099776;

RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,  
 RA Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,  
 RA Steshenko V., Park S.H., Zhao B., Teplitzskaya E., Edwards J.R.,  
 RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,  
 RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,  
 RA Segal G., Qu X., Rzhetsky A., Zhang P., Cavanis E., De Jong P.J.,  
 RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;  
 RT "The genomic sequence of the accidental pathogen Legionella  
 RT pneumophila";  
 RL Science 305:1196-1196(2004).

DR EMBL; AB017354; ANU28513.1; -; Genomic\_DNA.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 149 AA; 16374 MW; 76C1CB2C5D08DF23 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 149;  
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

DB 37 KSVFFA 42

RESULT 49

Q51314 9NOSO

ID Q51314 9NOSO PRELIMINARY; PRT; 150 AA.

AC Q51314

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24; Last annotation update)

DE Ssdna replicating plasmid encoding a replication-associated protein  
 DE (repA) and three ORFs, complete cds.

OS Nostoc sp.

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI\_TaxID=1180;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Walton D.K., Gendel S.M., Atherly A.G.;  
 RA Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.

DR EMBL; M81381; AAA25514.1; -; Genomic\_DNA.

DR PIR; S27597; S27597.

SQ SEQUENCE 150 AA; 16660 MW; 7C34D00291E436A6 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 150;

Best Local Similarity 83.3%; Pred. No. 4.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

DB 36 KALFFA 41

RESULT 50

GUAD\_BACSU

ID GUAD\_BACSU STANDARD; PRT; 156 AA.

AC C34598;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Guanine deaminase (EC 3.5.4.3) (Guanase) (Guanine aminase) (Guanine

DE aminohydrolase) (GAH) (GDEase).

GN Names=guad; Synonyms=gde; OrderedLocuNames=BSU13170;

OC Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1423;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=168;

RA Devine K.M.;

RT "Sequence of the Bacillus subtilis genome between xlyA and ykoR.";

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=168;

RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;

RA Kunst F., Ogatawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Duesterhoft A., Ehrlich S.D., Emerson P.T.,

RA Ertan K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Ghim S.-Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,

RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hulio M.-F., Itaya M.,

RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M.,

RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,

RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,

RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,

RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,

RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,

RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,

RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,

RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,

RA Scoffone P., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,

RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,

RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,

RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,

RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,

RA Weitsengger T., Winters P., Wipat A., Yamamoto H., Yamane K.,

RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,



Yoshihawa H., Danchin A.;  
"The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.";  
Nature 390:249-256 (1997).  
[3]  
FUNCTION.  
STRAIN=168;  
MEDLINE=20533169; PubMed=1101664;  
NYgaard P., Bested S.M., Andersen K.A.K., Saxild H.H.;  
"Bacillus subtilis guanine deaminase is encoded by the yknA gene and is induced during growth with purines as the nitrogen source.";  
Microbiology 146:3061-3069 (2000).  
CC -1- FUNCTION: Catalyzes the hydrolytic deamination of guanine, producing xanthine and ammonia.  
CC -1- CATALYTIC ACTIVITY: Guanine + H(2)O = xanthine + NH(3).  
CC -1- COFACTOR: Zinc (By similarity).  
CC -1- PATHWAY: Purine catabolism.  
CC -1- INDUCTION: Expressed only during limited or partially limited nitrogen conditions. Can be induced to high levels in the presence of purines or intermediates of the purine catabolic pathway.  
CC Expression seems indirectly controlled by tnxA and glnX.  
CC -1- SIMILARITY: Belongs to the cytidine and deoxycytidylate deaminase family.  
-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
-----  
EMBL; AJ002571; CAA05596.1; -; Genomic DNA.  
DR EMBL; Z99110; CAB13174.1; -; Genomic\_DNA.  
DR PIR; F69857; F69857.  
DR PDB; 1TIY; X-ray; A/B=1-156.  
DR PDB; 1WKQ; X-ray; A/B=1-156.  
DR Subtilis; BG13240; Guad.  
DR InterPro; IPR002125; CMP\_dCMP\_Zn\_bd.  
DR Pfam; PF00383; dCMP\_cyt\_deam; 1.  
DR PROSITE; PS00903; Cyt\_dCMP\_DEAMINASES; 1.  
KW 3D-structure; Complete proteome; Hydrolase; Metal-binding;  
Purine metabolism; Zinc.  
FT METAL 53 53 Zinc (By similarity).  
FT METAL 83 83 Zinc (By similarity).  
FT METAL 86 86 Zinc (By similarity).  
SQ SEQUENCE 156 AA; 17156 MW; B6498345A98BC214 CRC64;  
  
Query Match 89.7%; Score 26; DB 1; Length 156;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KAVFFA 6  
|||:  
Db 96 KAVFYA 101  
  
RESULT 51  
Q5WBB0\_BACSK  
ID Q5WBB0\_BACSK PRELIMINARY; PRT; 156 AA.  
AC Q5WBB0;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Guanine deaminase (EC 3.5.4.3).  
GN Name=gde; OrderedLocusNames=ABC3819;  
OS Bacillus clausii (strain KSM-K16).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=66692;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=KSM-K16;  
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,  
RA Kawai S., Ito S., Horikoshi K.;  
RT "The complete genome sequence of the alkaliphilic *Bacillus clausii*"

```

GN Name=fumX; OrderedLocusNames=AQ_1679;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AB000750; AAC07546.1; -; Genomic_DNA.
DR PIR; E70445; E70445.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR004647; TtDB_fumA_fumB.
DR Pfam; PF05683; Fumerase_C_1.
DR TIGRFAMs; TIGR00723; ttdB_fumA_fumB; 1.
KW Complete proteome.
SQ SEQUENCE 185 AA; 20441 MW; CBA8320A226E2558 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 185;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KAVFFA 6
|||:|
Db 117 KAVVFA 122

RESULT 54
CSRPI CHICK STANDARD; PRT; 191 AA.
AC P67966; P32965;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cysteine-rich protein 1 (CRP1) (CRP).
GN Name=CSRPI; Synonyms=CSRP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryonic fibroblast;
RX MEDLINE=94124603; PubMed=8294495; DOI=10.1083/jcb.124.1.117;
RA Crawford A.W., Pino J.D., Beckerle M.C.;
RT "Biochemical and molecular characterization of the chicken cysteine-
RT rich protein, a developmentally regulated LIM-domain protein that is
RT associated with the actin cytoskeleton.";
RL J. Cell Biol. 124:117-127(1994).
[2]
RN [2]
RP PROTEIN SEQUENCE OF 1-49; 69-83; 111-129 AND 177-188.
RX MEDLINE=93107157; PubMed=1469049; DOI=10.1083/jcb.119.6.1573;
RA Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
RT "Zyxin and cCRP: two interactive LIM domain proteins associated with
RT the cytoskeleton.";
RL J. Cell Biol. 119:1573-1587(1992).
[3]
RN [3]
RP ZINC-BINDING.
RX MEDLINE=93281587; PubMed=8506279;
RA Michelsen J.W., Schmeichel K.L., Beckerle M.C., Winge D.R.;
RT "The LIM motif defines a specific zinc-binding protein domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4404-4408(1993).
[4]
RN [4]
RP MUTAGENESIS.
RX MEDLINE=94209279; PubMed=8157637;
RA Michelsen J.W., Sewell A.K., Louis H.A., Olsen J.I., Davis D.R.,
RA Winge D.R., Beckerle M.C.;

```

---

```

RT "Mutational analysis of the metal sites in an LIM domain.";
RL J. Biol. Chem. 269:11108-11113(1994).
[5]
RN [5]
RP STRUCTURE BY NMR OF C-TERMINAL LIM DOMAIN.
RX MEDLINE=95393167; PubMed=7664053;
RA Perez-Alvarado G.C., Miles C., Michelsen J.W., Louis H.A., Winge D.R.;
RT "Structure of the carboxy-terminal LIM domain from the cysteine rich
RT protein CRP.";
RL Nat. Struct. Biol. 1:388-398(1994).
CC -1- FUNCTION: Heat stable protein, that interacts with zyxin. May be a
CC component of a signal transduction pathway that mediates adhesion-
CC stimulated changes in gene expression.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Associates with the actin cytoskeleton.
CC -1- TISSUE SPECIFICITY: Most prominent in tissues that are enriched in
CC smooth muscle cells, such as gizzard, stomach, and intestine.
CC Lower level in the heart, no expression in liver, skeletal muscle,
CC or brain.
CC -1- DEVELOPMENTAL STAGE: Expression levels increase dramatically
CC during smooth muscle maturation.
CC -1- DOMAIN: Glycine-rich repeats mediate the association with the
CC actin cytoskeleton (Probable).
CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X73831; CAAS2053.1; -; mRNA.
DR PIR; A49648; A49648.
DR PIR; B44358; B44358.
DR PIR; C44358; C44358.
DR PDB; 1B8T; NMR; A=1-191.
DR PDB; 1CTI; NMR; @=107-191.
DR InterPro; IPR001781; LIM_Zn_bd.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS50023; LIM_DOMAIN_2; 2.
KW 3D-structure; Direct protein sequencing; LIM domain; Metal-binding;
KW Nuclear protein; Repeat; Zinc.
FT INIT MET 0 0
FT DOMAIN 9 60 LIM zinc-binding 1.
FT DOMAIN 117 168 LIM zinc-binding 2.
FT MOTIF 63 68 Nuclear localization signal (Potential).
FT COMPBIAS 62 77 Gly-rich.
FT COMPBIAS 174 185 Gly-rich.
FT STRAND 7 8
FT TURN 10 12
FT STRAND 15 16
FT STRAND 22 24
FT TURN 25 26
FT STRAND 27 29
FT TURN 31 33
FT STRAND 35 35
FT TURN 37 39
FT STRAND 42 42
FT STRAND 48 51
FT TURN 52 53
FT STRAND 54 57
FT HELIX 58 65
FT STRAND 115 116
FT TURN 118 120
FT STRAND 123 124
FT STRAND 130 132
FT TURN 133 134
FT STRAND 135 137
FT TURN 139 141
FT STRAND 143 143
FT TURN 145 147

```

FT STRAND 150 150  
FT STRAND 156 159  
FT TURN 160 161  
FT STRAND 162 165  
FT HELIX 166 172  
FT TURN 173 173  
SQ SEQUENCE 191 AA; 20254 MW; BC1A45013C7BDA38 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 191;  
Best Local Similarity 83.3%; Pred. No. 5.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
DB 14 KAVYFA 19

## RESULT 55

CSRPI\_COTJA STANDARD; PRT; 191 AA.  
ID CSRPI\_COTJA  
AC P67967; P32965;  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Cysteine-rich protein 1 (CRPI) (CRP).  
GN Name=CSRPI; Synonyms=CSR;  
OS Coturnix coturnix japonica (Japanese quail).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Coturnix.  
OC NCBI\_TaxID=93934;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RP TISSUE=Embryonic fibroblast;  
RX MEDLINE=96081967; PubMed=7499425; DOI=10.1074/jbc.270.48.28945;  
RA Weiskirchen R., Pino J.D., Macalima T., Bieter K., Beckerle M.C.;  
RT "The cysteine-rich protein family of highly related LIM domain proteins.";  
RL J. Biol. Chem. 270:28946-28954 (1995).  
CC -!- FUNCTION: Heat stable protein, that interacts with zyxin. May be a component of a signal transduction pathway that mediates adhesion-stimulated changes in gene expression.  
CC -!- SUBUNIT: Monomer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Associates with the actin cytoskeleton (By similarity).  
CC -!- DOMAIN: Glycine-rich repeats mediate the association with the actin cytoskeleton (Probable).  
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; Z28333; CAA82187.1; -; mRNA.  
CC PIR; S38879; S38879.

CC InterPro; IPR001781; LIM\_Zn\_bd.  
CC Pfam; PF00412; LIM; 2.

CC ProDom; PD000094; LIM; 2.

CC SMART; SM00132; LIM; 2.

CC PROSITE; PS00478; LIM DOMAIN 1; 2.

CC PROSITE; PS50023; LIM DOMAIN 2; 2.

KW LIM domain; Metal-binding; Nuclear protein; Repeat; Zinc.

FT INIT\_MET 0 0 By similarity.

FT DOMAIN 9 60 LIM zinc-binding 1.

FT DOMAIN 117 168 LIM zinc-binding 2.

FT MOTIF 63 68 Nuclear localization signal (Potential).

FT COMPIAS 62 77 Gly-rich.

FT COMPIAS 174 185 Gly-rich.

SQ SEQUENCE 191 AA; 20254 MW; BC1A45013C7BDA38 CRC64;

Query Match

89.7%; Score 26; DB 1; Length 191;

Best Local Similarity 83.3%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
DB 14 KAVYFA 19

## RESULT 56

QRR88 DEIRA  
ID QRR88\_DEIRA PRELIMINARY; PRT; 229 AA.  
AC QRR88;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Molybdenum cofactor biosynthesis protein D/E.  
GN OrderedLocusNames=DR2607;  
OS Deinococcus radiodurans.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;  
OC Deinococcaceae; Deinococcus.  
OC NCBI\_TaxID=1299;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RP STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;  
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;  
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,  
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,  
RA Fraser C.M.;  
RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";  
RL Science 286:1571-1577 (1999).  
DR EMBL; AE002090; AAP12145.1; -; Genomic\_DNA.  
DR PIR; E75252; E75252.  
DR HSSP; P30748; INVI.  
DR TIGR; DR2607; -.  
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.  
DR GO; GO:0006790; P:sulfur metabolism; IEA.  
DR InterPro; IPR003448; Mo\_biosynth\_Moae.  
DR InterPro; IPR010034; Moad.  
DR InterPro; IPR003749; This.  
DR PANTHER; PTHR10311; Mo\_biosynth\_Moae; 1.  
DR Pfam; PF02391; Moae; 1.  
DR Pfam; PF02597; This; 1.  
DR TIGRFAMs; TIGR01682; moad; 1.  
KW Complete proteome.

SQ SEQUENCE 229 AA; 25311 MW; CD0F8B7060118B38 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 229;

Best Local Similarity 83.3%; Pred. No. 6.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
DB 4 RAVFFA 9

## RESULT 57

Q67QUL SYNTH  
ID Q67QUL SYNTH PRELIMINARY; PRT; 232 AA.  
AC Q67QUL;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=STH967;  
OS Symbiobacterium thermophilum.  
OC Bacteria; Actinobacteria; Symbiobacterium.  
OC NCBI\_TaxID=2734;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=IAM14863;  
RX PubMed=15383646; DOI=10.1093/nar/gkh830;  
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,  
RA Morimura K., Ikeda H., Hattori M., Beppu T.;  
RT "Genome sequence of *Symbiobacterium thermophilum*, an uncultivable  
bacterium that depends on microbial commensalism.";  
RL Nucleic Acids Res. 32:4937-4944 (2004).  
DR EMBL; AP006840; BAD39952.1; -; Genomic\_DNA.  
DR InterPro; IPR005834; Dehal like\_hydro.  
DR Pfam; PF00702; Hydrolase; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 232 AA; 24811 MW; D830F748F8D4D67E CRC64;

Query Match 89.7%; Score 26; DB 2; Length 232;  
Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 3 KALFFA 8  
|||||

RESULT 58  
Q527F8 MAGGR PRELIMINARY; PRT; 233 AA.  
AC Q527F8;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=MG05732.4;  
OS Magnaporthe grisea 70-15.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.  
OX NCBI\_TaxID=242507;  
[1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
RA Alt-zahra M., Allen T., Allen T., An P., Anderson M., Anderson S.,  
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,  
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,  
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,  
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,  
RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,  
RA Gnrke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,  
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
RA Horan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
RA Jaffe D., Jones C., Kamal M., Kanat A., Kanvaseis M., Karlsson E.,  
RA Kells C., Kieu A., Kisher P., Kodira C., Kulbokas E., Labutti K.,  
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
RA Lindblad-coh K., Liu X., Lokitysang T., Lokitysang Y., Lucien O.,  
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,  
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,  
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Menes L.,  
RA Mesirov J., Mihalov A., Minova T., Mikkelsen T., Mlenga V., Moru K.,  
RA Moses J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotoaho B.,  
RA O'Neill K., Oaman S., Parker S., Perrin D., Phunthang P., Piquani B.,  
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe P.,  
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,  
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
RA Stetson K., Stone K., Stone S., Stubbs M., Talamas J., Tchuinga P.,  
RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,  
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,

RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
RA Wangi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
RA Zimmer A., Zody M., Lander E.;  
RT "The genome sequence of *Magnaporthe grisea*.";  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Zhu H., Blackmon B.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL; AACU01000565; EAA54941.1; -; Genomic\_DNA.  
DR Hypothetical protein.  
KW Hypothetical protein.  
SQ SEQUENCE 233 AA; 25744 MW; C25C02486B86B34C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 233;  
Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 192 RAVFFA 197  
|||||

RESULT 59  
O30760 RHOSH PRELIMINARY; PRT; 233 AA.  
AC O30760;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Autoinducer synthesis regulator.  
GN Names=cerR;  
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1063;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX MEDLINE=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:7530-7537 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2.4.1T;  
RX PubMed=98053869; PubMed=9393720;  
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;  
RT "A quorum-sensing system in the free-living photosynthetic bacterium  
RT Rhodobacter sphaeroides.";  
RL J. Bacteriol. 179:753

```

DR PRINTS; PR00038; HTHLUXR.
DR ProDom; PD000307; HTH LUXR; 1.
DR SMART; SM00421; HTH LUXR; 1.
SQ SEQUENCE 233 AA; 26080 MW; 127DDE8E6DB8D48 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 233;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 92 RAVFFPA 97

RESULT 60
Q9N2Y5_CABEL PRELIMINARY; PRT; 235 AA.
AC Q9N2Y5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Y71G10AR.3.
GN ORFNames=Y71G10AR.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AC024856; AAF60868.4; -; Genomic DNA.
DR Ensembl; Y71G10AR.3; Caenorhabditis elegans.
DR WormBase; WBGene00022137; Y71G10AR.3.
DR WormPep; Y71G10AR.3; CE36900.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 235 AA; 27638 MW; 206BEC3C9570D089 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 235;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 47 KAVFFS 52

RESULT 61
Q5UEW2_9PROT PRELIMINARY; PRT; 266 AA.
AC Q5UEW2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative sulfatase (Fragment).
GN ORFNames=Red2C11_75;
OS uncultured alpha proteobacterium BBAC2C11.
OC Bacteria; Proteobacteria; Alphaproteobacteria; SAR116 cluster;
OC environmental samples.
OX NCBI_TaxID=295349;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sabehi G.; Beja O.;
RT "SAR116.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY744399; AAV31659.1; -; Genomic DNA.
DR GO; GO:0008484; F:sulfuric ester hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000917; Sulfatase.

DR PRINTS; PF00884; Sulfatase; 1.
FT NON TER 266
SQ SEQUENCE 266 AA; 29908 MW; 518924D95F9043A7 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 232 KALFFPA 237

RESULT 62
Q5GU79_XANOR PRELIMINARY; PRT; 268 AA.
AC Q5GU79;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=XO04490;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KACC10331 / KX085;
RX PubMed=15673718; DOI=10.1093/nar/gki206;
RA Lee B.-M.; Park Y.-J.; Park D.-S.; Kang H.-W.; Kim J.-G.; Song E.-S.;
RA Park I.-C.; Yoon U.-H.; Hahn J.-H.; Koo B.-S.; Lee G.-B.; Kim H.;
RA Park H.-S.; Yoon K.-O.; Kim J.-H.; Jung C.-H.; Koh N.-H.; Seo J.-S.;
RA Go S.-J.;
RT "The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
RT the bacterial blight pathogen of rice."
RL Nucleic Acids Res. 33:577-586(2005).
DR EMBL; AE013598; AAW77744.1; -; Genomic DNA.
DR InterPro; IPR005184; DUF306_MetA_HslJ.
DR Pfam; PF01724; META; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 268 AA; 28691 MW; 7757B113FF1816S9 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 2 RAVFFPA 7

RESULT 63
Q7QS35_GIALA PRELIMINARY; PRT; 276 AA.
AC Q7QS35;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_661_5852.6682.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G.; McArthur A.G.; Adam R.D.; Alek S.B.; Gillin F.D.;
RA Olsen G.J.; Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

```



```
Db          240 KAVYFA 245

RESULT 67
VGI2_ICHV1
ID VGI2_ICHV1 STANDARD; PRT; 299 AA.
AC Q00165;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical gene 12 zinc-binding protein.
GN Name=12;
OS Ictalurid herpesvirus 1 (ICHV-1) (Channel catfish herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Ictalurivirus.
OX NCBI_TaxID=10401;
RN [1]_TaxID=10401;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Auburn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RL "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M75136; AAA88193.1; -; Genomic DNA.
CC EMBL; M75136; AAA88115.1; -; Genomic DNA.
CC PIR; D36787; ZBBE13.
CC DR InterPro: IPR001841; Znf_RING.
CC DR SMART: SM00184; RING; 1_RING.
CC KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 299 AA; 33108 MW; B78295A90A647EB CRC64;

Query Match          89.7%; Score 26; DB 1; Length 299;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVYFA 6
:|||||
DB 39 KAVYFA 44

RESULT 68
Q8GX90_ARATH PRELIMINARY; PRT; 318 AA.
ID Q8GX90;
AC Q8GX90;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein At2g32880.
GN Name=At2g32880;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK118361; BAC42975.1; -; mRNA.
DR InterPro: IPR002083; MATH.
DR Pfam; PF00917; MATH; 2.
DR SMART; SM00061; MATH; 2.
DR PROSITE; PS01444; MATH; 2.
KW Hypothetical protein.
SQ SEQUENCE 318 AA; 36701 MW; 14B0D9BF9E0C7BD CRC64;
```

```
Query Match          89.7%; Score 26; DB 2; Length 318;
Best Local Similarity 83.3%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVYFA 6
:|||||
DB 137 KAVYFA 142

RESULT 69
Q6ASCI_DESPS PRELIMINARY; PRT; 321 AA.
ID Q6ASCI;
AC Q6ASCI;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Related to glycosyltransferase involved capsular polysaccharide
DE biosynthesis.
GN OrderedLocusNames=DP0013;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
RA Rabus R., Ruppel A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR522870; CAG34742.1; -; Genomic DNA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR InterPro: IPR001173; Glyco trans 2.
DR Pfam; PF00535; Glycos transf 2; 1.
DR Complete proteome; Transf erase.
SQ SEQUENCE 321 AA; 37861 MW; B3DEC2F91FB040BD CRC64;

Query Match          89.7%; Score 26; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVYFA 6
:|||||
DB 190 KAVYFA 195

RESULT 70
Q9EZ99_ZYMMO PRELIMINARY; PRT; 340 AA.
ID Q9EZ99; Q5NL26;
AC Q9EZ99; Q5NL26;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Tryptophanyl-tRNA synthase (EC 6.1.1.2).
GN Name=trpS; OrderedLocusNames=ZMO1640;
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ZM4;
RA Shin I.S., Kang H.S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / CP4;
RX PubMed=15592456; DOI=10.1038/nbt1045;
```



Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J., Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M., Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.-Y., Kang H.L., Lee S.-J., Lee K.J., Kang H.S.,  
 "The genome sequence of the ethanologenic bacterium *Zymomonas mobilis* ZM4".  
 Nat. Biotechnol. 23:63-68 (2005).  
 CC -1- SUBUNIT: ATP + L-tryptophan + tRNA (Trp) = AMP + diphosphate + L-tryptophyl-tRNA (Trp).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 DR EMBL: AF300471; AAG42413.1; -; Genomic DNA.  
 DR EMBL: AK008692; AAV90264.1; -; Genomic DNA.  
 DR HSSP: P00953; 1MAU.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0016874; F:ligase activity; IEA.  
 DR GO: GO:0004830; F:tryptophan-tRNA ligase activity; IEA.  
 DR GO: GO:0006412; P:protein biosynthesis; IEA.  
 DR GO: GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.  
 DR InterPro: IPR002305; tRNA-synt 1b.  
 DR InterPro: IPR001412; tRNA-synt 1.  
 DR InterPro: IPR002306; Trp tRNA-synt 1b.  
 DR Pfam: PF00579; tRNA-synt 1b; 1.  
 DR PRINTS: PR01039; TRNASINTHRP.  
 DR TIGRFAMs: TIGR00233; trps; 1.  
 DR PROSITE: PS00178; AA tRNA LIGASE I; 1.  
 KW ATP-binding; Aminoacyl-tRNA synthetase; Complete proteome; Ligase;  
 KW Nucleotide-binding; Protein biosynthesis.  
 SQ SEQUENCE 340 AA; 37475 MW; 383EACB86ABEB883 CRC64;  
 Query Match 89.7%; Score 26; DB 2; Length 340;  
 Best Local Similarity 83.3%; Pred. No. 8.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 :|||||  
 DB 81 RAVFFA 86  
 RESULT 71  
 CYSN\_METCA STANDARD; PRT; 348 AA.  
 ID CYSN\_METCA STANDARD; PRT; 348 AA.  
 AC Q609Q1;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Sulfate/thiosulfate import ATP-binding protein cysA (EC 3.6.3.25)  
 GN (Sulfate-transferring ATPase).  
 GN Name=cysA; OrderedLocustNames=MCA1181;  
 OS Methylococcus capsulatus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;  
 OC Methylococcaceae; Methylococcus.  
 NCBI\_TaxID=414;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RP STRAIN=Bath / NCIMB 11132;  
 RC PubMed=15383840; DOI=10.1371/journal.pbio.0020303;  
 RA Ward N.L., Larsen O., Sakwa J., Bruseck L., Khouri H.M., Durkin A.S., Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E., Mache B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E., Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R., Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J., Grindberg S.H., Holt I.E., Eidhammer I., Jonassen I., Vanaken S., Uterback T.R., Feldblyum T.V., Fraser C.M., Lilienhaug J.R., Eisen J.A.;  
 RT "Genomic insights into methanotrophy: the complete genome sequence of *Methylococcus capsulatus* (Bath).";  
 RL PLoS Biol. 2:1616-1628 (2004).  
 CC -1- FUNCTION: Part of the ABC transporter complex cysAWTP involved in sulfate/thiosulfate import. Responsible for energy coupling to the transport system (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + sulfate(Out) = ADP + phosphate + sulfate(In).  
 CC

Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J., Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M., Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.-Y., Kang H.L., Lee S.-J., Lee K.J., Kang H.S.,  
 "The genome sequence of the ethanologenic bacterium *Zymomonas mobilis* ZM4".  
 Nat. Biotechnol. 23:63-68 (2005).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA (Trp) = AMP + diphosphate + L-tryptophyl-tRNA (Trp).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 DR EMBL: AF300471; AAG42413.1; -; Genomic DNA.  
 DR EMBL: AK008692; AAV90264.1; -; Genomic DNA.  
 DR HSSP: P00953; 1MAU.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0016874; F:ligase activity; IEA.  
 DR GO: GO:0004830; F:tryptophan-tRNA ligase activity; IEA.  
 DR GO: GO:0006412; P:protein biosynthesis; IEA.  
 DR GO: GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.  
 DR InterPro: IPR002305; tRNA-synt 1b.  
 DR InterPro: IPR001412; tRNA-synt 1.  
 DR InterPro: IPR002306; Trp tRNA-synt 1b.  
 DR Pfam: PF00579; tRNA-synt 1b; 1.  
 DR PRINTS: PR01039; TRNASINTHRP.  
 DR TIGRFAMs: TIGR00233; trps; 1.  
 DR PROSITE: PS00178; AA tRNA LIGASE I; 1.  
 KW ATP-binding; Aminoacyl-tRNA synthetase; Complete proteome; Ligase;  
 KW Nucleotide-binding; Protein biosynthesis.  
 SQ SEQUENCE 340 AA; 37475 MW; 383EACB86ABEB883 CRC64;  
 Query Match 89.7%; Score 26; DB 2; Length 340;  
 Best Local Similarity 83.3%; Pred. No. 8.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 :|||||  
 DB 81 RAVFFA 86  
 RESULT 71  
 CYSN\_METCA STANDARD; PRT; 348 AA.  
 ID CYSN\_METCA STANDARD; PRT; 348 AA.  
 AC Q609Q1;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Sulfate/thiosulfate import ATP-binding protein cysA (EC 3.6.3.25)  
 GN (Sulfate-transferring ATPase).  
 GN Name=cysA; OrderedLocustNames=MCA1181;  
 OS Methylococcus capsulatus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;  
 OC Methylococcaceae; Methylococcus.  
 NCBI\_TaxID=414;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RP STRAIN=Bath / NCIMB 11132;  
 RC PubMed=15383840; DOI=10.1371/journal.pbio.0020303;  
 RA Ward N.L., Larsen O., Sakwa J., Bruseck L., Khouri H.M., Durkin A.S., Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E., Mache B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E., Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R., Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J., Grindberg S.H., Holt I.E., Eidhammer I., Jonassen I., Vanaken S., Uterback T.R., Feldblyum T.V., Fraser C.M., Lilienhaug J.R., Eisen J.A.;  
 RT "Genomic insights into methanotrophy: the complete genome sequence of *Methylococcus capsulatus* (Bath).";  
 RL PLoS Biol. 2:1616-1628 (2004).  
 CC -1- FUNCTION: Part of the ABC transporter complex cysAWTP involved in sulfate/thiosulfate import. Responsible for energy coupling to the transport system (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + sulfate(Out) = ADP + phosphate + sulfate(In).  
 CC

-1- SUBUNIT: The complex is composed of two ATP-binding proteins (cysA), two transmembrane proteins (cysE and cysW) and a solute-binding protein (cysP) (Probable).  
 -1- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).  
 -1- SIMILARITY: Belongs to the ABC transporter family. Sulfate/tungstate importer (TC 3.A.1.6) subfamily.  
 -1- SIMILARITY: Contains 1 ABC transporter domain.  
 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 EMBL: AF017282; AAU92759.1; -; Genomic DNA.  
 TIGR: MCA1181;  
 InterPro: IPR003593; AAA ATPase.  
 InterPro: IPR003439; ABC\_transp\_like.  
 InterPro: IPR005866; Sulph\_transpct.  
 Pfam: PF00005; ABC\_tran; 1.  
 ProDom: PD000006; ABC transporter; 1.  
 SMART: SM00382; AAA; 1.  
 TIGRFAMs: TIGR00968; 3a0106s01; 1.  
 PROSITE: PS00211; ABC\_TRANSPORTER\_1; 1.  
 PROSITE: PS00993; ABC\_TRANSPORTER\_2; 1.  
 KW ATP-binding; Complete proteome; Hydrolase; Inner membrane; Membrane;  
 KW Nucleotide-binding; Sulfate transport; Transport.  
 FT DOMAIN 3 237 ABC transporter.  
 FT NP\_BIND 35 42 ATP (By similarity).  
 SQ SEQUENCE 348 AA; 38768 MW; 05F3EF976A11885 CRC64;  
 Query Match 89.7%; Score 26; DB 1; Length 348;  
 Best Local Similarity 83.3%; Pred. No. 9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KAVFFA 6  
 :|||||  
 DB 271 KALFFA 276  
 RESULT 72  
 Q83WJ3\_SHIFL PRELIMINARY; PRT; 352 AA.  
 ID Q83WJ3\_SHIFL PRELIMINARY; PRT; 352 AA.  
 AC Q83WJ3; Q7UB67;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Putative resistance protein.  
 GN Name=ythN; OrderedLocustNames=S3802, SF3944;  
 OS Shigella flexneri.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Shigella.  
 NCBI\_TaxID=623;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=301 / Serotype 2a



RA Schwartz D.C., Blattner F.R.;  
 RT "Complete genome sequence and comparative genomics of Shigella  
 flexneri serotype 2a strain 2457T.";  
 RL Infect. Immun. 71:2775-2786(2003).  
 DR EMBL; AE005674; AAN45379.2; -; Genomic\_DNA.  
 DR EMBL; AB016990; AAP18819.1; -; Genomic\_DNA.  
 DR InterPro; IPR011701; MFS\_1.  
 DR Pfam; PF07690; MFS\_1; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 352 AA; 38913 MW; 2CEA79CE6252270B CRC64;

Query Match 89.7%; Score 26; DB 2; Length 352;  
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 :|||||  
 Db 332 KAVFFA 337

RESULT 73  
 Q72FT5 DESVH  
 ID Q72FT5\_DESVH PRELIMINARY; PRT; 352 AA.  
 AC Q72FT5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Membrane protein, putative.  
 GN OrderedLocNames=DVU0128;  
 OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;  
 OC Desulfovibrionaceae; Desulfovibrio.  
 OX NCBI\_TaxID=882;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15077118; DOI=10.1038/nbt959;  
 RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,  
 RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,  
 RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,  
 RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,  
 RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,  
 RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,  
 RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;  
 RT "The genome sequence of the anaerobic, sulfate-reducing bacterium  
 Desulfovibrio vulgaris Hildenborough.";  
 RL Nat. Biotechnol. 22:554-559(2004).  
 DR EMBL; AB017309; AAS94612.1; -; Genomic\_DNA.  
 DR TIGR; DVU0128; -;  
 DR InterPro; IPR002549; UPF0118.  
 DR Pfam; PF01594; UPF0118; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 352 AA; 36026 MW; 787856A87A10B493 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 352;  
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 :|||||  
 Db 23 KALFFA 28

RESULT 74  
 Q6MI90 DBEBA  
 ID Q6MI90\_DBEBA PRELIMINARY; PRT; 383 AA.  
 AC Q6MI90;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Putative polysaccharide deacetylase precursor (EC 3.5.1.-).  
 GN OrderedLocNames=Bd3279;  
 OS Bdellovibrio bacteriovorus.

OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;  
 OC Bdellovibrionaceae; Bdellovibrio.  
 OX NCBI\_TaxID=959;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN-HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;  
 RX PubMed=14752164; DOI=10.1126/science.1093027;  
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,  
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,  
 RA Sockett R.E., Schuster S.C.;  
 RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a  
 genomic perspective.";  
 RL Science 303:689-692(2004).  
 DR EMBL; BX842655; CAE78090.1; -; Genomic\_DNA.  
 DR GO; GO:0016810; F:hydrolase activity, acting on carbon-nitrog. . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR002509; Polysac-deacet.  
 DR Pfam; PF01522; Polysacc-deac\_1; 1.  
 KW Complete proteome; Hydrolase; Signal.  
 FT SIGNAL 11 Potential.  
 SQ SEQUENCE 383 AA; 42819 MW; 7A1A4EF645C565BC CRC64;

Query Match 89.7%; Score 26; DB 2; Length 383;  
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 :|||||  
 Db 197 KAMFFA 202

RESULT 75  
 Q4HML6 CAMLA  
 ID Q4HML6\_CAMLA PRELIMINARY; PRT; 390 AA.  
 AC Q4HML6;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Cyanate MFS transporter, putative.  
 GN ORFNames=CLA1389;  
 OS Campylobacter lari RM2100.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=306263;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=RM2100;  
 RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,  
 RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,  
 RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,  
 RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,  
 RA Nelson K.E.;  
 RT "Major structural and novel potential virulence mechanisms from the  
 genomes of multiple Campylobacter species.";  
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.

DR EMBL; AAFK01000001; EAL55536.1; -; Genomic\_DNA.  
 SQ SEQUENCE 390 AA; 42990 MW; 29E9CF925C147383 CRC64;  
 Query Match 89.7%; Score 26; DB 2; Length 390;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
 :|||||  
 Db 75 KALFFA 80

Search completed: December 29, 2005, 17:47:22  
 Job time : 90.1936 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds  
(without alignments)  
13.656 Million cell updates/sec

Title: US-10-009-122-7  
Perfect score: 29  
Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Published Applications AA New:  
1: /cgm2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgm2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgm2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgm2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cgm2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep:\*  
6: /cgm2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgm2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgm2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	660	7	US-11-186-284-125
2	29	100.0	708	6	US-10-821-234-917
3	25	86.2	210	6	US-10-467-657-6318
4	25	86.2	560	6	US-10-623-155-225
5	25	86.2	563	6	US-10-821-234-1067
6	24	82.8	19	6	US-10-923-605-5
7	24	82.8	19	6	US-10-934-818-5
8	24	82.8	40	7	US-11-016-706-36
9	24	82.8	40	7	US-11-098-674-12
10	24	82.8	42	6	US-10-923-605-1
11	24	82.8	42	6	US-10-934-818-1
12	24	82.8	42	7	US-11-016-706-37
13	24	82.8	43	6	US-10-934-818-6
14	24	82.8	43	6	US-10-250-581-1
15	24	82.8	43	6	US-10-250-581-1
16	24	82.8	288	6	US-10-467-657-1272
17	24	82.8	423	6	US-10-525-710-44
18	24	82.8	489	6	US-10-467-657-7846
19	24	82.8	770	6	US-10-982-545-15
20	24	82.8	770	6	US-10-789-273-38
21	23	79.3	9	6	US-10-982-891-44
22	23	79.3	114	6	US-10-467-657-5012
23	23	79.3	283	7	US-11-082-389-252
24	23	79.3	283	7	US-11-082-389-254
25	23	79.3	310	6	US-10-454-437-328
					Sequence 125, App
					Sequence 917, App
					Sequence 6318, Ap
					Sequence 225, App
					Sequence 1067, Ap
					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 36, Appl
					Sequence 12, Appl
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 37, Appl
					Sequence 6, Appli
					Sequence 1, Appli
					Sequence 1272, Ap
					Sequence 44, Appl
					Sequence 7846, Ap
					Sequence 15, Appl
					Sequence 38, Appl
					Sequence 48, Appl
					Sequence 5012, Ap
					Sequence 252, App
					Sequence 254, App
					Sequence 328, App

26	79.3	411	6	US-10-793-626-2080	Sequence 2080, Ap
27	79.3	557	6	US-10-467-657-5540	Sequence 5540, Ap
28	79.3	974	6	US-10-995-561-895	Sequence 895, App
29	79.3	997	6	US-10-995-561-896	Sequence 896, App
30	75.9	190	6	US-10-467-657-3436	Sequence 3436, Ap
31	75.9	211	6	US-10-821-234-1372	Sequence 1372, Ap
32	75.9	216	6	US-10-467-657-5976	Sequence 5976, Ap
33	75.9	269	7	US-11-179-977-11	Sequence 11, Appl
34	75.9	335	7	US-11-092-353-2	Sequence 2, Appli
35	75.9	341	7	US-10-131-826A-256	Sequence 256, App
36	75.9	341	7	US-11-099-691-6	Sequence 6, Appli
37	75.9	397	7	US-10-467-657-2684	Sequence 2684, Ap
38	75.9	478	7	US-11-092-353-4	Sequence 4, Appli
39	75.9	550	6	US-10-467-657-234	Sequence 234, App
40	75.9	550	6	US-10-467-657-924	Sequence 924, App
41	75.9	645	6	US-10-510-386-32	Sequence 32, Appl
42	75.9	989	6	US-10-821-234-975	Sequence 4, Appli
43	75.9	1070	7	US/11/062	Sequence 7, Appli
44	75.9	1095	7	US/11/062	Sequence 20, Appl
45	75.9	1169	7	US-11-077-550-20	Sequence 14, Appl
46	72.4	28	6	US-10-250-581-14	Sequence 17, Appl
47	72.4	28	6	US-10-250-581-17	Sequence 14, Appl
48	72.4	28	6	US-10-250-581-14	Sequence 17, Appl
49	72.4	28	6	US-10-250-581-17	Sequence 15, Appl
50	72.4	40	6	US-10-250-581-15	Sequence 18, Appl
51	72.4	40	6	US-10-250-581-18	Sequence 15, Appl
52	72.4	40	6	US-10-250-581-15	Sequence 18, Appl
53	72.4	42	6	US-10-250-581-16	Sequence 16, Appl
54	72.4	42	6	US-10-250-581-19	Sequence 19, Appl
55	72.4	42	6	US-10-250-581-16	Sequence 16, Appl
56	72.4	42	6	US-10-250-581-19	Sequence 19, Appl
57	72.4	42	6	US-10-467-657-4978	Sequence 4978, Ap
58	72.4	54	6	US-11-123-896-344	Sequence 344, App
59	72.4	71	7	US-11-123-896-335	Sequence 335, App
60	72.4	73	7	US-11-123-896-335	Sequence 335, App
61	72.4	105	6	US-10-467-657-9209	Sequence 9209, Ap
62	72.4	105	7	US-11-000-463-759	Sequence 759, App
63	72.4	115	6	US-10-793-626-1554	Sequence 1554, Ap
64	72.4	127	6	US-10-467-657-3152	Sequence 3152, Ap
65	72.4	134	6	US-10-467-657-6860	Sequence 6860, Ap
66	72.4	134	6	US-10-467-657-4112	Sequence 4112, Ap
67	72.4	153	6	US-10-467-657-9046	Sequence 9046, Ap
68	72.4	167	6	US-10-467-657-5306	Sequence 5306, Ap
69	72.4	189	6	US-10-467-657-6854	Sequence 6854, Ap
70	72.4	189	6	US-10-467-657-7856	Sequence 7856, Ap
71	72.4	191	6	US-10-467-657-818	Sequence 818, App
72	72.4	213	6	US-10-981-873-40	Sequence 40, Appl
73	72.4	227	6	US-10-980-388-86	Sequence 86, Appl
74	72.4	230	6	US-10-510-386-198	Sequence 198, App
75	72.4	244	6	US-10-454-437-238	Sequence 238, App
76	72.4	244	6	US-10-454-437-240	Sequence 240, App
77	72.4	264	6	US-10-873-528-70	Sequence 70, Appl
78	72.4	299	6	US-10-467-657-4424	Sequence 4424, Ap
79	72.4	355	6	US-10-467-657-7996	Sequence 7996, Ap
80	72.4	358	6	US-10-467-657-7030	Sequence 7030, Ap
81	72.4	366	6	US-10-467-657-7024	Sequence 7024, Ap
82	72.4	372	6	US-10-467-657-7964	Sequence 7964, Ap
83	72.4	372	6	US-10-467-657-590	Sequence 590, App
84	72.4	406	6	US-10-467-657-7420	Sequence 7420, Ap
85	72.4	418	6	US-10-467-657-5788	Sequence 5788, Ap
86	72.4	422	6	US-10-525-710-40	Sequence 40, Appl
87	72.4	429	6	US-10-858-730-79	Sequence 79, Appl
88	72.4	439	6	US-10-783-626-2408	Sequence 2408, Ap
89	72.4	481	6	US-10-995-561-959	Sequence 959, App
90	72.4	483	6	US-10-793-626-3132	Sequence 3132, Ap
91	72.4	495	6	US-10-613-744-5	Sequence 5, Appli
92	72.4	500	6	US-10-957-569-18	Sequence 18, Appl
93	72.4	550	7	US-11-055-822-866	Sequence 866, App
94	72.4	613	6	US-10-467-657-5796	Sequence 5796, Ap
95	72.4	616	6	US-10-613-744-4	Sequence 4, Appli
96	72.4	716	6	US-10-131-826A-512	Sequence 512, App
97	72.4	716	7	US-11-147-047-52	Sequence 52, Appl
98	72.4	801	6	US-10-467-657-6470	Sequence 6470, Ap

99	21	72.4	897	6	US-10-821-234-1523	Sequence 1523, Ap	172	20	69.0	338	6	US-10-467-657-6798	Sequence 6798, Ap
100	21	72.4	898	7	US-11-099-691-7	Sequence 7, Appli	173	20	69.0	347	6	US-10-467-657-2014	Sequence 2014, Ap
101	21	72.4	1141	6	US-10-995-561-1009	Sequence 1009, Ap	174	20	69.0	355	6	US-10-454-437-102	Sequence 102, Ap
102	21	72.4	1141	6	US-10-995-561-1010	Sequence 1010, Ap	175	20	69.0	355	7	US-11-068-686-4	Sequence 4, Appli
103	20	69.0	5	7	US-11-098-674-1	Sequence 1, Appli	176	20	69.0	356	7	US-11-075-185-16	Sequence 16, Appli
104	20	69.0	9	7	US-11-032-498-28	Sequence 28, Appli	177	20	69.0	357	6	US-10-467-657-2500	Sequence 2500, Ap
105	20	69.0	28	6	US-10-250-581-2	Sequence 2, Appli	178	20	69.0	357	6	US-10-467-657-6648	Sequence 6648, Ap
106	20	69.0	28	6	US-10-250-581-2	Sequence 2, Appli	179	20	69.0	363	6	US-10-995-561-602	Sequence 602, Ap
107	20	69.0	38	6	US-10-467-657-2058	Sequence 2058, Ap	180	20	69.0	365	6	US-10-624-932-24	Sequence 24, Appli
108	20	69.0	40	6	US-10-250-581-3	Sequence 3, Appli	181	20	69.0	376	6	US-10-995-561-844	Sequence 844, Ap
109	20	69.0	40	6	US-10-250-581-3	Sequence 3, Appli	182	20	69.0	376	6	US-10-995-561-848	Sequence 848, Ap
110	20	69.0	42	6	US-10-250-581-4	Sequence 4, Appli	183	20	69.0	380	6	US-10-624-932-20	Sequence 20, Appli
111	20	69.0	42	6	US-10-250-581-4	Sequence 4, Appli	184	20	69.0	380	6	US-10-624-932-22	Sequence 22, Appli
112	20	69.0	47	6	US-10-467-657-5436	Sequence 5436, Ap	185	20	69.0	380	6	US-10-995-561-846	Sequence 846, Ap
113	20	69.0	48	6	US-10-467-657-4322	Sequence 4322, Ap	186	20	69.0	380	7	US-11-108-528-28	Sequence 28, Appli
114	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	187	20	69.0	387	6	US-10-467-657-5522	Sequence 5522, Ap
115	20	69.0	75	6	US-10-467-657-1496	Sequence 1496, Ap	188	20	69.0	390	6	US-10-995-561-847	Sequence 847, Ap
116	20	69.0	92	6	US-10-467-657-2378	Sequence 2378, Ap	189	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
117	20	69.0	95	6	US-10-467-657-8785	Sequence 8785, Ap	190	20	69.0	396	6	US-10-510-386-238	Sequence 238, Ap
118	20	69.0	100	7	US-11-123-896-137	Sequence 137, App	191	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appli
119	20	69.0	104	6	US-10-821-234-1227	Sequence 1227, App	192	20	69.0	400	6	US-10-793-626-1056	Sequence 1056, Ap
120	20	69.0	107	6	US-10-793-626-1586	Sequence 1586, Ap	193	20	69.0	401	7	US-11-055-822-336	Sequence 336, Ap
121	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	194	20	69.0	402	6	US-10-467-657-9070	Sequence 9070, Ap
122	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appli	195	20	69.0	402	7	US-11-000-463-449	Sequence 449, App
123	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appli	196	20	69.0	413	6	US-10-467-657-11858	Sequence 11858, Ap
124	20	69.0	131	6	US-10-467-657-9073	Sequence 9073, Ap	197	20	69.0	426	6	US-10-467-657-2120	Sequence 2120, Ap
125	20	69.0	131	6	US-10-467-657-9195	Sequence 9195, Ap	198	20	69.0	428	7	US-11-000-463-448	Sequence 448, Ap
126	20	69.0	137	6	US-10-793-626-530	Sequence 530, App	199	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, Ap
127	20	69.0	137	6	US-10-467-657-6584	Sequence 6584, App	200	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
128	20	69.0	135	6	US-10-467-657-2420	Sequence 2420, Ap	201	20	69.0	450	6	US-10-467-657-7094	Sequence 7094, Ap
129	20	69.0	156	6	US-10-793-626-2452	Sequence 2452, Ap	202	20	69.0	450	6	US-10-467-657-8028	Sequence 8028, Ap
130	20	69.0	168	7	US-11-000-463-824	Sequence 824, App	203	20	69.0	451	6	US-10-467-657-7104	Sequence 7104, Ap
131	20	69.0	175	6	US-10-467-657-7504	Sequence 7504, Ap	204	20	69.0	453	7	US-11-082-389-198	Sequence 198, App
132	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	205	20	69.0	456	6	US-10-467-657-4150	Sequence 4150, Ap
133	20	69.0	196	6	US-10-793-626-630	Sequence 630, App	206	20	69.0	472	6	US-10-467-657-2268	Sequence 2268, Ap
134	20	69.0	196	6	US-10-967-527A-26	Sequence 26, Appli	207	20	69.0	485	6	US-10-821-234-934	Sequence 934, App
135	20	69.0	201	6	US-10-467-657-458	Sequence 458, App	208	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appli
136	20	69.0	202	7	US-11-082-389-364	Sequence 364, App	209	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
137	20	69.0	207	6	US-10-467-657-1816	Sequence 1816, Ap	210	20	69.0	494	6	US-10-467-657-4376	Sequence 4376, Ap
138	20	69.0	211	6	US-10-467-657-6932	Sequence 6932, Ap	211	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appli
139	20	69.0	215	6	US-10-131-826A-4	Sequence 4, Appli	212	20	69.0	507	6	US-10-467-657-1612	Sequence 1612, Ap
140	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	213	20	69.0	513	6	US-10-467-657-5464	Sequence 5464, Ap
141	20	69.0	227	6	US-10-467-657-1514	Sequence 1514, Ap	214	20	69.0	514	7	US-11-186-284-228	Sequence 228, App
142	20	69.0	228	6	US-10-793-626-1862	Sequence 1862, Ap	215	20	69.0	523	6	US-10-131-826A-246	Sequence 246, App
143	20	69.0	228	6	US-10-467-657-568	Sequence 568, App	216	20	69.0	524	6	US-10-689-742-13	Sequence 13, Appli
144	20	69.0	228	6	US-10-467-657-4838	Sequence 4838, Ap	217	20	69.0	525	7	US-11-082-389-350	Sequence 350, App
145	20	69.0	229	6	US-10-131-826A-410	Sequence 410, App	218	20	69.0	528	6	US-10-793-626-1930	Sequence 1930, Ap
146	20	69.0	233	6	US-10-821-234-1322	Sequence 1322, Ap	219	20	69.0	540	6	US-10-858-730-293	Sequence 293, App
147	20	69.0	239	6	US-10-980-388-78	Sequence 78, Appli	220	20	69.0	554	6	US-11-000-463-240	Sequence 240, App
148	20	69.0	240	6	US-10-467-657-6276	Sequence 6276, Ap	221	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
149	20	69.0	242	7	US-10-821-234-1073	Sequence 1073, Ap	222	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
150	20	69.0	254	6	US-11-103-957-27	Sequence 27, App	223	20	69.0	560	7	US-11-080-991-62	Sequence 62, Appli
151	20	69.0	255	7	US-11-185-111-36	Sequence 36, Appli	224	20	69.0	572	6	US-10-467-657-1022	Sequence 1022, Ap
152	20	69.0	257	7	US-11-102-240-94	Sequence 94, Appli	225	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
153	20	69.0	269	6	US-10-467-657-330	Sequence 330, App	226	20	69.0	582	7	US-11-090-439-58	Sequence 58, Appli
154	20	69.0	272	6	US-10-467-657-2520	Sequence 2520, Ap	227	20	69.0	592	6	US-10-467-962B-95	Sequence 95, Appli
155	20	69.0	288	6	US-10-873-528-18	Sequence 18, Appli	228	20	69.0	592	6	US-10-524-647-112	Sequence 112, App
156	20	69.0	291	6	US-10-432-483-12	Sequence 12, Appli	229	20	69.0	599	6	US-10-467-657-3972	Sequence 3972, Ap
157	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appli	230	20	69.0	614	7	US-11-126-841A-2	Sequence 2, Appli
158	20	69.0	292	7	US-11-102-883-22	Sequence 22, Appli	231	20	69.0	614	7	US-11-126-841A-13	Sequence 13, Appli
159	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	232	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
160	20	69.0	311	6	US-10-793-626-2450	Sequence 2450, Ap	233	20	69.0	677	6	US-10-131-826A-230	Sequence 230, App
161	20	69.0	316	7	US-10-467-657-2334	Sequence 2334, Ap	234	20	69.0	693	6	US-10-467-657-6176	Sequence 6176, Ap
162	20	69.0	316	7	US-11-082-389-62	Sequence 62, Appli	235	20	69.0	721	6	US-10-467-962B-49	Sequence 49, Appli
163	20	69.0	318	6	US-10-131-826A-374	Sequence 374, App	236	20	69.0	724	7	US-11-184-380-4	Sequence 4, Appli
164	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	237	20	69.0	741	6	US-10-467-657-6266	Sequence 6266, Ap
165	20	69.0	324	6	US-10-467-657-7692	Sequence 7692, Ap	238	20	69.0	835	7	US-11-186-283-2	Sequence 2, Appli
166	20	69.0	334	6	US-10-467-657-8440	Sequence 8440, Ap	239	20	69.0	835	7	US-11-186-283-8	Sequence 8, Appli
167	20	69.0	325	6	US-10-454-437-142	Sequence 142, App	240	20	69.0	852	6	US-10-467-657-5004	Sequence 5004, Ap
168	20	69.0	330	6	US-10-510-386-82	Sequence 82, Appli	241	20	69.0	858	6	US-10-613-744-6	Sequence 6, Appli
169	20	69.0	333	7	US-11-082-389-202	Sequence 202, App	242	20	69.0	907	7	US-11-103-957-82	Sequence 82, Appli
170	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap	243	20	69.0	916	6	US-10-467-657-4242	Sequence 4242, Ap
171	20	69.0	338	6	US-10-467-657-136	Sequence 136, App	244	20	69.0	964	7	US-11-103-957-13	Sequence 13, Appli

245 20 69.0 1027 6 US-10-793-626-3106  
 246 20 69.0 1076 6 US-10-467-657-3708  
 247 20 69.0 1144 6 US-10-467-962B-89  
 248 20 69.0 1259 6 US-10-467-657-5510  
 249 20 69.0 1274 6 US-10-454-437-360  
 250 20 69.0 1362 7 US-11-043-633-33  
 251 20 69.0 1363 7 US-11-043-633-32  
 252 20 69.0 1368 7 US-11-043-633-34  
 253 20 69.0 1531 7 US-11-103-957-15  
 254 20 69.0 2004 6 US-10-467-657-84  
 255 20 69.0 2004 6 US-10-467-657-6322  
 256 20 69.0 3433 6 US-10-714-781A-67  
 257 20 69.0 3623 6 US-10-995-561-593  
 258 20 69.0 4128 6 US-10-770-726-77  
 259 19 65.5 28 6 US-10-250-581-5  
 260 19 65.5 28 6 US-10-250-581-8  
 261 19 65.5 28 6 US-10-250-581-11  
 262 19 65.5 28 6 US-10-250-581-5  
 263 19 65.5 28 6 US-10-250-581-8  
 264 19 65.5 28 6 US-10-250-581-11  
 265 19 65.5 39 6 US-10-467-657-2174  
 266 19 65.5 40 6 US-10-250-581-6  
 267 19 65.5 40 6 US-10-250-581-9  
 268 19 65.5 40 6 US-10-250-581-12  
 269 19 65.5 40 6 US-10-250-581-6  
 270 19 65.5 40 6 US-10-250-581-9  
 271 19 65.5 42 6 US-10-250-581-12  
 272 19 65.5 42 6 US-10-250-581-7  
 273 19 65.5 42 6 US-10-250-581-10  
 274 19 65.5 42 6 US-10-250-581-13  
 275 19 65.5 42 6 US-10-250-581-7  
 276 19 65.5 42 6 US-10-250-581-10  
 277 19 65.5 42 6 US-10-250-581-13  
 278 19 65.5 50 6 US-10-467-657-7892  
 279 19 65.5 52 6 US-10-467-657-3656  
 280 19 65.5 83 6 US-10-467-657-5366  
 281 19 65.5 95 7 US-11-055-822-238  
 282 19 65.5 95 7 US-11-055-822-632  
 283 19 65.5 95 7 US-11-055-822-1102  
 284 19 65.5 96 6 US-10-467-657-3380  
 285 19 65.5 97 6 US-10-650-326B-2  
 286 19 65.5 97 6 US-10-995-561-900  
 287 19 65.5 98 6 US-10-467-657-3490  
 288 19 65.5 102 6 US-10-667-295-43  
 289 19 65.5 102 6 US-10-793-626-2592  
 290 19 65.5 107 6 US-10-467-657-1018  
 291 19 65.5 113 7 US-11-073-605-10  
 292 19 65.5 124 6 US-10-467-657-8548  
 293 19 65.5 128 6 US-10-793-626-1208  
 294 19 65.5 138 6 US-10-467-657-2052  
 295 19 65.5 141 6 US-10-667-295-42  
 296 19 65.5 141 6 US-10-467-657-5544  
 297 19 65.5 150 7 US-11-109-156-32  
 298 19 65.5 153 6 US-10-467-657-7674  
 299 19 65.5 153 6 US-10-467-657-8432  
 300 19 65.5 157 7 US-11-116-144-167

ALIGNMENTS

RESULT 1  
 US-11-186-284-125  
 ; Sequence 125, Application US/11186284  
 ; Publication No. US20050266493A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; APPLICANT: Berger, Allison  
 ; APPLICANT: Guillemette, Tracy L.  
 ; APPLICANT: Kamatkar, Shubhangi  
 ; APPLICANT: Schlegel, Robert  
 ; APPLICANT: Monahan, John E.  
 ; APPLICANT: Thibodeau, Stephen N.

Sequence 3106, Ap  
 Sequence 5708, Ap  
 Sequence 89, Appl  
 Sequence 5510, Ap  
 Sequence 360, Appl  
 Sequence 33, Appl  
 Sequence 32, Appl  
 Sequence 34, Appl  
 Sequence 15, Appl  
 Sequence 84, Appl  
 Sequence 6322, Ap  
 Sequence 67, Appl  
 Sequence 593, Appl  
 Sequence 77, Appl  
 Sequence 5, Appl  
 Sequence 8, Appl  
 Sequence 11, Appl  
 Sequence 5, Appl  
 Sequence 8, Appl  
 Sequence 11, Appl  
 Sequence 12, Appl  
 Sequence 10, Appl  
 Sequence 13, Appl  
 Sequence 7, Appl  
 Sequence 10, Appl  
 Sequence 13, Appl  
 Sequence 7892, Ap  
 Sequence 3656, Ap  
 Sequence 238, App  
 Sequence 632, App  
 Sequence 1102, Ap  
 Sequence 3380, Ap  
 Sequence 2, Appl  
 Sequence 900, App  
 Sequence 3490, Ap  
 Sequence 43, Appl  
 Sequence 2592, Ap  
 Sequence 1018, Ap  
 Sequence 10, Appl  
 Sequence 8548, Ap  
 Sequence 1208, Ap  
 Sequence 2052, Ap  
 Sequence 42, Appl  
 Sequence 5544, Ap  
 Sequence 32, Appl  
 Sequence 7674, Ap  
 Sequence 8432, Ap  
 Sequence 167, App

APPLICANT: BURGART, Lawrence J.  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; TITLE OF INVENTION: THERAPY OF COLON CANCER  
 ; FILE REFERENCE: MPM01-029P2RNM  
 ; CURRENT APPLICATION NUMBER: US/11/186,284  
 ; CURRENT FILING DATE: 2005-07-21  
 ; PRIOR APPLICATION NUMBER: US/10/301,822  
 ; PRIOR FILING DATE: 2002-11-21  
 ; PRIOR APPLICATION NUMBER: US 60/339,971  
 ; PRIOR FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: US 60/361,978  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: US 60/381,988  
 ; PRIOR FILING DATE: 2002-05-20  
 ; NUMBER OF SEQ ID NOS: 228  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 125  
 ; LENGTH: 660  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-11-186-284-125

Query Match 100.0%; Score 29; DB 7; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||  
 Db 531 KAVFFA 536

RESULT 2  
 US-10-821-234-917  
 ; Sequence 917, Application US/10821234  
 ; Publication No. US20050255114A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Labat, Ivan  
 ; APPLICANT: Stache-Crain, Birgit  
 ; APPLICANT: Andarmani, Susan  
 ; APPLICANT: Tang, Y. Tom  
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 ; FILE REFERENCE: 821A  
 ; CURRENT APPLICATION NUMBER: US/10/821,234  
 ; CURRENT FILING DATE: 2004-04-07  
 ; PRIOR APPLICATION NUMBER: US 60/462,047  
 ; PRIOR FILING DATE: 2003-04-07  
 ; NUMBER OF SEQ ID NOS: 1704  
 ; SOFTWARE: pt\_seq\_genes Version 1.0  
 ; SEQ ID NO 917  
 ; LENGTH: 708  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-821-234-917

Query Match 100.0%; Score 29; DB 6; Length 708;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
 |||||  
 Db 579 KAVFFA 584

RESULT 3  
 US-10-467-657-6318  
 ; Sequence 6318, Application US/10467657  
 ; Publication No. US20050260581A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SpA  
 ; APPLICANT: FONTANA Maria Rita  
 ; APPLICANT: PIZZA Mariagrazia  
 ; APPLICANT: MASIGNANI Vega

```
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6318
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6318

Query Match      86.2%; Score 25; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      116 KAVFF 120

RESULT 4
US-10-623-155-225
; Sequence 225, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-225

Query Match      86.2%; Score 25; DB 6; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      537 KAVFF 541

RESULT 5
US-10-821-234-1067
; Sequence 1067, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt_SEQ_genes Version 1.0
; SEQ ID NO 1067

; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence

; LENGTH: 563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1067

Query Match      86.2%; Score 25; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      540 KAVFF 544

RESULT 6
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_RES
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match      82.8%; Score 24; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 6.3;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      4 KLVFFA 9

RESULT 7
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match      82.8%; Score 24; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 6.3;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      4 KLVFFA 9

RESULT 8
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match      82.8%; Score 24; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 9
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elmova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match      82.8%; Score 24; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 10
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match      82.8%; Score 24; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 11
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1
```

```
Query Match      82.8%; Score 24; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 12
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match      82.8%; Score 24; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 13
US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match      82.8%; Score 24; DB 6; Length 43;

Query Match      82.8%; Score 24; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 14
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 15
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 16
US-10-467-657-1272
; Sequence 1272, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 1272  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1272

Query Match 82.8%; Score 24; DB 6; Length 288;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6  
Db 44 AVFFA 48

## RESULT 17

US-10-525-710-44  
; Sequence 44, Application US/10525710  
; Publication No. US20050260721A1  
; GENERAL INFORMATION:  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Kolprogge, Corinna  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Hafner, Stefan  
; TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing  
; TITLE REFERENCE: 13111-00006-US  
; CURRENT APPLICATION NUMBER: US/10/525,710  
; CURRENT FILING DATE: 2005-02-24  
; PRIOR APPLICATION NUMBER: PCT/EP 2003/009453  
; PRIOR FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: DE 102 39 082.7  
; PRIOR FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 44  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
US-10-525-710-44

Query Match 82.8%; Score 24; DB 6; Length 423;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
Db 146 KAIFF 150

## RESULT 18

US-10-467-657-7846  
; Sequence 7846, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 7846  
; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-7846

Query Match 82.8%; Score 24; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6  
Db 28 AVFFA 32

## RESULT 19

US-10-982-545-15  
; Sequence 15, Application US/10982545  
; Publication No. US20050244890A1  
; GENERAL INFORMATION:  
; APPLICANT: Davies, Huw Alun  
; APPLICANT: McGuire, James  
; APPLICANT: Simonsen, Anja Hviid  
; APPLICANT: Blennow, Kaj  
; APPLICANT: Podust, Vladimir  
; APPLICANT: CIPHERGEN Biosystems, Inc.  
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease  
; FILE REFERENCE: 016866-011550US  
; CURRENT APPLICATION NUMBER: US/10/982,545  
; CURRENT FILING DATE: 2004-11-06  
; PRIOR APPLICATION NUMBER: US 60/518,360  
; PRIOR FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US 60/526,753  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: US 60/546,423  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/547,250  
; PRIOR FILING DATE: 2004-02-23  
; PRIOR APPLICATION NUMBER: US 60/558,896  
; PRIOR FILING DATE: 2004-04-02  
; PRIOR APPLICATION NUMBER: US 60/572,617  
; PRIOR FILING DATE: 2004-05-18  
; PRIOR APPLICATION NUMBER: US 60/586,503  
; PRIOR FILING DATE: 2004-07-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease  
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),  
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,  
; OTHER INFORMATION: Alzheimer's disease amyloid protein  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)..(17)  
; OTHER INFORMATION: signal peptide  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(40)  
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-N1), A-beta 1-40  
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (18)..(687)  
; OTHER INFORMATION: soluble APP-alpha  
; FEATURE:  
; NAME/KEY: PEPTIDE



```

; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; OTHER INFORMATION: C31
US-10-982-545-15

Query Match      82.8%; Score 24; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      687 KLVFFA 692

RESULT 20
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurliq
; APPLICANT: Saidanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06

```

```

; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-38

Query Match      82.8%; Score 24; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      687 KLVFFA 692

RESULT 21
US-10-982-891-44
; Sequence 44, Application US/10982891
; Publication No. US20050244844A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, ALPHONSE
; APPLICANT: CAYLA, XAVIER
; APPLICANT: REBOLLO, ANGELITA
; TITLE OF INVENTION: METHODS OF SCREENING OF PPI-INTERACTING POLYPEPTIDES OR PROTEINS
; TITLE OF INVENTION: PEPTIDES INHIBITING PPIc BINDING TO Bcl-2 PROTEINS, BCL-XL AND
; TITLE OF INVENTION: BCL-W, AND USES THEREOF
; FILE REFERENCE: 260990USOCONT
; CURRENT APPLICATION NUMBER: US/10/982,891
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: PCT/EP03/05453
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: EP 02291170
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: MAMMALIAN
US-10-982-891-44

Query Match      79.3%; Score 23; DB 6; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.4e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      3 KAVMFA 8

RESULT 22
US-10-467-657-5012
; Sequence 5012, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5012
; LENGTH: 114
; TYPE: PRT

```

```

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5012

Query Match          79.3%; Score 23; DB 6; Length 114;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 34 RAVFFS 39

RESULT 23
US-11-082-389-252
; Sequence 252, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 252
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-254

Query Match          79.3%; Score 23; DB 7; Length 283;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6
Db 264 AIFFA 268

RESULT 25
US-10-454-437-328
; Sequence 328, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5012

Query Match          79.3%; Score 23; DB 6; Length 114;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 34 RAVFFS 39

RESULT 24
US-11-082-389-254
; Sequence 254, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig

```

```
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 328
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-328

Query Match          79.3%; Score 23; DB 6; Length 310;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 AVFFA 6
      |:|||
Db      63 AIFFA 67

RESULT 26
US-10-793-626-2080
; Sequence 2080, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2080
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2080

Query Match          79.3%; Score 23; DB 6; Length 411;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 AVFFA 6
      |:|||
Db      304 AIFFA 308

RESULT 27
US-10-467-657-5540
; Sequence 5540, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
```

```
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5540
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5540

Query Match          79.3%; Score 23; DB 6; Length 557;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
Db      166 KAVMFA 171

RESULT 28
US-10-995-561-895
; Sequence 895, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 895
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-895

Query Match          79.3%; Score 23; DB 6; Length 974;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
Db      497 KAVLFA 502

RESULT 29
US-10-995-561-896
; Sequence 896, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-896

Query Match          79.3%; Score 23; DB 6; Length 997;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVEFA 6
      |||||
Db      520 KAVLFA 525
```

```

RESULT 30
US-10-467-657-3436
; Sequence 3436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3436
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3436

```

```

Query Match      75.9%; Score 22; DB 6; Length 190;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 KAVPPA 6
Db      46 KTVFYA 51

```

```

RESULT 31
US-10-821-234-1372
; Sequence 1372, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1372

```

```

Query Match      75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 KAVPPA 6
Db      33 KTVYFA 38

```

```

RESULT 32
US-10-467-657-5976
; Sequence 5976, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita

```

```

; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5976
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5976

```

```

Query Match      75.9%; Score 22; DB 6; Length 216;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVPPF 5
Db      8 KSVFF 12

```

```

RESULT 33
US-11-179-977-11
; Sequence 11, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GC511-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Bacillus
US-11-179-977-11

```

```

Query Match      75.9%; Score 22; DB 7; Length 269;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 KAVPPA 6
Db      193 KAAFFS 198

```

```

RESULT 34
US-11-092-353-2
; Sequence 2, Application US/11092353
; Publication No. US20050272653A1
; GENERAL INFORMATION:
; APPLICANT: Knopf, John
; APPLICANT: Seehra, Jasbir
; TITLE OF INVENTION: BMP-3 PROPEPTIDES AND RELATED METHODS
; FILE REFERENCE: PHPP-P01-002
; CURRENT APPLICATION NUMBER: US/11/092,353
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: US 60/557,100
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSBQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-092-353-2

```

Query Match 75.9%; Score 22; DB 7; Length 335;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
DB 79 KAVFF 83

RESULT 35  
US-10-131-826A-256  
; Sequence 256, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tunas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 256  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-256

Query Match 75.9%; Score 22; DB 6; Length 341;  
Best Local Similarity 80.0%; Pred. No. 3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
DB 102 KALFF 106

RESULT 36  
US-11-099-691-6  
; Sequence 6, Application US/11099691  
; Publication No. US20050260644A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE PHARMACEUTICALS, INC.  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: LAL, Preeti  
; APPLICANT: YUE, Henry  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: YANG, Junming  
; TITLE OF INVENTION: CELL SIGNALING PROTEINS  
; FILE REFERENCE: PF-0521 PCT  
; CURRENT APPLICATION NUMBER: US/11/099,691  
; CURRENT FILING DATE: 2005-04-06  
; PRIOR APPLICATION NUMBER: US/09/700,444  
; PRIOR FILING DATE: 2002-08-26  
; PRIOR APPLICATION NUMBER: 60/085,343  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/098,010  
; PRIOR FILING DATE: 1998-08-26  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PERL Program  
; SEQ ID NO 6  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc-feature  
; FEATURE:  
; OTHER INFORMATION: Incyte Clone 2472655  
US-11-099-691-6

Query Match 75.9%; Score 22; DB 7; Length 341;  
Best Local Similarity 80.0%; Pred. No. 3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
DB 102 KALFF 106

RESULT 37  
US-10-467-657-2684  
; Sequence 2684, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2684  
; LENGTH: 397  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2684

Query Match 75.9%; Score 22; DB 6; Length 397;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVPPA 6  
 |||||  
 Db 309 KADFFA 314

## RESULT 38

US-11-092-353-4  
 ; Sequence 4, Application US/11092353  
 ; Publication No. US20050272653A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knopf, John  
 ; APPLICANT: Sehbra, Jasbir  
 ; TITLE OF INVENTION: BMP-3 PROPEPTIDES AND RELATED METHODS  
 ; FILE REFERENCE: PHPP-P01-002  
 ; CURRENT APPLICATION NUMBER: US/11/092,353  
 ; CURRENT FILING DATE: 2005-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/557,100  
 ; PRIOR FILING DATE: 2004-03-26  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 478  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-092-353-4

Query Match 75.9%; Score 22; DB 7; Length 478;  
 Best Local Similarity 80.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPP 5  
 |||||  
 Db 112 KAVFF 116

## RESULT 39

US-10-467-657-234  
 ; Sequence 234, Application US/10467657  
 ; Publication No. US20050260581A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SPA  
 ; APPLICANT: FONTANA Maria Rita  
 ; APPLICANT: PIZZA Mariagrazia  
 ; APPLICANT: MASIGNANI Vega  
 ; APPLICANT: MONACI Elisabetta  
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/467,657  
 ; CURRENT FILING DATE: 2003-08-11  
 ; PRIOR APPLICATION NUMBER: GB-0103424.8  
 ; PRIOR FILING DATE: 2001-02-12  
 ; NUMBER OF SEQ ID NOS: 9218  
 ; SOFTWARE: SeqWin99, version 1.04  
 ; SEQ ID NO 234  
 ; LENGTH: 550  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria gonorrhoeae  
 US-10-467-657-234

Query Match 75.9%; Score 22; DB 6; Length 550;  
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPP 5  
 |||||  
 Db 176 RAVPP 180

## RESULT 40

US-10-467-657-924  
 ; Sequence 924, Application US/10467657  
 ; Publication No. US20050260581A1  
 ; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA  
 ; APPLICANT: FONTANA Maria Rita  
 ; APPLICANT: PIZZA Mariagrazia  
 ; APPLICANT: MASIGNANI Vega  
 ; APPLICANT: MONACI Elisabetta  
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/467,657  
 ; CURRENT FILING DATE: 2003-08-11  
 ; PRIOR APPLICATION NUMBER: GB-0103424.8  
 ; PRIOR FILING DATE: 2001-02-12  
 ; NUMBER OF SEQ ID NOS: 9218  
 ; SOFTWARE: SeqWin99, version 1.04  
 ; SEQ ID NO 924  
 ; LENGTH: 550  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria gonorrhoeae  
 US-10-467-657-924

Query Match 75.9%; Score 22; DB 6; Length 550;  
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPP 5  
 |||||  
 Db 176 RAVPP 180

## RESULT 41

US-10-510-386-32  
 ; Sequence 32, Application US/10510386  
 ; Publication No. US20050244922A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andersen, Jens Tonne  
 ; APPLICANT: Clausen, Ib Groth  
 ; APPLICANT: Jorgensen, Steen Troels  
 ; APPLICANT: Olsen, Peter Bjarke  
 ; APPLICANT: Rasmussen, Michael Dolberg  
 ; TITLE OF INVENTION: Improved Bacillus Host Cell  
 ; FILE REFERENCE: 10294.204-US  
 ; CURRENT APPLICATION NUMBER: US/10/510,386  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 248  
 ; SOFTWARE: Patentin version 3.3  
 ; SEQ ID NO 32  
 ; LENGTH: 645  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus licheniformis  
 US-10-510-386-32

Query Match 75.9%; Score 22; DB 6; Length 645;  
 Best Local Similarity 66.7%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVPPA 6  
 |||||  
 Db 123 KGLFFA 128

## RESULT 42

US-10-821-234-975  
 ; Sequence 975, Application US/10821234  
 ; Publication No. US20050255114A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Labat, Ivan  
 ; APPLICANT: Stache-Crain, Birgit  
 ; APPLICANT: Andarmani, Susan  
 ; APPLICANT: Tang, Y. Tom  
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 ; FILE REFERENCE: 821A  
 ; CURRENT APPLICATION NUMBER: US/10/821,234  
 ; CURRENT FILING DATE: 2004-04-07  
 ; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 975\_  
; LENGTH: 989  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-975

Query Match 75.9%; Score 22; DB 6; Length 989;  
Best Local Similarity 66.7%; Pred. No. 8.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
DB 312 ESVFFA 317

RESULT 43  
US/11/062  
; Sequence 4, Application US/11062471A  
; Publication No. US2005025503A1  
; GENERAL INFORMATION:  
; APPLICANT: SHONE, Clifford Charles  
; APPLICANT: SUTTON, John Mark  
; APPLICANT: HALLIS, Basam  
; APPLICANT: SILMAN, Nigel  
; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells  
; FILE REFERENCE: 1581.080001  
; CURRENT APPLICATION NUMBER: US/11/062,471A  
; CURRENT FILING DATE: 2005-02-22  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: 09/831,050  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: PCT/GB99/03699  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: GB 9824282.9  
; PRIOR FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1070  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker,  
US/11/062,471A-4

Query Match 75.9%; Score 22; DB 7; Length 1070;  
Best Local Similarity 80.0%; Pred. No. 9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
DB 762 KSVFF 766

RESULT 44  
US/11/062  
; Sequence 7, Application US/11062471A  
; Publication No. US2005025503A1  
; GENERAL INFORMATION:  
; APPLICANT: SHONE, Clifford Charles  
; APPLICANT: SUTTON, John Mark  
; APPLICANT: HALLIS, Basam  
; APPLICANT: SILMAN, Nigel  
; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells  
; FILE REFERENCE: 1581.080001  
; CURRENT APPLICATION NUMBER: US/11/062,471A  
; CURRENT FILING DATE: 2005-02-22  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: 09/831,050  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: PCT/GB99/03699  
; PRIOR FILING DATE: 1999-11-05

; PRIOR APPLICATION NUMBER: GB 9824282.9  
; PRIOR FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 1095  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human ;  
US/11/062,471A-7

Query Match 75.9%; Score 22; DB 7; Length 1095;  
Best Local Similarity 80.0%; Pred. No. 9.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
DB 787 KSVFF 791

RESULT 45  
US-11-077-550-20  
; Sequence 20, Application US/11077550  
; Publication No. US2005024435A1  
; GENERAL INFORMATION:  
; APPLICANT: Shone, Clifford Charles  
; APPLICANT: Quinn, Conrad Padraig  
; APPLICANT: Foster, Keith Alan  
; APPLICANT: Chaddock, John  
; APPLICANT: Marks, Philip  
; APPLICANT: Sutton, J. Mark  
; APPLICANT: Stancombe, Patrick  
; APPLICANT: Wayne, Jonathan  
; TITLE OF INVENTION: Recombinant Toxin Fragments  
; FILE REFERENCE: 1581.0130004  
; CURRENT APPLICATION NUMBER: US/11/077,550  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: 10/241,596  
; PRIOR FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: 09/255,829  
; PRIOR FILING DATE: 1999-02-23  
; PRIOR APPLICATION NUMBER: PCT/GB97/02273  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 08/782,893  
; PRIOR FILING DATE: 1996-12-27  
; PRIOR APPLICATION NUMBER: GB9625996.5  
; PRIOR FILING DATE: 1996-12-13  
; PRIOR APPLICATION NUMBER: GB9617671.4  
; PRIOR FILING DATE: 1996-08-23  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 1169  
; TYPE: PRT  
; ORGANISM: Clostridium botulinum  
US-11-077-550-20

Query Match 75.9%; Score 22; DB 7; Length 1169;  
Best Local Similarity 80.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5  
DB 983 KSVFF 987

RESULT 46  
US-10-250-581-14  
; Sequence 14, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...

;; TITLE OF INVENTION: Soluble cyclic analogs....  
;; FILE REFERENCE: 16069  
;; CURRENT APPLICATION NUMBER: US/10/250,581  
;; CURRENT FILING DATE: 2004-01-14  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: Patent In Version 2.1  
;; SEQ ID NO 14  
;; LENGTH: 28  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (17)  
;; OTHER INFORMATION: Xaa=Orn  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (17)..(21)  
;; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
;; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-14

Query Match 72.4%; Score 21; DB 6; Length 28;  
Best Local Similarity 80.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
| |||  
Db 16 KXVFF 20

RESULT 47  
US-10-250-581-17  
;; Sequence 17, Application US/10250581  
;; Publication No. US20040116337A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
;; TITLE OF INVENTION: Soluble cyclic analogs....  
;; FILE REFERENCE: 16069  
;; CURRENT APPLICATION NUMBER: US/10/250,581  
;; CURRENT FILING DATE: 2004-01-14  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: Patent In Version 2.1  
;; SEQ ID NO 17  
;; LENGTH: 28  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (17)  
;; OTHER INFORMATION: Xaa=Dab  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (17)..(21)  
;; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
;; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-17

Query Match 72.4%; Score 21; DB 6; Length 28;  
Best Local Similarity 80.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
| |||  
Db 16 KXVFF 20

RESULT 48  
US-10-250-581-14  
;; Sequence 14, Application US/10250581  
;; Publication No. US20040116337A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
;; TITLE OF INVENTION: Soluble cyclic analogs....

;; FILE REFERENCE: 16069  
;; CURRENT APPLICATION NUMBER: US/10/250,581  
;; CURRENT FILING DATE: 2004-01-14  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: Patent In Version 2.1  
;; SEQ ID NO 14  
;; LENGTH: 28  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (17)  
;; OTHER INFORMATION: Xaa=Orn  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (17)..(21)  
;; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
;; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-14

Query Match 72.4%; Score 21; DB 6; Length 28;  
Best Local Similarity 80.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
| |||  
Db 16 KXVFF 20

RESULT 49  
US-10-250-581-17  
;; Sequence 17, Application US/10250581  
;; Publication No. US20040116337A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
;; TITLE OF INVENTION: Soluble cyclic analogs....  
;; FILE REFERENCE: 16069  
;; CURRENT APPLICATION NUMBER: US/10/250,581  
;; CURRENT FILING DATE: 2004-01-14  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: Patent In Version 2.1  
;; SEQ ID NO 17  
;; LENGTH: 28  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (17)  
;; OTHER INFORMATION: Xaa=Dab  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (17)..(21)  
;; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
;; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-17

Query Match 72.4%; Score 21; DB 6; Length 28;  
Best Local Similarity 80.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVPF 5  
| |||  
Db 16 KXVFF 20

RESULT 50  
US-10-250-581-15  
;; Sequence 15, Application US/10250581  
;; Publication No. US20040116337A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
;; TITLE OF INVENTION: Soluble cyclic analogs....  
;; FILE REFERENCE: 16069



; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 15  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Orn  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-15

Query Match 72.4%; Score 21; DB 6; Length 40;  
Best Local Similarity 80.0%; Pred. No. 60;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5  
|  
|  
|  
|  
Db 16 KXVFF 20

RESULT 51  
US-10-250-581-18  
; Sequence 18, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 18  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Dab  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-18

Query Match 72.4%; Score 21; DB 6; Length 40;  
Best Local Similarity 80.0%; Pred. No. 60;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5  
|  
|  
|  
|  
Db 16 KXVFF 20

RESULT 52  
US-10-250-581-15  
; Sequence 15, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 15  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Orn  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-15

Query Match 72.4%; Score 21; DB 6; Length 40;  
Best Local Similarity 80.0%; Pred. No. 60;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5  
|  
|  
|  
|  
Db 16 KXVFF 20

RESULT 53  
US-10-250-581-18  
; Sequence 18, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 18  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Dab  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-18

Query Match 72.4%; Score 21; DB 6; Length 40;  
Best Local Similarity 80.0%; Pred. No. 60;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5  
|  
|  
|  
|  
Db 16 KXVFF 20

RESULT 54  
US-10-250-581-16  
; Sequence 16, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 16  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Orn  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-16

Query Match 72.4%; Score 21; DB 6; Length 42;  
Best Local Similarity 80.0%; Pred. No. 63;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
|  
|  
|  
|  
Db 16 KXVFF 20

RESULT 55  
US-10-250-581-19  
; Sequence 19, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 19  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Dab  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-19

Query Match 72.4%; Score 21; DB 6; Length 42;  
Best Local Similarity 80.0%; Pred. No. 63;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
|  
|  
|  
|  
Db 16 KXVFF 20

RESULT 56  
US-10-250-581-16  
; Sequence 16, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 16  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Orn  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-16

Query Match 72.4%; Score 21; DB 6; Length 42;  
Best Local Similarity 80.0%; Pred. No. 63;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
|  
|  
|  
|  
Db 16 KXVFF 20

RESULT 57  
US-10-250-581-19  
; Sequence 19, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 19  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Dab  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-19

Query Match 72.4%; Score 21; DB 6; Length 42;  
Best Local Similarity 80.0%; Pred. No. 63;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
|  
|  
|  
|  
Db 16 KXVFF 20

RESULT 58  
US-10-467-657-4978  
; Sequence 4978, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:

```
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4978
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4978
```

```
Query Match 72.4%; Score 21; DB 6; Length 54;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 AVFFA 6
Db 41 SVFFA 45
```

```
RESULT 59
US-11-123-896-344
; Sequence 344, Application US/11/123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Tulipa gesneriana
US-11-123-896-344
```

```
Query Match 72.4%; Score 21; DB 7; Length 71;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KAVFF 5
Db 3 RAIFF 7
```

```
RESULT 60
US-11-123-896-335
; Sequence 335, Application US/11/123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
```

```
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Tulipa gesneriana
US-11-123-896-335
```

```
Query Match 72.4%; Score 21; DB 7; Length 73;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KAVFF 5
Db 5 RAIFF 9
```

```
RESULT 61
US-10-467-657-9209
; Sequence 9209, Application US/10/467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9209
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9209
```

```
Query Match 72.4%; Score 21; DB 6; Length 105;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KAVFFA 6
Db 3 QTVFFA 8
```

```
RESULT 62
US-11-000-463-759
; Sequence 759, Application US/11/000463
; Publication No. US2005026423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
```

; APPLICANT: Cao, Yi-Cheng  
; APPLICANT: Drmanac, Radofe T.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 785C1P4CN  
; CURRENT APPLICATION NUMBER: US/11/000,463  
; CURRENT FILING DATE: 2004-11-29  
; PRIOR APPLICATION NUMBER: 10/291,265  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: PCT/US01/02623  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/922,279  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 759  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-000-463-759

Query Match 72.4%; Score 21; DB 7; Length 105;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6  
Db 68 AVFFA 72

RESULT 63  
US-10-793-626-1554  
; Sequence 1554, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1554  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1554

Query Match 72.4%; Score 21; DB 6; Length 115;  
Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6  
Db 23 SVFFA 27

RESULT 64  
US-10-467-657-3152  
; Sequence 3152, Application US/10467657  
; Publication No. US20050260581A1

; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 3152  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3152

Query Match 72.4%; Score 21; DB 6; Length 127;  
Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6  
Db 52 ALFFA 56

RESULT 65  
US-10-467-657-6860  
; Sequence 6860, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6860  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6860

Query Match 72.4%; Score 21; DB 6; Length 134;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6  
Db 78 ALFFA 82

RESULT 66  
US-10-467-657-4112  
; Sequence 4112, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

```
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4112
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4112

Query Match          72.4%; Score 21; DB 6; Length 153;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 AVFFA 6
DB      111 AVYFA 115

RESULT 67
US-10-467-657-9046
; Sequence 9046, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9046
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9046

Query Match          72.4%; Score 21; DB 6; Length 162;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      87 RAYFFA 92

RESULT 68
US-10-467-657-5306
; Sequence 5306, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5306
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5306

Query Match          72.4%; Score 21; DB 6; Length 167;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      159 KAVAF 164

RESULT 69
US-10-467-657-6854
; Sequence 6854, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6854
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6854

Query Match          72.4%; Score 21; DB 6; Length 189;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 AVFFA 6
DB      87 ALFFA 91

RESULT 70
US-10-467-657-7856
; Sequence 7856, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7856
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7856

Query Match          72.4%; Score 21; DB 6; Length 189;
```

Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6  
|:|:|  
Db 87 ALFFA 91

## RESULT 71

US-10-467-657-818  
; Sequence 818, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 818  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-818

Query Match 72.4%; Score 21; DB 6; Length 191;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
|:|:|  
Db 122 QAVFF 126

## RESULT 72

US-10-981-873-40  
; Sequence 40, Application US/10981873  
; Publication No. US20050250680A1  
; GENERAL INFORMATION:  
; APPLICANT: Walensky, Loren D.  
; APPLICANT: Korsmeyer, Stanley J.  
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND  
; FILE REFERENCE: 00530-124001  
; CURRENT APPLICATION NUMBER: US/10/981,873  
; PRIOR FILING DATE: 2004-11-05  
; PRIOR APPLICATION NUMBER: US 60/517,848  
; PRIOR FILING DATE: 2003-11-05  
; PRIOR APPLICATION NUMBER: US 60/591,548  
; PRIOR FILING DATE: 2004-07-27  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-981-873-40

Query Match 72.4%; Score 21; DB 6; Length 213;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
|:|:|  
Db 203 KAVFF 207

## RESULT 73

US-10-980-388-86  
; Sequence 86, Application US/10980388  
; Publication No. US20050255490A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Farodi, Luis A.  
; APPLICANT: Hiebsch, Ronald R.  
; APPLICANT: Lind, Peter  
; APPLICANT: Kaytes, Paul S.  
; APPLICANT: Ruff, Valerie  
; APPLICANT: Huff, Rita M.  
; APPLICANT: Wood, Linda S.  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App  
; FILE REFERENCE: 00325.US1  
; CURRENT APPLICATION NUMBER: US/10/980,388  
; CURRENT FILING DATE: 2004-11-02  
; PRIOR APPLICATION NUMBER: US/09/791,932  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/184,305  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,304  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,303  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,397  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,247  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/188,880  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/217,369  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/217,370  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/218,492  
; PRIOR FILING DATE: 2000-07-20  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 86  
; LENGTH: 227  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-980-388-86

Query Match 72.4%; Score 21; DB 6; Length 227;  
Best Local Similarity 60.0%; Pred. No. 3.3e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5  
|:|:|  
Db 81 KSIFP 85

## RESULT 74

US-10-510-386-198  
; Sequence 198, Application US/10510386  
; Publication No. US20050244922A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Jens Tonne  
; APPLICANT: Clausen, Ib Groth  
; APPLICANT: Jorgensen, Steen Troels  
; APPLICANT: Olsen, Peter Bjarke  
; APPLICANT: Rasmussen, Michael Dolberg  
; TITLE OF INVENTION: Improved Bacillus Host Cell  
; FILE REFERENCE: 10294.204-US  
; CURRENT APPLICATION NUMBER: US/10/510,386  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 248  
; SOFTWARE: PatentIn version 3.3

```
; SEQ ID NO 198
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-198

Query Match      72.4%; Score 21; DB 6; Length 230;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      94 KAAFF 98

RESULT 75
US-10-454-437-238
; Sequence 238, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schröder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128PCPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 238
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-238

Query Match      72.4%; Score 21; DB 6; Length 244;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      20 KAVFSA 25
```

Search completed: December 29, 2005, 18:50:17  
Job time : 5.29032 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds  
(without alignments)  
37.818 Million cell updates/sec

Title: US-10-009-122-7

Perfect score: 29

Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications AA Main.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	3	US-09-867-847-16
2	29	100.0	6	3	US-09-867-847-24
3	29	100.0	6	3	US-09-915-092-6
4	29	100.0	6	3	US-09-915-092-14
5	29	100.0	6	3	US-09-747-408-7
6	29	100.0	6	3	US-09-747-408-15
7	29	100.0	6	5	US-10-728-028-5
8	29	100.0	6	5	US-10-728-028-14
9	29	100.0	6	5	US-10-845-958-14
10	29	100.0	6	5	US-10-825-958-22
11	29	100.0	37	4	US-10-641-924-6
12	29	100.0	37	4	US-10-642-255-6
13	29	100.0	74	4	US-10-115-223-19
14	29	100.0	74	4	US-10-115-223-25
15	29	100.0	74	4	US-10-402-212-19
16	29	100.0	74	4	US-10-402-212-25
17	29	100.0	108	4	US-10-115-223-20
18	29	100.0	108	4	US-10-115-223-26
19	29	100.0	108	4	US-10-402-212-20
20	29	100.0	108	4	US-10-402-212-26
21	29	100.0	193	4	US-10-115-223-18
22	29	100.0	193	4	US-10-115-223-24
23	29	100.0	193	4	US-10-402-212-18
24	29	100.0	193	4	US-10-402-212-24
25	29	100.0	222	4	US-10-115-223-17
26	29	100.0	222	4	US-10-402-212-17
27	29	100.0	228	4	US-10-115-223-23

29	100.0	228	4	US-10-402-212-23	Sequence 23, Appl
29	100.0	261	5	US-10-795-159-697	Sequence 97, App
29	100.0	429	4	US-10-115-223-45	Sequence 45, Appl
29	100.0	429	4	US-10-402-212-45	Sequence 45, Appl
29	100.0	468	5	US-10-450-763-54360	Sequence 54360, A
29	100.0	660	3	US-09-391-104-19	Sequence 19, Appl
29	100.0	660	3	US-09-801-196-35	Sequence 35, Appl
29	100.0	660	3	US-09-818-715-208	Sequence 208, App
29	100.0	660	4	US-10-219-329-14	Sequence 14, Appl
29	100.0	660	4	US-10-301-822-125	Sequence 125, App
29	100.0	660	4	US-10-153-185-14	Sequence 14, Appl
29	100.0	660	4	US-10-219-561-14	Sequence 14, Appl
29	100.0	660	4	US-10-131-985-25	Sequence 25, Appl
29	100.0	660	4	US-10-447-315-3	Sequence 3, Appli
29	100.0	660	4	US-10-032-376A-14	Sequence 14, Appl
29	100.0	660	4	US-10-335-207-14	Sequence 14, Appl
29	100.0	660	4	US-10-480-621-1	Sequence 1, Appli
29	100.0	660	4	US-10-474-794-208	Sequence 208, App
29	100.0	660	5	US-10-601-059-14	Sequence 14, Appl
29	100.0	660	5	US-10-872-198-131	Sequence 131, App
29	100.0	660	5	US-10-901-417-25	Sequence 25, Appl
29	100.0	660	5	US-10-979-159-208	Sequence 208, App
29	100.0	660	5	US-10-287-436A-489	Sequence 489, App
29	100.0	660	5	US-10-287-436A-1185	Sequence 1185, Ap
29	100.0	660	6	US-11-021-951-131	Sequence 131, App
29	100.0	660	6	US-11-031-488-14	Sequence 14, Appl
29	100.0	663	4	US-10-115-223-30	Sequence 30, Appl
29	100.0	663	4	US-10-402-212-30	Sequence 30, Appl
29	100.0	718	4	US-10-369-493-4873	Sequence 4873, Ap
29	100.0	737	4	US-10-369-493-7633	Sequence 7633, Ap
29	100.0	770	4	US-10-437-963-138526	Sequence 138526, A
29	100.0	1330	5	US-10-450-763-54358	Sequence 54358, A
28	96.6	383	4	US-10-369-493-4941	Sequence 4941, Ap
28	96.6	383	4	US-10-369-493-7699	Sequence 7699, Ap
29	89.7	49	4	US-10-424-599-278606	Sequence 278606, A
29	89.7	61	4	US-10-424-599-150066	Sequence 150066, A
29	89.7	65	5	US-10-926-683-1595	Sequence 1595, Ap
29	89.7	89	4	US-10-425-115-359391	Sequence 359391, A
29	89.7	103	4	US-10-424-599-210814	Sequence 210814, A
29	89.7	108	4	US-10-437-963-114838	Sequence 114838, A
29	89.7	124	4	US-10-424-599-182643	Sequence 182643, A
29	89.7	131	4	US-10-767-701-41102	Sequence 41102, A
29	89.7	138	5	US-10-450-763-39449	Sequence 39449, A
29	89.7	172	4	US-10-437-963-172959	Sequence 172959, A
29	89.7	206	4	US-10-767-701-31699	Sequence 31699, A
29	89.7	208	5	US-10-450-763-39451	Sequence 39451, A
29	89.7	210	4	US-10-282-122A-61639	Sequence 61639, A
29	89.7	258	4	US-10-425-115-286732	Sequence 286732, A
29	89.7	270	4	US-10-437-963-176878	Sequence 176878, A
29	89.7	308	4	US-10-425-115-332957	Sequence 332957, A
29	89.7	314	4	US-10-425-115-286735	Sequence 286735, A
29	89.7	320	4	US-10-425-114-43310	Sequence 43310, A
29	89.7	320	4	US-10-425-114-64659	Sequence 64659, A
29	89.7	323	4	US-10-437-963-117099	Sequence 117099, A
29	89.7	334	3	US-09-933-767-348	Sequence 348, App
29	89.7	334	4	US-10-004-860-348	Sequence 348, App
29	89.7	334	4	US-10-023-282-348	Sequence 348, App
29	89.7	421	3	US-09-741-669-400	Sequence 400, App
29	89.7	421	3	US-10-282-122A-42751	Sequence 42751, A
29	89.7	441	5	US-10-821-273-34	Sequence 34, Appl
29	89.7	556	5	US-10-820-474A-119	Sequence 119, App
29	89.7	715	4	US-10-282-122A-75547	Sequence 75547, A
29	89.7	859	4	US-10-437-963-201533	Sequence 201533, A
29	89.7	1042	4	US-10-282-122A-61918	Sequence 61918, A
29	89.7	1166	4	US-10-437-963-128203	Sequence 128203, A
29	89.7	1172	5	US-10-450-763-36972	Sequence 36972, A
29	89.7	1719	4	US-10-437-963-142580	Sequence 142580, A
25	86.2	5	3	US-09-850-061A-40	Sequence 40, Appl
25	86.2	5	4	US-10-721-774-40	Sequence 40, Appl
25	86.2	6	3	US-09-867-847-18	Sequence 18, Appl
25	86.2	6	3	US-09-867-847-26	Sequence 26, Appl
25	86.2	6	3	US-09-915-092-8	Sequence 8, Appli
25	86.2	6	3	US-09-915-092-16	Sequence 16, Appl



101	25	86.2	25	6	3	US-09-747-408-9	Sequence 9, Appli	174	25	86.2	256	5	US-10-733-923-20752	Sequence 20752, A
102	25	86.2	25	6	3	US-09-747-408-17	Sequence 17, Appli	175	25	86.2	268	4	US-10-369-493-20071	Sequence 20071, A
103	25	86.2	25	6	5	US-10-728-028-8	Sequence 8, Appli	176	25	86.2	268	4	US-10-425-115-308997	Sequence 308997, A
104	25	86.2	25	6	5	US-10-728-028-16	Sequence 16, Appli	177	25	86.2	282	3	US-09-845-713A-2	Sequence 2, Appli
105	25	86.2	25	6	5	US-10-825-958-16	Sequence 16, Appli	178	25	86.2	282	4	US-10-435-696-35	Sequence 35, Appli
106	25	86.2	25	6	5	US-10-825-958-24	Sequence 24, Appli	179	25	86.2	289	4	US-10-425-115-215163	Sequence 215163, A
107	25	86.2	25	22	4	US-10-425-115-347015	Sequence 347015, A	180	25	86.2	297	4	US-10-425-115-73046	Sequence 73046, A
108	25	86.2	25	25	3	US-09-764-877-1260	Sequence 1260, Ap	181	25	86.2	303	5	US-09-908-0067A-5	Sequence 5, Appli
109	25	86.2	25	25	4	US-10-242-515-1260	Sequence 1260, Ap	182	25	86.2	314	3	US-09-491-067A-5	Sequence 16, Appli
110	25	86.2	25	34	5	US-10-499-352A-444	Sequence 444, App	183	25	86.2	317	4	US-10-425-115-225676	Sequence 225676, A
111	25	86.2	25	37	4	US-10-641-924-7	Sequence 7, Appli	184	25	86.2	322	3	US-09-816-028A-48	Sequence 48, Appli
112	25	86.2	25	37	4	US-10-642-255-7	Sequence 7, Appli	185	25	86.2	322	3	US-09-886-055-253	Sequence 253, App
113	25	86.2	25	39	4	US-10-424-599-220682	Sequence 220682, A	186	25	86.2	322	3	US-09-804-291-253	Sequence 253, App
114	25	86.2	25	55	4	US-10-424-599-171652	Sequence 171652, A	187	25	86.2	322	4	US-10-017-161-156	Sequence 156, App
115	25	86.2	25	60	4	US-10-437-963-173619	Sequence 173619, A	188	25	86.2	322	4	US-10-303-161-48	Sequence 48, Appli
116	25	86.2	25	62	4	US-10-424-599-197144	Sequence 197144, A	189	25	86.2	322	4	US-10-303-118-48	Sequence 48, Appli
117	25	86.2	25	62	4	US-10-424-599-212719	Sequence 212719, A	190	25	86.2	322	4	US-10-303-128-48	Sequence 48, Appli
118	25	86.2	25	63	4	US-10-424-599-217238	Sequence 217238, A	191	25	86.2	322	4	US-10-303-134-48	Sequence 48, Appli
119	25	86.2	25	63	4	US-10-029-386-28659	Sequence 28659, A	192	25	86.2	322	4	US-10-303-162-48	Sequence 48, Appli
120	25	86.2	25	66	4	US-10-425-115-367811	Sequence 367811, A	193	25	86.2	322	4	US-10-387-629-76	Sequence 76, Appli
121	25	86.2	25	69	4	US-10-424-599-201270	Sequence 201270, A	194	25	86.2	322	4	US-10-292-798-134	Sequence 134, App
122	25	86.2	25	70	4	US-10-425-115-292851	Sequence 292851, A	195	25	86.2	322	4	US-10-343-650A-582	Sequence 582, App
123	25	86.2	25	71	4	US-10-424-599-170927	Sequence 170927, A	196	25	86.2	322	4	US-10-473-518-2	Sequence 2, Appli
124	25	86.2	25	75	4	US-10-425-115-299056	Sequence 299056, A	197	25	86.2	322	4	US-10-820-536-48	Sequence 48, Appli
125	25	86.2	25	80	4	US-10-243-552-570	Sequence 570, App	198	25	86.2	322	4	US-10-845-408-48	Sequence 48, Appli
126	25	86.2	25	80	4	US-10-437-963-111335	Sequence 111335, A	199	25	86.2	322	4	US-10-845-412-48	Sequence 48, Appli
127	25	86.2	25	81	4	US-10-425-115-299931	Sequence 299931, A	200	25	86.2	322	5	US-10-846-219-48	Sequence 48, Appli
128	25	86.2	25	81	4	US-10-424-599-245453	Sequence 245453, A	201	25	86.2	322	5	US-10-821-604-48	Sequence 48, Appli
129	25	86.2	25	87	4	US-10-437-963-133986	Sequence 133986, A	202	25	86.2	322	5	US-10-847-993-48	Sequence 48, Appli
130	25	86.2	25	89	4	US-10-425-115-302836	Sequence 302836, A	203	25	86.2	322	5	US-10-821-573-48	Sequence 48, Appli
131	25	86.2	25	90	4	US-10-424-599-147666	Sequence 147666, A	204	25	86.2	322	5	US-10-850-807-48	Sequence 48, Appli
132	25	86.2	25	95	4	US-10-425-115-296215	Sequence 296215, A	205	25	86.2	322	5	US-10-850-125-48	Sequence 48, Appli
133	25	86.2	25	95	4	US-10-437-963-197590	Sequence 197590, A	206	25	86.2	322	5	US-10-830-825-48	Sequence 48, Appli
134	25	86.2	25	98	4	US-10-425-115-364147	Sequence 364147, A	207	25	86.2	322	5	US-10-962-334-48	Sequence 48, Appli
135	25	86.2	25	99	4	US-10-437-963-150181	Sequence 150181, A	208	25	86.2	322	5	US-10-830-997-48	Sequence 48, Appli
136	25	86.2	25	109	4	US-10-437-963-105773	Sequence 105773, A	209	25	86.2	322	5	US-10-962-235-48	Sequence 48, Appli
137	25	86.2	25	109	4	US-10-425-115-226514	Sequence 226514, A	210	25	86.2	322	5	US-10-961-882-48	Sequence 48, Appli
138	25	86.2	25	117	3	US-09-864-761-71128	Sequence 371128, A	211	25	86.2	322	5	US-10-819-316-253	Sequence 253, App
139	25	86.2	25	117	4	US-10-425-115-362628	Sequence 362628, A	212	25	86.2	322	5	US-10-819-316-531	Sequence 531, App
140	25	86.2	25	127	4	US-10-767-701-47243	Sequence 47243, A	213	25	86.2	327	4	US-10-437-963-109308	Sequence 109308, A
141	25	86.2	25	128	4	US-10-425-115-192450	Sequence 192450, A	214	25	86.2	332	4	US-10-274-694-2	Sequence 2, Appli
142	25	86.2	25	129	4	US-10-424-599-278483	Sequence 278483, A	215	25	86.2	332	4	US-10-369-493-11167	Sequence 11167, A
143	25	86.2	25	130	4	US-10-424-599-170319	Sequence 170319, A	216	25	86.2	332	4	US-10-369-493-22884	Sequence 22884, A
144	25	86.2	25	132	4	US-10-029-386-28941	Sequence 28941, A	217	25	86.2	332	5	US-10-332-448-2	Sequence 2, Appli
145	25	86.2	25	133	4	US-10-424-599-270652	Sequence 270652, A	218	25	86.2	347	3	US-09-939-484-6	Sequence 6, Appli
146	25	86.2	25	133	4	US-10-425-115-305393	Sequence 305393, A	219	25	86.2	347	3	US-09-939-483-6	Sequence 6, Appli
147	25	86.2	25	135	4	US-10-437-963-141578	Sequence 141578, A	220	25	86.2	354	6	US-11-097-143-6189	Sequence 6189, Ap
148	25	86.2	25	140	4	US-10-424-599-151465	Sequence 151465, A	221	25	86.2	366	4	US-10-424-599-278238	Sequence 278238, A
149	25	86.2	25	150	4	US-10-335-977-6540	Sequence 6540, Ap	222	25	86.2	373	4	US-10-437-963-167534	Sequence 167534, A
150	25	86.2	25	155	4	US-10-424-599-200083	Sequence 200083, A	223	25	86.2	380	4	US-10-369-493-7986	Sequence 7986, Ap
151	25	86.2	25	171	4	US-10-424-599-229782	Sequence 229782, A	224	25	86.2	382	4	US-10-369-493-11163	Sequence 11163, A
152	25	86.2	25	175	4	US-10-437-963-122124	Sequence 122124, A	225	25	86.2	411	4	US-10-282-122A-77801	Sequence 77801, A
153	25	86.2	25	180	4	US-10-424-599-252237	Sequence 252237, A	226	25	86.2	415	4	US-10-282-122A-68770	Sequence 68770, A
154	25	86.2	25	186	5	US-10-481-032A-218	Sequence 218, App	227	25	86.2	416	6	US-10-055-475-14	Sequence 14, Appli
155	25	86.2	25	186	5	US-10-481-032A-228	Sequence 228, App	228	25	86.2	416	6	US-11-042-922-14	Sequence 14, Appli
156	25	86.2	25	188	4	US-10-437-963-172476	Sequence 172476, A	229	25	86.2	430	4	US-10-058-636-2	Sequence 2, Appli
157	25	86.2	25	190	4	US-10-437-963-173798	Sequence 173798, A	230	25	86.2	430	4	US-10-799-016-2	Sequence 2, Appli
158	25	86.2	25	198	4	US-10-437-963-172452	Sequence 172452, A	231	25	86.2	454	3	US-09-993-811-12	Sequence 12, Appli
159	25	86.2	25	201	4	US-10-732-923-17850	Sequence 17850, A	232	25	86.2	472	5	US-10-472-928-4158	Sequence 4158, Ap
160	25	86.2	25	202	5	US-10-732-923-19034	Sequence 19034, A	233	25	86.2	473	5	US-10-617-320-3273	Sequence 3273, Ap
161	25	86.2	25	209	4	US-10-424-599-280085	Sequence 280085, A	234	25	86.2	481	6	US-11-097-143-3162	Sequence 3162, Ap
162	25	86.2	25	210	4	US-10-282-122A-65447	Sequence 65447, A	235	25	86.2	507	4	US-10-223-070-9	Sequence 9, Appli
163	25	86.2	25	210	4	US-10-282-122A-66099	Sequence 66099, A	236	25	86.2	514	4	US-10-055-475-13	Sequence 13, Appli
164	25	86.2	25	224	4	US-10-424-599-245461	Sequence 245461, A	237	25	86.2	514	6	US-11-042-922-13	Sequence 13, Appli
165	25	86.2	25	224	4	US-10-424-599-257424	Sequence 257424, A	238	25	86.2	530	3	US-09-804-014A-28	Sequence 28, Appli
166	25	86.2	25	246	6	US-11-097-143-2748	Sequence 2748, Ap	239	25	86.2	532	3	US-09-993-811-6	Sequence 6, Appli
167	25	86.2	25	247	4	US-10-335-977-6541	Sequence 6541, Ap	240	25	86.2	532	3	US-09-875-321-13	Sequence 13, Appli
168	25	86.2	25	247	4	US-10-335-977-6542	Sequence 6542, Ap	241	25	86.2	532	3	US-09-804-014A-31	Sequence 31, Appli
169	25	86.2	25	247	5	US-10-732-923-19035	Sequence 19035, A	242	25	86.2	532	4	US-10-162-012-13	Sequence 13, Appli
170	25	86.2	25	249	4	US-10-369-493-10584	Sequence 10584, A	243	25	86.2	532	4	US-10-254-010-2	Sequence 2, Appli
171	25	86.2	25	254	4	US-10-369-493-16714	Sequence 16714, A	244	25	86.2	532	4	US-10-162-102-13	Sequence 13, Appli
172	25	86.2	25	255	5	US-10-732-923-20940	Sequence 20940, A	245	25	86.2	532	5	US-10-916-061-13	Sequence 13, Appli
173	25	86.2	25	255	6	US-11-097-143-29655	Sequence 29655, A	246	25	86.2	539	4	US-10-282-122A-48163	Sequence 48163, A

```

247 25 86.2 552 4 US-10-282-122A-49134
248 25 86.2 558 4 US-10-282-122A-50632
249 25 86.2 560 3 US-09-735-705-225
250 25 86.2 560 3 US-09-850-716A-225
251 25 86.2 560 3 US-09-897-778-225
252 25 86.2 560 3 US-09-943-075A-6
253 25 86.2 560 3 US-09-738-626-5465
254 25 86.2 560 4 US-10-039-272-2
255 25 86.2 560 4 US-10-007-700-225
256 25 86.2 560 4 US-10-117-982-225
257 25 86.2 560 4 US-10-463-106-2
258 25 86.2 560 4 US-10-295-027-1258
259 25 86.2 560 4 US-10-313-986-225
260 25 86.2 560 4 US-10-309-290-152
261 25 86.2 560 4 US-10-408-765A-466
262 25 86.2 560 5 US-10-775-972-225
263 25 86.2 560 5 US-10-723-860-1128
264 25 86.2 560 5 US-10-922-124-225
265 25 86.2 560 5 US-10-978-758-6
266 25 86.2 560 5 US-10-631-467-821
267 25 86.2 561 5 US-10-450-763-39378
268 25 86.2 563 4 US-10-282-122A-50907
269 25 86.2 572 4 US-10-227-884-42
270 25 86.2 572 4 US-10-230-163-42
271 25 86.2 572 4 US-10-230-338-42
272 25 86.2 572 4 US-10-218-631-42
273 25 86.2 572 4 US-10-230-414-42
274 25 86.2 572 4 US-10-232-224-42
275 25 86.2 572 4 US-10-216-159A-42
276 25 86.2 572 4 US-10-218-849-42
277 25 86.2 572 4 US-10-227-873-42
278 25 86.2 572 4 US-10-227-883-42
279 25 86.2 572 4 US-10-219-076-42
280 25 86.2 572 4 US-10-230-434-42
281 25 86.2 572 4 US-10-219-003-42
282 25 86.2 572 4 US-10-219-075-42
283 25 86.2 572 4 US-10-219-464-42
284 25 86.2 572 4 US-10-219-466-42
285 25 86.2 572 4 US-10-219-479-42
286 25 86.2 572 4 US-10-219-481-42
287 25 86.2 572 4 US-10-230-260-42
288 25 86.2 572 4 US-10-232-231-42
289 25 86.2 572 4 US-10-232-233-42
290 25 86.2 572 4 US-10-216-165-42
291 25 86.2 572 4 US-10-218-956-42
292 25 86.2 572 4 US-10-219-468-42
293 25 86.2 572 4 US-10-219-478-42
294 25 86.2 572 4 US-10-219-536-42
295 25 86.2 572 4 US-10-233-205-42
296 25 86.2 572 4 US-10-219-072-42
297 25 86.2 572 4 US-10-219-470-42
298 25 86.2 572 4 US-10-219-474-42
299 25 86.2 572 4 US-10-219-524-42
300 25 86.2 572 4 US-10-219-528-42

```

# ALIGNMENTS

```

RESULT 1
US-09-867-847-16
; Sequence 16, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

```

```

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-16

```

```

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KAVFFA 6
Db 1 KAVFFA 6

```

```

RESULT 2
US-09-867-847-24
; Sequence 24, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-24

```

```

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KAVFFA 6
Db 1 KAVFFA 6

```

```

RESULT 3
US-09-915-092-6
; Sequence 6, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert

```

```

; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-6

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 4
US-09-915-092-14
; Sequence 14, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-14

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 5
US-09-747-408-7
; Sequence 7, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-7

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-7

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 6
US-09-747-408-15
; Sequence 15, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-15

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 7
US-10-728-028-6
; Sequence 6, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-728-028-6

```

```
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-6

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 8
US-10-728-028-14
; Sequence 14, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-14

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 9
US-10-825-958-14
; Sequence 14, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-14

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 10
US-10-825-958-22
; Sequence 22, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-22

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 11
US-10-641-924-6
; Sequence 6, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 5303SAUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
```

```
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-641-924-6

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      18 KAVFFA 23

RESULT 12
US-10-642-255-6
; Sequence 6, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyi, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; FILE REFERENCE: enOS
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-642-255-6

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      18 KAVFFA 23

RESULT 13
US-10-115-223-19
; Sequence 19, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
```

```
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-19

Query Match      100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 14
US-10-115-223-25
; Sequence 25, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-25

Query Match      100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 15
US-10-402-212-19
; Sequence 19, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
```

; PRIOR FILING DATE: 1996-05-31  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-402-212-19

Query Match 100.0%; Score 29; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 64 KAVFFA 69  
|||||

## RESULT 16

US-10-402-212-25  
; Sequence 25, Application US/10402212  
; Publication No. US20040063790A1  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter C.  
; APPLICANT: Cheresch, David A.  
; APPLICANT: Silletti, Steven A.  
; APPLICANT: The Scripps Research Institute  
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS  
; FILE REFERENCE: TSRI-419.3  
; CURRENT APPLICATION NUMBER: US/10/402,212  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 10/115,223  
; PRIOR FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: 09/194,468  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,869  
; PRIOR FILING DATE: 1996-05-31  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-10-402-212-25

Query Match 100.0%; Score 29; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 64 KAVFFA 69  
|||||

## RESULT 17

US-10-115-223-20  
; Sequence 20, Application US/10115223  
; Publication No. US20030176334A1  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheresch, David A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/10/115,223  
; CURRENT FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: US/09/194,468  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773

; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-223-20

Query Match 100.0%; Score 29; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 64 KAVFFA 69  
|||||

## RESULT 18

US-10-115-223-26  
; Sequence 26, Application US/10115223  
; Publication No. US20030176334A1  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheresch, David A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/10/115,223  
; CURRENT FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: US/09/194,468  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-10-115-223-26

Query Match 100.0%; Score 29; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 64 KAVFFA 69  
|||||

## RESULT 19

US-10-402-212-20  
; Sequence 20, Application US/10402212  
; Publication No. US20040063790A1  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter C.  
; APPLICANT: Cheresch, David A.  
; APPLICANT: Silletti, Steven A.  
; APPLICANT: The Scripps Research Institute  
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS  
; FILE REFERENCE: TSRI-419.3  
; CURRENT APPLICATION NUMBER: US/10/402,212  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 10/115,223

```
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-20

Query Match          100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 20
US-10-402-212-26
; Sequence 26, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresh, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-26

Query Match          100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 21
US-10-115-223-18
; Sequence 18, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-18

Query Match          100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 22
US-10-115-223-24
; Sequence 24, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-24

Query Match          100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 23
US-10-402-212-18
; Sequence 18, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
```

```
; APPLICANT: Chereah, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-18
```

```
Query Match      100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
        |||||
Db      64 KAVFFA 69
```

```
RESULT 24
US-10-402-212-24
; Sequence 24, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Chereah, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-24
```

```
Query Match      100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
        |||||
Db      64 KAVFFA 69
```

```
RESULT 25
US-10-115-223-17
; Sequence 17, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Chereah, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-17
```

```
Query Match      100.0%; Score 29; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
        |||||
Db      93 KAVFFA 98
```

```
RESULT 26
US-10-402-212-17
; Sequence 17, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Chereah, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-17
```

```
Query Match      100.0%; Score 29; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



QY 1 KAVFFA 6  
| | | | |  
Db 93 KAVFFA 98

## RESULT 27

US-10-115-223-23  
; Sequence 23, Application US/10115223  
; Publication No. US20030176334A1  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Chersesh, David A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/10/115,223  
; CURRENT FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: US/09/194,468  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-10-115-223-23

Query Match 100.0%; Score 29; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
| | | | |  
Db 99 KAVFFA 104

## RESULT 28

US-10-402-212-23  
; Sequence 23, Application US/10402212  
; Publication No. US20040063790A1  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter C.  
; APPLICANT: Chersesh, David A.  
; APPLICANT: Silletti, Steven A.  
; APPLICANT: The Scripps Research Institute  
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS  
; FILE REFERENCE: TSRI-419.3  
; CURRENT APPLICATION NUMBER: US/10/402,212  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 10/115,223  
; PRIOR FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: 09/194,468  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,869  
; PRIOR FILING DATE: 1996-05-31  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-10-402-212-23

Query Match 100.0%; Score 29; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
| | | | |  
Db 99 KAVFFA 104

## RESULT 29

US-10-795-159-697  
; Sequence 697, Application US/10795159  
; Publication No. US20050221439A1  
; GENERAL INFORMATION:  
; APPLICANT: BAKALETZ et al.  
; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE  
; FILE REFERENCE: 28335/38815A  
; CURRENT APPLICATION NUMBER: US/10/795,159  
; CURRENT FILING DATE: 2004-03-05  
; PRIOR APPLICATION NUMBER: US 60/453,134  
; PRIOR FILING DATE: 2003-03-06  
; NUMBER OF SEQ ID NOS: 771  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 697  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: H. influenzae  
US-10-795-159-697

Query Match 100.0%; Score 29; DB 5; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
| | | | |  
Db 205 KAVFFA 210

## RESULT 30

US-10-115-223-45  
; Sequence 45, Application US/10115223  
; Publication No. US20030176334A1  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Chersesh, David A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF  
; FILE REFERENCE: MER0049S  
; CURRENT APPLICATION NUMBER: US/10/115,223  
; CURRENT FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: US/09/194,468  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,896  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 429  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-223-45

Query Match 100.0%; Score 29; DB 4; Length 429;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
| | | | |  
Db 300 KAVFFA 305

; OTHER INFORMATION: Fibronectin type II domain identified by Pfam, accession name  
; OTHER INFORMATION: fn2, E-value=4.4e-55, Pfam score of 147.1

; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(468)  
; OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-450-763-54360

Query Match 100.0%; Score 29; DB 5; Length 468;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 361 KAVFFA 366

RESULT 33

US-09-391-104-19  
; Sequence 19, Application US/09391104  
; Publication No. US20020031817A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Palduto, Michael T.  
; APPLICANT: Magnuson, Scott R.  
; APPLICANT: Morgan, Douglas W.  
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,  
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
; TITLE OF INVENTION: OF USING SAME  
; FILE REFERENCE: 6073.US.P1  
; CURRENT APPLICATION NUMBER: US/09/391,104  
; PRIOR FILING DATE: 1999-09-07  
; PRIOR APPLICATION NUMBER: US 08/814,394  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 660  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-391-104-19

Query Match 100.0%; Score 29; DB 3; Length 660;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 531 KAVFFA 536

RESULT 34

US-09-801-196-35  
; Sequence 35, Application US/09801196  
; Patent No. US20020037827A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Kai  
; APPLICANT: Smith, Ryan  
; APPLICANT: Fajardo, Mark  
; APPLICANT: Moss, Patrick  
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)  
; TITLE OF INVENTION: EXPRESSED IN SKIN CELLS  
; FILE REFERENCE: 240083.509  
; CURRENT APPLICATION NUMBER: US/09/801,196  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 660  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-801-196-35

RESULT 31

US-10-402-212-45  
; Sequence 45, Application US/10402212  
; Publication No. US20040063790A1  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter C.  
; APPLICANT: Cheresch, David A.  
; APPLICANT: Silletti, Steven A.  
; APPLICANT: The Scripps Research Institute  
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS  
; FILE REFERENCE: TSRI-419.3  
; CURRENT APPLICATION NUMBER: US/10/402,212  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 10/115,223  
; PRIOR FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: 09/194,468  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,869  
; PRIOR FILING DATE: 1996-05-31  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 429  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-402-212-45

Query Match 100.0%; Score 29; DB 4; Length 429;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
Db 300 KAVFFA 305

RESULT 32

US-10-450-763-54360  
; Sequence 54360, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 54360  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (221)..(258)  
; OTHER INFORMATION: Type II fibronectin collagen-binding domain proteins domain  
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00023, p-value=4.682e-3  
; OTHER INFORMATION: raw score of 24.31  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (167)..(264)

```
Query Match      100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536

RESULT 35
US-09-918-715-208
; Sequence 208, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-208

Query Match      100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536

RESULT 36
US-10-219-329-14
; Sequence 14, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Weart, Ilona f.
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035W01
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-14

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536

RESULT 37
US-10-301-822-125
; Sequence 125, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-125

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536

RESULT 38
US-10-153-185-14
; Sequence 14, Application US/10153185
; Publication No. US20030148959A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Soheil
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-14

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536
```

Db 531 KAVFFA 536

## RESULT 39

US-10-219-561-14  
; Sequence 14, Application US/10219561  
; Publication No. US20030166567A1

## GENERAL INFORMATION:

; APPLICANT: Quirk, Stephen  
; APPLICANT: Malik, Sohail  
; APPLICANT: Villanueva, Julie M.

; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds

; FILE REFERENCE: 1443.008052

; CURRENT APPLICATION NUMBER: US/10/219,561

; CURRENT FILING DATE: 2002-08-15

; PRIOR APPLICATION NUMBER: US 10/032,376

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: US 10/153,185

; PRIOR FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US 60/312,726

; PRIOR FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 660

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-219-561-14

## Query Match

Best Local Similarity 100.0%; Score 29; DB 4; Length 660;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 531 KAVFFA 536

## RESULT 40

US-10-131-985-25

; Sequence 25, Application US/10131985

; Publication No. US20030199440A1

## GENERAL INFORMATION:

; APPLICANT: Dack, Kevin N

; APPLICANT: Davies, Michael J

; APPLICANT: Fish, Paul V

; APPLICANT: Huggins, Jonathan P

; APPLICANT: McIntosh, Fraser S

; APPLICANT: Occleston, Nicholas L

; TITLE OF INVENTION: Composition

; FILE REFERENCE: PCS 10391A

; CURRENT APPLICATION NUMBER: US/10/131,985

; CURRENT FILING DATE: 2002-04-25

; PRIOR APPLICATION NUMBER: US/09/726,295

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: GB 9930768.8

; PRIOR FILING DATE: 1999-12-29

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 660

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-131-985-25

## Query Match

Best Local Similarity 100.0%; Score 29; DB 4; Length 660;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 531 KAVFFA 536

## RESULT 41

US-10-447-315-3

; Sequence 3, Application US/10447315

; Publication No. US20040071687A1

## GENERAL INFORMATION:

; APPLICANT: Rafii, Shahin

; APPLICANT: Heissig, Beate

; APPLICANT: Hattori, Koichi

; APPLICANT: Cornell Research Foundation, Inc.

; TITLE OF INVENTION: Adult Stem Cell Recruitment

; FILE REFERENCE: 1676.006US1

; CURRENT APPLICATION NUMBER: US/10/447,315

; CURRENT FILING DATE: 2003-05-28

; PRIOR APPLICATION NUMBER: US 60/383,658

; PRIOR FILING DATE: 2002-05-28

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 660

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-447-315-3

## Query Match

Best Local Similarity 100.0%; Score 29; DB 4; Length 660;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 531 KAVFFA 536

## RESULT 42

US-10-032-376A-14

; Sequence 14, Application US/10032376A

; Publication No. US20040127420A1

## GENERAL INFORMATION:

; APPLICANT: Quirk, Steven

; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing

; FILE REFERENCE: 1443.008US1

; CURRENT APPLICATION NUMBER: US/10/032,376A

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/312,726

; PRIOR FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 660

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-032-376A-14

## Query Match

Best Local Similarity 100.0%; Score 29; DB 4; Length 660;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 531 KAVFFA 536

## RESULT 43

US-10-335-207-14

; Sequence 14, Application US/10335207

; Publication No. US20040127421A1

## GENERAL INFORMATION:

; APPLICANT: Malik, Sohail

; APPLICANT: Quirk, Stephen

; TITLE OF INVENTION: Method to Increase Fibronectin

; FILE REFERENCE: 1443.047US1

; CURRENT APPLICATION NUMBER: US/10/335,207

```
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-14

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 44
US-10-480-621-1
; Sequence 1, Application US/10480621
; Publication No. US20040175817A1
; GENERAL INFORMATION:
; APPLICANT: Jepson, Holly
; APPLICANT: Minshull, Claire
; APPLICANT: Paupetit, Richard
; APPLICANT: Rowsell, Sian
; TITLE OF INVENTION: A CRYSTALLISED CATALYTIC DOMAIN OF MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE 9 (MMP9) AND THE USE OF
; TITLE OF INVENTION: ITS THREE DIMENSIONAL STRUCTURE TO DESIGN
; TITLE OF INVENTION: MMP9 MODULATORS
; FILE REFERENCE: 06275-377US1
; CURRENT APPLICATION NUMBER: US/10/480,621
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/SE02/01266
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: SE 0102298-7
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-621-1

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 45
US-10-474-794-208
; Sequence 208, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-208

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 46
US-10-601-059-14
; Sequence 14, Application US/10601059
; Publication No. US20040259802A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shu-Ping
; APPLICANT: Quirk, Stephen
; APPLICANT: Kimberly-Clark Worldwide, Inc.
; TITLE OF INVENTION: Anti-Chondrosarcoma Compounds
; FILE REFERENCE: 1443.064US1
; CURRENT APPLICATION NUMBER: US/10/601,059
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 10/335,207
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/219,329
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/US02/26319
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-601-059-14

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 47
US-10-872-198-131
; Sequence 131, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
```

```

; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-131

```

```

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

```

```

RESULT 48
US-10-901-417-25
; Sequence 25, Application US/10901417
; Publication No. US20050026836A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: Mcintosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/901,417
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/10/131,985
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-417-25

```

```

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

```

```

RESULT 49
US-10-979-159-208
; Sequence 208, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler

```

```

; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-208

```

```

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

```

```

RESULT 50
US-10-287-436A-489
; Sequence 489, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 489
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-489

```

```

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

```

```

RESULT 51
US-10-287-436A-1185
; Sequence 1185, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446

```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1185
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-1185

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 52
US-11-021-951-131
; Sequence 131, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMEIER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.000205
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-131

Query Match      100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 53
US-11-031-488-14
; Sequence 14, Application US/11031488
; Publication No. US20050239710A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/11/031,488

; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-488-14

Query Match      100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 54
US-10-115-223-30
; Sequence 30, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER00495
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-30

Query Match      100.0%; Score 29; DB 4; Length 663;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      534 KAVFFA 539

RESULT 55
US-10-402-212-30
; Sequence 30, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresh, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
```

; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 10/115,223  
; PRIOR FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: 09/194,468  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: PCT/US97/09158  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/018,773  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: 60/015,869  
; PRIOR FILING DATE: 1996-05-31  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 663  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-10-402-212-30

Query Match 100.0%; Score 29; DB 4; Length 663;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPFA 6  
Db 534 KAVPFA 539

## RESULT 56

; Sequence 4873, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 4873  
; LENGTH: 718  
; TYPE: PRT  
; ORGANISM: Burkholderia fungorum  
US-10-369-493-4873

Query Match 100.0%; Score 29; DB 4; Length 718;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPFA 6  
Db 576 KAVPFA 581

## RESULT 57

; Sequence 7633, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 4873  
; LENGTH: 718  
; TYPE: PRT  
; ORGANISM: Burkholderia fungorum  
US-10-369-493-4873

; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 7633  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Burkholderia cepacia  
US-10-369-493-7633

Query Match 100.0%; Score 29; DB 4; Length 737;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPFA 6  
Db 576 KAVPFA 581

## RESULT 58

; Sequence 138526, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 138526  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_39906C.1.pep  
US-10-437-963-138526

Query Match 100.0%; Score 29; DB 4; Length 770;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPFA 6  
Db 555 KAVPFA 560

## RESULT 59

; Sequence 54358, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/09631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23



```
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54358
; LENGTH: 1330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (579)..(616)
; OTHER INFORMATION: Type II fibronectin collagen-binding domain proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00023, p-value=4.682e-3
; OTHER INFORMATION: raw score of 24.31
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (271)..(451)
; OTHER INFORMATION: Matrixin domain identified by Pfam, accession name
; OTHER INFORMATION: Peptidase_M10, E-value=3.7e-109, Pfam score of 376.1
US-10-450-763-54358

Query Match      100.0%; Score 29; DB 5; Length 1330;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      768 KAVFFA 773

RESULT 60
US-10-369-493-4941
; Sequence 4941, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4941
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4941

Query Match      96.6%; Score 28; DB 4; Length 383;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      167 KAIFFA 172

RESULT 61
US-10-369-493-7699
; Sequence 7699, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 150066
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4941
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-7699

Query Match      96.6%; Score 28; DB 4; Length 383;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      164 KAIFFA 169

RESULT 62
US-10-424-599-278606
; Sequence 278606, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278606
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93603C.1.pap
US-10-424-599-278606

Query Match      89.7%; Score 26; DB 4; Length 49;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      15 RAVFFA 20

RESULT 63
US-10-424-599-150066
; Sequence 150066, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 150066
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
```

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_106530C.1.pep  
US-10-424-599-150066

Query Match 89.7%; Score 26; DB 4; Length 61;  
Best Local Similarity 83.3%; Pred. No. 3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|:||||  
Db 53 KSVFFA 58

## RESULT 64

US-10-926-683-1595  
; Sequence 1595, Application US/10926683  
; Publication No. US20050106595A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.025CPI  
; CURRENT APPLICATION NUMBER: US/10/926,683  
; CURRENT FILING DATE: 2004-08-25  
; PRIOR APPLICATION NUMBER: US/09/471,276  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 09/057,719  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 09/069,047  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: PCT/IB99/00712  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 1622  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1595  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-926-683-1595

Query Match 89.7%; Score 26; DB 5; Length 65;  
Best Local Similarity 83.3%; Pred. No. 3.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|:||||  
Db 54 KAVFFS 59

## RESULT 65

US-10-425-115-359391  
; Sequence 359391, Application US/10425115  
; Publication No. US2004021472A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 359391  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_90934C.1.pep  
US-10-425-115-359391

Query Match 89.7%; Score 26; DB 4; Length 89;

Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|:||||  
Db 54 KAVFFS 59

## RESULT 66

US-10-424-599-210814  
; Sequence 210814, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 210814  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_32392C.1.pep  
US-10-424-599-210814

Query Match 89.7%; Score 26; DB 4; Length 103;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6  
|:||||  
Db 44 KALFFA 49

## RESULT 67

US-10-437-963-114838  
; Sequence 114838, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 114838  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(108)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_18490C.1.pep  
US-10-437-963-114838

Query Match 89.7%; Score 26; DB 4; Length 108;  
Best Local Similarity 83.3%; Pred. No. 5.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||

Db 48 KAVFYA 53

RESULT 68  
US-10-424-599-182643  
; Sequence 182643, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 182643  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(124)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_13593C.1.pep  
US-10-424-599-182643

Query Match 89.7%; Score 26; DB 4; Length 124;  
Best Local Similarity 83.3%; Pred. No. 6.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||

Db 65 KAVFFS 70

RESULT 69  
US-10-767-701-41102  
; Sequence 41102, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 41102  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1929\_1.pep  
US-10-767-701-41102

Query Match 89.7%; Score 26; DB 4; Length 131;  
Best Local Similarity 83.3%; Pred. No. 6.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||

Db 42 KAVFFA 47

RESULT 70  
US-10-450-763-39449  
; Sequence 39449, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PC7/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 39449  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-450-763-39449

Query Match 89.7%; Score 26; DB 5; Length 138;  
Best Local Similarity 83.3%; Pred. No. 6.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||

Db 49 RAVFFA 54

RESULT 71  
US-10-437-963-172959  
; Sequence 172959, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 172959  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_71044C.1.pep  
US-10-437-963-172959

Query Match 89.7%; Score 26; DB 4; Length 172;  
Best Local Similarity 83.3%; Pred. No. 8.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6  
|||||

Db 145 RAVFFA 150

RESULT 72  
US-10-767-701-31699  
; Sequence 31699, Application US/10767701